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(71) Applicant *(for all designated States except US)*: **STICHTING VOOR DE TECHNISCHE WETENSCHAPPEN** [NL/NL]; Van Vollenhovenlaan 661, NL-3527 JP Utrecht (NL).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **SMIT, August, Benjamin** [NL/NL]; Achillesstraat 28 II, NL-1076 RC Amsterdam (NL). **SIXMA, Titia, Karen** [NL/NL]; Ingen Houszstraat 61, NL-3514 HV Utrecht (NL).

(74) Agent: **VOSSIUS & PARTNER**; Siebertstr. 4, D-81675 München (DE).

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(54) Title: WATER-SOLUBLE LIGAND-BINDING PROTEINS AND ANALOGS OF LIGAND-GATED ION CHANNELS, CRYSTALS THEREOF AND THEIR USE FOR SCREENING LIGANDS OF LIGAND-GATED ION CHANNELS

(57) Abstract: Provided are water-soluble ligand-binding proteins derived from molluscs and analogs of ligand-gated ion channels, crystals thereof and their use for screening ligands of ligand-gated ion channels. In particular, water-soluble ligand-binding proteins are provided that are capable of forming multimers and are amenable to crystallization. The crystal structure of one of these proteins, an acetylcholine binding protein (AChBP) is provided, which can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and thus for screening of drugs that act on these ion channels. Furthermore, chimeric proteins are provided that are capable of binding a ligand of a ligand-gated receptor, and comprising at least the amino acids of the AChBP determining solubility of the AChBP, in the same positions as in the AChBP, and furthermore comprising amino acids determining binding to said ligand.

WATER-SOLUBLE LIGAND-BINDING PROTEINS AND ANALOGS OF LIGAND-GATED ION CHANNELS, CRYSTALS THEREOF AND THEIR USE FOR SCREENING LIGANDS OF LIGAND-GATED ION CHANNELS

SUMMARY OF THE INVENTION

Novel water-soluble ligand-binding proteins have been identified and isolated, which have a ligand-binding profile substantially similar to that of ligand-gated ion channels. DNA molecules encoding such proteins have been cloned and characterized. The biological and structural properties of these proteins are disclosed, as is the amino acid and nucleotide sequence. The recombinant DNA molecules, and portions thereof, are useful for isolating homologues of the DNA molecules, identifying and isolating genomic equivalents of the DNA molecules, and identifying, detecting or isolating mutant forms of the DNA molecules. Using a recombinant expression system functional DNA molecules encoding the water-soluble ligand-binding proteins as well as chimeras have been functionally produced. Furthermore, the water-soluble ligand-binding proteins could be crystallized revealing the three dimensional (3D) structure and enabling the modeling of the 3D structure of the ligand-binding domain of ligand-gated ion channels. The invention is further in the field of the development of new drugs that are capable of selectively intervening in neuronal signaling pathways. The invention is more in particular concerned with providing new analogues of the channel-coupled receptors, crystal structures thereof and to their use in screening ligands for these receptors.

Several documents are cited throughout the text of this specification either by name or are referred to by numerals within parenthesis. Full bibliographic citations may be found at the end of the specification immediately preceding the claims. Each of the documents cited herein (including any manufacturer's specifications, instructions, etc.) are hereby incorporated herein by reference; however, there is no admission that any document cited is indeed prior art as to the present invention.

BACKGROUND OF THE INVENTION

The communication in the central nervous system (CNS) occurs through a complex interaction of electrical and chemical signals. Molecules bearing chemical information are called neurotransmitters. The chemical information is converted in electric currents on the post-synaptic membrane, which is specialised in recognising and binding neurotransmitters by means of protein receptors. The specific binding of a ligand to one type of such receptors, the ionotropic receptors, induces a fast opening of the ion channel coupled to the receptor. An important group of ionotropic receptors is the superfamily of the channel-coupled receptors, also referred to as ligand-gated receptors, including the 7-amino-butyric acid ($GABA_A$) receptor, the glycine receptor, the serotonin-3 (5-HT3) receptor and both neuronal and muscle-type nicotinic acetylcholine receptors (nAChR). These receptors share certain structural features such as (1) a 15-residue cysteine loop between amino acids 128 and 142 corresponding to the Torpedo AChR α unit, (2) four trans-membrane domains, (3) similar subunit arrangements, and (4) homologies in amino acid sequence. Activation of these receptors causes a change in electrical current and hyperpolarisation of the cell membrane and consequently an inhibition of the electrical activity of the cell. The $GABA_A$ receptor and the glycine receptor are coupled to a chloride-selective channel, and thus the inhibition of the electrical activity leads to inhibition of the cell response. On the other hand, activation of the 5-HT3 receptor and the nAChRs provokes an excitatory response on the cell because they are connected to a cation-selective channel (Na+, K+, Ca2+). The AChRs are the best studied of the ligand-gated receptors; for a review, see Arias, Brain Research Reviews, 25 (1997)133-191 and Arias, Neurochem. Int. 36 (2000), 595-645). Mutations in these ligand-gated ion-channels (LGICs) lead to diseases such as congenital myasthenia gravis, epilepsy, startle syndrome and alcohol sensitivity (Vafa and Schofield, Int. Rev. Neurobiol. 42, 285-332; 1998). NAChRs mediate nicotine addiction in chronic tobacco users. Since nicotine binding to these receptors also has a positive effect on Alzheimer's disease, Parkinson's disease and schizophrenia these receptors present an important drug target (Paterson and Nordberg, A. Neuronal nicotinic receptors in the human brain. Prog. Neurobiol. 61, 75-111; 2000).

The development of new active compounds that can selectively or - as the case may be - a-selectively bind to the channel-coupled receptors, is of utmost importance for the understanding of the processes occurring in the nervous system and for the treatment of disturbances of neural conditions. The development of such active compounds requires the availability of a reliable model system for the corresponding receptors. The primary structural features (amino acid sequences) of the various

receptors have been largely elucidated by now. Certain subunits of the AChRs have been found to be determinant in the pharmacological specificity or affinity of the receptor for its ligand (Corringer et al., J. Neuroscience 18 (1998), 648-657). However, the study of the ligand binding properties of the receptor proteins is hampered by the fact that the spatial structure of the proteins - which is decisive in the binding of ligands - is still unknown. This is partly because crystallisation of the receptor proteins has been unsuccessful up to now.

The above-defined technical problem is solved by the present invention by providing the embodiments characterized in the claims.

Accordingly, in one aspect the present invention relates to a water-soluble protein derived from a mollusc being capable of binding a ligand of a ligand-gated receptor.

It has been found according to the invention that acetylcholine-binding proteins (AChBP) of certain molluscs show a surprising structural similarity with the channel-coupled receptors on the one hand and have interesting physical properties, such as water-solubility, on the other hand. The molluscan AChBPs are capable of forming multimers, especially pentamers, and of binding specific toxins such as α-bungarotoxin. These multimers may be homogeneous (identical units) or heterogeneous (different units). These properties make them eminently suitable as model systems for studying the binding of candidate ligands to the channel-coupled receptors. It has been possible to produce these molluscan AChBPs in recombinant systems, thus allowing convenient and large-scale production thereof. Moreover, it is feasible to construct hybrid proteins sharing the physical properties of the mollusc AChBP with the pharmacological properties of the (human) channel-coupled receptors, thus providing new dedicated tools for screening ligands for these receptors.

The AChBP is a naturally occurring analogue of the extracellular domains of the α-subunits of the neuronal nicotinic acetylcholine receptors (nAChRs). In contrast to the nAChRs, it lacks domains to form a transmembrane ion channel, but alike the nAChRs it assembles into a homo-pentamer (Figure 6). Moreover, AChBP has ligand-binding characteristics that are typical for a nicotinic receptor. The 3-dimensional structure of AChBP was solved by X-ray crystallography at 2.7Å resolution (current R_{factor} = 27.9 %, R_{free} = 30.0 %). In crystals, as in solution, AChBP forms a stable homo-pentamer with dimensions comparable to those of the ligand-binding domain of the nAChR, as determined in EM studies by Unwin, Struct. Struct. Biol 121 (1998), 181-190. The high-resolution crystal structure of AChBP, along with

biochemical and pharmacological data, supports the extrapolation of AChBP as a good mimic of ligand-binding domains of ligand-gated ion channels including nAChR, 5-HT3R, $GABA_{A,C}R$ and GlyR.

Four AChBPs according to the present invention are exemplified herein, isolated and cloned from the CNS of *Lymnaea stagnalis* (L-AChBP_T1 and L-AChBP_T2) and *Bulinus truncatus* (B-AChBP_T1 and B-AChBP_T2). L-AChBP_T1 and 2 are 229 amino acid proteins with a signal sequence of 19 amino acids (224 and 21 amino acids, respectively, for B-AChBP_T1 and 2; see also Figure 1) and have sequence homology with the extracellular domains of the subunits of ligand-gated ion channels (Figure 3), in particular with those of the nAChRs (Figure 4 and 5). The mass of the purified AChBP from Lymnaea has been determined by mass-spectrometry. The glycosylated form has a mass of about 24720 Da and the de-glycosylated form of about 23832 Da. In SDS-PAGE the glycosylated AChBP migrates between the 14 and 26 kDA marker proteins. Hydrophopicity plots of the AChBPs are shown in Figure 2, which reveal those regions of the ligand-binding proteins that are particularly hydrophilic and thus may be replaced at least in part or essential amino acids thereof in the ligand-binding domain of the ligand-gated ion channel. Sequence conservation is particularly high in the so-called loop areas (reviewed by Arias, Neurochem. Int. 36 (2000), 595-645), which contain the residues involved in ligand-binding. The cysteine residues characteristic for the Cys-loop family of ligand gated receptors are conserved in AChBP. Also the double cysteine typically found in the alpha subunits of the nAChR is present. AChBP protein sequence ends at the position where in the nAChRs the first predicted transmembrane domain would start. The ligand-binding characteristics of AChPBs are described in Example 4 and summerized in Table 2.

The terms "channel coupled receptors", "ligand-gated receptor", "ligand-gated ion channel" are used interchangeable herein. However, in context with the natural occurring, in particular human molecules the term "ligand-gated ion channel" is preferably used. The water-soluble ligand-binding protein of the invention can also be characterized as a ligand-binding protein having at least 10%, more preferably at least 12%, still more preferably at least 15% and most preferably at least 20% amino acid sequence identity to a vertebrate ligand-gated ion channel but missing any trans-membrane domain. A ligand-gated receptor of the present invention is characterized by having substantially the same ligand-binding characteristics of a vertebrate, preferably mammalian, most preferably human ligand-gated ion channel but comprising at least one alteration in the original amino acid sequence, said

alteration resulting in the presence of an amino acid determining or contributing to the water-solubility of the water-soluble ligand-protein found in molluscs, in particular snails such as those described in more detail below.

The terms "ligand-binding protein", "ligand-binding domain" and "ligand-binding receptor" are meant to at least include the portion of a water-soluble ligand-binding protein or corresponding modified ligand-gated ion channel required for binding a ligand. Minimally the ligand-binding domain consists of a peptide containing that domain. However the use of this term is meant to include a ligand- binding domain or protein that is comprised by a larger portion of, for example, ligand-gated ion channel, such as a fully reconstituted nicotinic acetylcholine receptor.

As shown in Figure 3 the nicotinic acetylcholine receptor (nAChR) belongs to a well-understood member of the ligand-gated ion channels superfamily. The members of this signaling protein group, including 5-HT3, glycine, $GABA_A$, and $GABA_C$ receptors, are thought to share common secondary, tertiary, and quaternary structures on the basis of a high degree of sequence similarity. Therefore, it is expected that the novel findings in respect to the exemplified AChBP equally apply to the other members of the mentioned ligand-gated ion channels superfamily. Thus, either water-soluble protein being capable of binding a ligand of any of those ligand-gated ion channels may be found in molluscs or the present 5-HT3, $GABA_A$, and glycine receptors can be modified such as to substantially retain their binding affinity.

Accordingly, the ligand of the water-soluble ligand-binding protein is preferably acetylcholine, gamma-amino-butyric acid (GABA), glycine, nicotine or serotonin. Isolation of such water-soluble ligand-binding proteins can be done as described in Example 1 for the AChBP of the present invention. Instead of α-bungarotoxin other known ligands or can be used for affinity purification. Most preferably, water-soluble ligand-binding protein of the invention is a acetylcholine-binding protein (AChBP). Preferably, the ligand-binding protein displays substantially the binding characteristics shown in Table 2.

The acetylcholine-binding proteins to be used according to the invention are originally derived from aquatic molluscan species, especially species from the class of the snails (Gastropoda), in particular from the order of the lunged snails (Pulmonata). The order of the Pulmonata is divided into the suborders of the Basommatophora (mostly aquatic snails), Systellommatophora and Stylommatophora (mostly land snails). The Basommatophora include the families of the Acroloxidae (e.g. genus Acroloxus), Lymnaeidae (e.g. genera Galba, Stagnicola, Radix and Lymnaea),

Physidae (e.g. genera Physa and Aplexa) and Planorbidae (e.g. genera Planorbis, Anisus, Ancylus, Gyraulus, Biomphalaria and Bulinus). Examples of suitable species are *Lymnaea stagnalis* (pond snail) and *Bulinus truncatus*. The isolation of the AChBPs from these snails, cloning of the cDNA encoding these AChBPs and their characterization including the full amino acid sequences is described in the examples. The cDNA and amino acid sequences of the AChBPs of *Lymnaea stagnalis* are depicted in SEQ ID Nos. 1 and 2 (L-AChBP_T1) and SEQ ID Nos. 3 and 4 (L-AChBP_T2). Those of *Bulinus truncatus* are depicted in SEQ ID Nos. 5 and 6 (B-AChBP_T1) and SEQ ID Nos. 7 and 8 (B-AChBP_T2). Features of these proteins are further described in the examples and the accompanying figures.

While a water-soluble ligand-binding protein derived form a Pulmonata species, preferably from a Basommatophora species is preferred, it will be appreciated that the present invention generally relates to any water-soluble protein being capable of binding a ligand of a ligand-gated receptor comprising an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence as depicted in any one of SEQ ID Nos. 2, 4, 6 or 8 or a functional equivalent thereof, or a fragment of at least 5 continuous amino acids thereof;

(b) an amino acid sequence having at least 30% amino acid identity to the amino acid sequence of any one of SEQ ID Nos. 2, 4, 6 or 8; and

(c) an amino acid sequence resulting in a protein which is detectable by a monoclonal or polyclonal antibody which recognises, preferably with a binding affinity of at least 10^{-7}M, a protein comprising an amino acid sequence of (a) or (b).

Identity or similarity, as known in the art, are relationships between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. Both identity and similarity can be readily calculated (Computational Molecular Biology, Lesk, ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part I, Griffin and Griffin, eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, Academic Press, 1987; and Sequence Analysis Primer, Gribskov and Devereux, eds., M Stockton Press, New

York, 1991). While there exist a number of methods to measure identity and similarity between two polynucleotide or two polypeptide sequences, both terms are well known to skilled artisans (von Heinje, supra; Gribskov and Devereux, supra; and Carillo and Lipman SIAM J. Applied Math. 48 (1988), 1073). Methods commonly employed to determine identity or similarity between sequences include, but are not limited to those disclosed in Carillo and Lipman; see supra. Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux et al., Nucleic Acids Research 12 (1984), 387), BLASTP, BLASTN, psi BLAST and FASTA (Atschul et al., J. Molec. Biol. 215 (1990), 403).

In another embodiment, the present invention relates to a water-soluble protein being capable of binding a ligand of a ligand-gated receptor comprising

(a) at least the amino acids of the water-soluble protein described above determining solubility of said protein, in the same or corresponding positions as in said protein; and

(b) at least 4 amino acids determining binding to said ligand.

Protein expression studies have shown that wild-type AChBP of the mollusc *Lymnaea stagnalis* can be produced in Pichia pastoris yeast. The yeast cells express AChBP in a homopentameric form and secrete the protein complex into the medium. The large amounts of AChBP per volume of medium produced (up to 2 mg per liter medium) and the large volumes of yeast that can be cultured allow a large-scale production of AChBP. Besides the wild-type AChBP, various AChBP mutants have been produced in Pichia pastoris. These include mutants containing the following single point mutations (the numbers refer to the amino acid position in the AChBP sequence of Lymnaea stagnalis depicted in SEQ ID No. 2 counted from the first amino acid of the signal peptide; the letter before the number indicates the original amino acid and the letter after the number indicates the mutant amino acid) N85D, H164Y, D194N, Y204P, Y211P and D213N.

Thus the invention pertains to water-soluble proteins derived from molluscan, preferably acetylcholine binding proteins (AChBP's), which are capable of forming multimers, and are capable of binding a ligand of a ligand-gated receptor. These proteins comprise, on the one hand, at least of the amino acids of the AChBP determining solubility of the AChBP in the same positions as in the AChBP, and, on

the other hand, amino acids determining binding to the ligand of the ligand-gated receptor. The degree of identity with the molluscan AChBP sequence can be defined by amino acid identity, of at least 15%, preferably 20%, more preferably 30%, still more preferably 40%, preferably at least 50 or even at least 60%, preferably more than 70%, more preferably more than 80% and most preferably at least 90% identity, or more, as determined, e.g., using the art-known BLAST algorithm. The amino acids determining binding to the ligand should comprise at least 4 amino acids, preferably at least 6 or even at least 8 amino acids, including a series of at least 3 or 4 amino acids, corresponding to the receptor sequence and preferably differing from the corresponding AChBP amino acids. Preferred embodiments of these proteins are further defined below. Usually, the water-soluble ligand-binding protein or domain as part of a for example chimeric ligand-gated ion channel will comprise 200-240 amino acids. The ligand is preferably acetylcholine, nicotine, lophotoxin, d-tubocurarine, carbamylcholine, galanthamine or epibatidine.

Said ligand-gated receptor can be derived from an arthropod (preferably insect), a plant (preferably a higher plant, most preferably a seed plant) or a chordate (preferably a mammalian, most preferably human), preferably said ligand-gated receptor is a nicotinic acetylcholine receptor.

Usually, the said amino acids in the water-soluble ligand-binding proteins of the invention, which determine solubility are in the same positions as in the AChBP having the amino acid sequence as depicted in any one of SEQ ID Nos. 2, 4, 6 or 8. The solubility determining regions are based on solvent accessibility in structure. The respective amino acid residues can be chosen for example according to Figure 10 or 11 in which the solvent accessible regions are indicated. Preferably, the water-soluble ligand-binding protein of the invention comprises an amino acid sequence having at least 40% amino acid identity to the amino acid sequence of the mature AChBP comprising the amino acid sequence of any one of SEQ ID Nos. 2, 4, 6 or 8, in which the ligand binding amino acids have been replaced with the corresponding amino acids of a ligand-gated receptor.

In one embodiment of the protein of the invention said solubility-determining amino acids (a) comprise hydrophilic amino acids (Asp, Glu, Arg, Lys) from the sequences 20-44, 73-81, 86-92, 112-120, 135-152, 166-189, 196-20, 209-213, and/or 219-227 of SEQ ID No. 2.

The amino acid sequences of L-AChBP_T1 (SEQ ID No. 2) and T2 (SEQ ID No. 4) are almost similar. For the sake of clarity, reference is always made to L-AChBP_T1 (SEQ ID No. 2). However, all references to amino acid residues within are valid for

both T1 and T2, with the noticeable exceptions of Arg(167) becoming Gly(167) and and Thr(203) becoming Ile(203). Furthermore, regarding the amino acid residues (domains) from L-AChBP_T1 and the corresponding residues from B-AChBP the following list provide those amino acid positions in which L-AChBP and B-AChBP differ. All amino acid residue numbers below correspond to their position within the amino acid sequence of the immature protein (numbering starting at methionine (1). One could also start numbering at the start of the amino acid sequence of the mature sequence (L(1)DRAD for L-AChBP and Q(1)IRW for B-AChBP). When using this second method (1st amino acid of the mature seq. = position 1) simply subtract 19 from the L-AChBP position numbers and 21 from the B-AChBP position numbers, for example Asp(36) becomes Asp(17) for L-AChBP) and Asp(15) for B-AChBP. For the further embodiments the positions are given for L-AChBP T1 (SEQ ID No. 2) followed by an indication of the corresponding amino acid positions in the amino acid sequence of L-AChBP_T2 (SEQ ID No. 4) and B-AChBP_T1 (SEQ ID No. 6) & B-AChBP_T2 (SEQ ID No. 8) in the form of (L-AChBP_T1&T2 : B-AChBP_T1&T2).

In a preferred embodiment said solubility determining amino acids (a) comprise amino acids Asp(36), Asp(68), Glu(115), Arg(137), Asp(143), Asp(148), Glu(150), Arg(167), Arg(189), Glu(215) of SEQ ID No.2, wherein Asp may be exchanged for Glu and vice versa and Lys may be exchanged for Arg and vice versa (L-AChBP_T1&T2 : B-AChBP_T1&T2; Asp(36) : Asp(36); Asp(68): Asp(68); Glu(115): Glu(116); Arg(137): Arg(138); Asp(143): Asp(144); Asp(148): Asp(149); Glu(150): Glu(151); Arg(167): Gly(167), in L-AChBP_T2 : Lys(168); Arg(189): Lys(190); Glu(215): Glu(216).

In a still more preferred embodiment the water-soluble ligand-binding protein comprises the amino acids Cys(142), Thr(149), Ala(153), Thr(154), Cys(155), Arg(156), Ile(157) and/or Lys(158) of SEQ ID No. 2. (L-AChBP_T1&T2 : B-AChBP_T1&T2; Cys(142): Cys(143); Thr(149): Thr(150); Ala(153): Ala(154); Thr(154): Thr(155); Cys(155): Cys(156); Arg(156): Arg(157); Ile(157): Ile(158); Lys(158): Lys(159). In a further embodiment the water-soluble ligand-binding protein comprises either in addition or alternatively the amino acids (b) Pro(39), Trp(77), Trp(101), Pro(103), Asp(194), and/or Ser(161) of SEQ ID No. 2 (L-AChBP_T1&T2 : B-AChBP_T1&T2; Pro(39): Pro(39); Trp(77): Trp(77); Trp(101): Trp(102); Pro(103): Pro(104); Ser(161): Ser(162); Asp(194): Ser(195).

In a still further embodiment the water-soluble ligand-binding protein comprises either

in addition or alternatively to the above described embodiments amino acid sequences 165-169 and/or 200-203 of SEQ ID No. 2 have been exchanged with the corresponding sequence of the ligand-gated receptor (L-AChBP_T1&T2 : B-AChBP_T1&T2; His(165)-Iso(169):. Asp(166)-Phe(170) (B-AChBP_T1) : Asp(166)-Leu(170) (B-AChBP_T2); Asn(200)-Thr(203); Iso(203) for L-AChBP_T2: Asn(201)-Lys(204).

The amino acids determining binding to the ligand of the nicotinic acetylcholine receptor include three stretches on the nAChR alpha subunits. These stretches contain amino acids that are conserved throughout the various nAChR alpha subunits and that are essential for ligand binding. These stretches (corresponding to the Torpedo alpha subunit) are (numbering of nAChR α7 as depicted in SEQ ID No. 9): Trp (108) - Tyr (115), Trp (108) and Tyr (115) being essential; Trp (171) - Tyr (173), the amino acids Trp (171) and Tyr (173) being essential; Tyr (210) - Tyr (217), the amino acids Tyr (210), Cys (212), Cys (213) and Tyr (217) being essential. In the chimeric proteins according to the invention, at least the essential amino acids of at least one of these stretches haven been substituted for the corresponding amino acids. Preferably, the entire stretches have been substituted.

In a particularly preferred embodiment of the invention, the water-soluble ligand-binding protein is capable of binding a ligand of an acetylcholine receptor, wherein in said protein at least one of the amino acid sequences Trp(101) - Tyr(T108), Trp(162) - His(164) and Tyr(204) - Tyr(211) of SEQ ID No. 2 has been exchanged with the corresponding sequence of the acetylcholine receptor (L-AChBP_T1&T2 : B-AChBP_T1&T2; Trp(101)-Tyr(108): Trp(102)-Tyr(109); Trp(162)-His(164): Trp(163)-His(165), (B-AChBP_T1) : Trp(163)-Phe(165) (B-AChBP_T2); Tyr(204)-Tyr(211): Tyr(205)-Tyr(212).

On the basis of homology to the AChBPs, it is possible to change amino acid residues in the original amino acid sequence of the ligand-gated ion channel, which are not critical to ligand-binding or essential for the tertiary and quaternary structure of the receptor but could be substituted to amino acid residues which according to the AChBP in particular the crystal structure contributes to their water-solubility. As a result the ligand-gated ion channel or its ligand-binding domain or the respective monomers and pentamers are for example expected to be more easily expressible in recombinant expression system and more importantly amenable to crystallization, allowing the construction of three-dimensional models of their ligand binding domains.

Thus, in another embodiment the present invention relates to a method for the production of a water-soluble ligand-gated receptor or a corresponding ligand-binding domain or for improving the water solubility and accessibility to crystallization of such a receptor or domain, said method comprising altering the amino acid sequence of the extracellular domain of a ligand-gated receptor by way of substituting, adding, deleting or modifying at least one amino acid at a position corresponding to an amino acid determining or contributing to the water-solubility of the above-described water-soluble ligand-binding protein of the present invention The method of the invention can be performed using conventional techniques known in the art, for example, by using amino acid deletion(s), insertion(s), substitution(s), addition(s), and/or recombination(s) and/or any other modification(s) known in the art either alone or in combination. Methods for introducing such modifications in the DNA sequence underlying the amino acid sequence of the ligand-binding domain a ligand-gated ion channel are well known to the person skilled in the art; see, e.g., Sambrook, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory (1989) N.Y.

The resulting ligand-gated receptor or ligand-binding domain retains comparable in vitro and preferably also in vivo ligand-binding activity to that of the ligand-gated ion channel, and more importantly, allow complete crystallization of the protein such that they may be characterized by X-ray crystallography. The X-ray crystallographic data can be used for example for identification and construction of possible therapeutic compounds in the treatment of various disease conditions.

As has been discussed herein before, the ligand-gated ion channel superfamily including nACh, 5-HT3, glycine, $GABA_A$, and $GABA_C$ receptors as well as invertebrate glutamate ion-channels and MOD-1 serotonin channel contain extracellular ligand binding domains that are homologous to the AChBP. Many of these receptors are promising drug targets. Therefore, the ligand-gated receptor to be modified is preferably one of those of the mentioned superfamily, most preferably it is nAChR.

Information on the nucleotide and amino acid sequences, structural elements, functional assays of the nAch, 5-HT3, glycine, $GABA_A$, and $GABA_C$ receptors can be found in the prior art. For example, the nicotinic receptors at the amino acid level are described in Corringer et al., Annu. Rev. Pharmacol. Toxicol. 40 (2000), 431-458. Means for retrieving nucleotide and amino acid sequences, performing sequence alignments in order to identify the most likely critical amino acid residues are described below and in the examples; for further general information see the review on periplasmic binding protein (PBP), an ancient protein module present in multiple drug receptors by Felder et al., PharmSci. 1(2) (1999).

In a preferred embodiment of the method of the present invention, said at least one amino acid is altered to the corresponding amino acid of the amino acid sequence depicted in any one of SEQ ID Nos. 2, 4, 6 or 8, or to a an equivalent amino acid, preferably in which said solubility-determining amino acids comprise solvent accessible regions in the crystal structure according to Figure 10 or 11. Preferred amino acid sequence positions and amino acid substitutions are described above for the AChBP and can be applied generally in the method of the present invention.

It is expected that the insertion of the loop Cys123-Cys136 of the mature AChBP SEQ ID No. 2 into the equivalent region (Cys127-Cys141) in the mature nicotinic α7 homopentamer ligand binding domain creates an easily expressed form of this protein. Likewise, this loop or an equivalent loop from other water-soluble ligand proteins of the present invention can be inserted into the equivalent region of other homopentameric ligand binding domains of ligand gated ion channels such as the glycine receptor and the 5-HT3 receptor to create an easily expressed form of those proteins.

Thus, in one embodiment, the present invention relates to any one of the above described methods, wherein loop Cys123-Cys136 of SEQ ID No. 2 is inserted into the corresponding region of the ligand binding domain of the ligand-gated receptor.

The above described water-soluble ligand-gated receptor or a corresponding ligand-binding domain are usually prepared by site-directed mutagenesis of the underlying encoding polynucleotide. Once the corresponding polynucleotide has been generated it can be used to express the altered ligand-gated receptor or a corresponding ligand-binding domain. Thus, the method of the present invention commonly comprises

(a) culturing a host cell transfected with and capable of expressing a polynucleotide comprising a nucleotide sequence encoding the altered amino acid sequence; and optionally

(b) recovering said water-soluble ligand-gated receptor or corresponding ligand-binding domain from the culture.

Methods for the expression and purification of the water-soluble ligand-gated receptor or corresponding ligand-binding domain of the present invention are described further below. Preferably, the expression system described in Examples 4 and 5, or corresponding expression systems are used.

The present invention also relates to the a water-soluble ligand-gated receptor and ligand-binding domain obtainable by the above described methods of the invention. Preferably, said water-soluble ligand-gated receptor exhibits a 10-fold, more preferably 100-fold, still more preferably 1000-fold and most preferably 10000-fold higher solubility in water than the corresponding wild type, preferably human ligand-gated receptor. However, improvements in water solubility of about 2 to 5 fold is also already advantageous. The average hydrophobicity may be in the range of –100 to –400. Accordingly, the present invention provides methods for the prediction and creation of mutants and chimeras of ligand binding domains of homopentameric acetylcholine receptor subtypes and of other homopentameric ion channels with increased solubility.

In one embodiment the water-soluble ligand-binding protein of the invention further comprises a spacer sequence allowing coupling with a carrier body. The spacer sequence may be an amino acid sequence encodable by a polynucleotide or other molecule such as polymethylene anchor groups commonly used in chip technology. The chimeric protein of the invention may further comprise a spacer sequence, which allows coupling of the protein to a carrier body. Such spacer sequence may be e.g. an oligo-histidine stretch attached to the C-terminus of the protein. Such an oligo-histidine stretch is capable of binding to Talon© metal affinity beads or similar carriers. Such binding stretches have no detectable influence on the pharmacological properties of the proteins. The chimeric proteins according to the invention can be used for screening of specific binding of potential drugs, in particular screening for modulators of ion-channel opening. Conventional in vitro screening techniques, such as phage display technology, can be used for this purpose. High-throughput assays, possibly in combination with combinatorial chemistry can also be used. Specific binding of test compounds to the (immobilised) chimeric proteins of the invention can be performed e.g. by competition binding assays using alpha bungarotoxin as a competitor. The invention also concerns test kits containing the proteins described above, together with further means for carrying out a screening test, such as carriers, labels, diluents, other chemicals etc.

In addition, the present invention relates to fusion proteins comprising the water-soluble ligand-binding protein of the invention or a binding fragment thereof and a fragment of a ligand-gated receptor. The term "fusion protein" as used herein refers to protein constructs that are the result of combining multiple protein domains or linker regions for the purpose of gaining the combined functions of the domains or

linker regions. This is may be accomplished by molecular cloning of the nucleotide sequences encoding such domains to produce a new polynucleotide sequence that encodes the desired fusion protein. Alternatively, creation of a fusion protein may be accomplished by chemically joining two proteins. A fusion protein of the present invention preferably comprises at least the ligand-binding domain of the AChBP or of a ligand-gated ion channel, which has been modified in accordance with the above described methods.

Nicotinic acetylcholine receptors are comprised of five subunits, selected from a related family of subunit proteins. The neuronal subunits fall into two main types depending on the presence or absence of a pair of vicinal cysteines close to the binding site for acetylcholine. Thus all α-subunits contain paired cysteine residues thought to play a role in binding of nicotinic agonists (Aplin and Wonnacott, 48 (1994), 473-477), whereas the β-subunits do not. There are ten known alpha subunits, α1 to α10, and at least four beta subunits, β1 to β4. Receptors comprise at least one alpha subunit which in some cell types combine with a beta subunit and in some cases a gamma, delta and epsilon subunit. For example, the AChR at the neuromuscular junction is believed to have an (α1)2β1γδ stoichiometry. Within the group of α-subunits there is marked diversity in the manner in which a complete functional nAChR is formed. The majority of the α subunits only form functional receptors when combined as a heteropentamer with β-subunits in the CNS (McGehee and Role, Annual Review of Physiology 57 (1995), 521-546). However, α7, α8 and α9 nAChR subunits and the related 5-HT3A subunit are capable of forming functional homopentameric receptors. In this respect it is interesting that the phylogenetic relationship between nAChR subunits suggest that α7, α8, α9 and the related 5-HT3A subunit are more related to each other than to the subunits which only form heteropentameric receptors. Sequence homologies indicate that the α7, α8 and α9 subunits form a distinct subgroup of the alpha subunits.

As is evident form the foregoing, the above described water-soluble ligand-binding protein or receptor or ligand-binding domain thereof can be used for forming complexes of homo- or heteromultimers, such as a dimer, pentamer or decamer consisting of at least one monomer of the mentioned proteins of the present invention. Preferably, these multimers constitute a function ligand-gated receptor. Preferably, said ligand-gated receptor is related to the nAchR.

The present invention also relates to the production of synthetic heteropentamers resembling heteropentameric gated ion-channels by mutation of AChBP, using

knowledge of the crystal structure about the primary and secondary contact regions; see infra. Preferably, said synthetic heteropentamers resembles a heteropentameric nicotinic acetylcholine receptor. Accordingly, the present invention more generally relates to a ligand-gated ion channel comprising any one of the above described water-soluble ligand-binding proteins or receptors of the invention as a monomer, homo- or heterodimer or -pentamer. This method therefore allows the prediction and creation of mutants and chimeras of nicotinic acetylcholine receptors and other ligand-gated ion channels that are insensitive or more sensitive to toxin binding, e.g. bungarotoxin, lophotoxin, conotoxin, and other toxins that inhibit ligand-gated ion channels. Preferably, said ligand-gated ion channel is less or more sensitive to binding of toxins such as bungarotoxin, lophotoxin or conotoxin compared to the wild type ligand-gated ion channel.

Further information and examples how to create chimeric ligand-binding proteins in accordance with the present invention is given in Example 10.

The nucleotide and amino acid sequences of the acetylcholine, 5-HT3, glycine, $GABA_A$, and $GABA_C$ receptors can be easily retrieved from public database, for example from the internet using http://www.ncbi.nlm.nih.gov/Entrez. The citations also include a reference to the corresponding publication also reporting on the functional expression of the respective receptor.

The use of recombinant acetylcholine-gated ion channels and functionally assays in the discovery of putative novel ligands has been described in Cosford, Pharm. Acta Helv. (2000), 74(2-3), 125-130. Furthermore, the cell-free expression and functional reconstitution of homo-oligomeric α7 nicotinic acetylcholine receptors into planar lipid bilayers has been reported by Lyford and Rosenberg, J. Biol. Chem. (1999), 274(36), 25675-25681. The use of functional assays of cloned and native muscarinic acetylcholine receptors for determining the selectivity profile of toxins has been described by Olianas et al. (J. Pharmacol. Exp. Ther. 288 (1999), 164-170). A system for the evaluation of pharmacological differences and similarities between 5-HT3 receptors stably transfected cells is provided by for example Bruss et al., Naunyn-Schmiedebergs Archives of Pharmacology 360 (1999), 225-33. The primary structure and functional expression of the 5-HT3 receptor is described in Maricq et al., Science 254 (1991), 432-437. Likewise, the stable expression of human glycine α1 and α2 receptor monomers in mouse L(tk-) cells and their use for the study of the physiology and pharmacology of functional glycine receptors is described in Wick et al., J. Neurosci. Methods 87 (1999), 97-103. An example for the measurement of the

pharmacology of recombinant $GABA_A$ receptor subtypes is described in Simpson et al., J. Neurosci. Methods 99 (2000), 91-100. Further examples for assay systems are given below.

The described methods as well as others known to the person skilled in the art can be used for example to

(1) express and characterise the water-soluble ligand-binding proteins and ligand-gated ion channels of the present invention; and

(2) use stably transfected cells expressing the above described ligand-gated ion channels for the identification of novel ligands.

The present invention also relates to polynucleotides encoding the water-soluble ligand-binding proteins and ligand-gated ion channels of the present invention, and multimers thereof, preferably dimers or pentamers. Such polynucleotide may be a DNA such as a cDNA, or an RNA such as mRNA or any other form of nucleic acid including synthetic or modified derivatives and may encode the polypeptide in a continuous sequence or in a number of sequences interrupted by intervening sequences. In which ever form it is present, the polynucleotide is an isolated polynucleotide in that it is removed from its naturally-occurring state. This aspect of the invention is based on the cloning of the cDNA for ligand-binding proteins. In a preferred embodiment, the polynucleotide comprises the nucleotide sequence of any one of SEQ ID Nos. 1, 3, 5 or 7, optionally including one or more mutations or deletions which do not substantially affect the activity of the polypeptide encoded thereby. Such mutations include those arising from the degeneracy of the genetic code, as well as those giving rise to any of the amino acid mutations or deletions discussed above. The polynucleotides of the invention preferably comprise

(a) a nucleotide sequence having at least 15 continuous nucleotides of the nucleotide sequence depicted in any one of SEQ ID Nos. 1, 3, 5 or 7 or a degenerated nucleotide sequence thereof; or

(b) a nucleotide sequence capable of hybridizing to a nucleotide sequence of (a) under stringent hybridisation conditions.

Typically, selective hybridization will occur when there is at least about 55% sequence identity -- preferably at least about 65%, more preferably at least about 75%, and most preferably at least about 90% -- over a stretch of at least about 14 nucleotides; see, e.g., Kanehisa, Nucleic Acids Res. 12 (1984), 203-213, herein incorporated by reference. Nucleic acid hybridization will be affected by such conditions as salt concentration, temperature, solvents, the base composition of the

hybridizing species, length of the complementary regions, and the number of nucleotide base mismatches between the hybridizing nucleic acids, as will be readily appreciated by those skilled in the art.

"Stringent hybridization conditions" and "stringent wash conditions" in the context of nucleic acid hybridization experiments depend upon a number of different physical parameters. The most important parameters include temperature of hybridization, base composition of the nucleic acids, salt concentration and length of the nucleic acid. One having ordinary skill in the art knows how to vary these parameters to achieve a particular stringency of hybridization. In general, "stringent hybridization" is performed at about 25°C below the thermal melting point (T m) for the specific DNA hybrid under a particular set of conditions.

"Stringent washing" is performed at temperatures about 5°C lower than the Tm for the specific DNA hybrid under a particular set of conditions. The Tm is the temperature at which 50% of the target sequence hybridizes to a perfectly matched probe; see Sambrook et al., page 9.51, hereby incorporated by reference. The Tm for a particular DNA-DNA hybrid can be estimated by the formula:

Tm = 81.5°C + 16.6 (log10[Na+]) + 0.41 (fraction G + C) - 0.63 (% formamide) - (600/l) where l is the length of the hybrid in base pairs.

The Tm for a particular RNA-RNA hybrid can be estimated by the formula:

Tm = 79.8°C + 18.5 (log10[Na+]) + 0.58 (fraction G + C) + 11.8 (fraction G + C)2 - 0.35 (% formamide) - (820/l).

The Tm for a particular RNA-DNA hybrid can be estimated by the formula:

Tm = 79.8°C + 18.5(log10[Na+]) + 0.58 (fraction G + C) + 11.8 (fraction G + C)2 - 0.50 (% formamide) - (820/l).

In general, the Tm decreases by 1-1.5°C for each 1% of mismatch between two nucleic acid sequences. Thus, one having ordinary skill in the art can alter hybridization and/or washing conditions to obtain sequences that have higher or lower degrees of sequence identity to the target nucleic acid. For instance, to obtain hybridizing nucleic acids that contain up to 10% mismatch from the target nucleic acid sequence, 10-15°C would be subtracted from the calculated Tm of a perfectly matched hybrid, and then the hybridization and washing temperatures adjusted accordingly. Probe sequences may also hybridize specifically to duplex DNA under certain conditions to form triplex or other higher order DNA complexes. The preparation of such probes and suitable hybridization conditions are well known in the art. An example of stringent hybridization conditions for hybridization of complementary nucleic acid sequences having more than 100 complementary residues on a filter in a Southern or Northern blot or for screening a library is 50%

formamide/6X SSC at 42°C for at least ten hours. Another example of stringent hybridization conditions is 6X SSC at 68°C for at least ten hours. An example of low stringency hybridization conditions for hybridization of complementary nucleic acid sequences having more than 100 complementary residues on a filter in a Southern or northern blot or for screening a library is 6X SSC at 42°C for at least ten hours. Hybridization conditions to identify nucleic acid sequences that are similar but not identical can be identified by experimentally changing the hybridization temperature from 68°C to 42°C while keeping the salt concentration constant (6X SSC), or keeping the hybridization temperature and salt concentration constant (e.g. 42°C and 6X SSC) and varying the formamide concentration from 50% to 0%. Hybridization buffers may also include blocking agents to lower background. These agents are well-known in the art; see Sambrook et al., pages 8.46 and 9.46-9.58, herein incorporated by reference. Wash conditions also can be altered to change stringency conditions. An example of stringent wash conditions is a 0.2x SSC wash at 65°C for 15 minutes (see Sambrook et al., for SSC buffer). Often the high stringency wash is preceded by a low stringency wash to remove excess probe. An exemplary medium stringency wash for duplex DNA of more than 100 base pairs is 1x SSC at 45°C for 15 minutes. An exemplary low stringency wash for such a duplex is 4x SSC at 40°C for 15 minutes. In general, signal-to-noise ratio of 2x or higher than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization.

By the provision of the nucleotide sequences of SEQ ID Nos. 1, 3, 5 and 7 as well as those encoding the amino acid sequences depicted in SEQ ID Nos. 2, 4, 6 and 8 it is possible to isolate identical or similar nucleic acid molecules which encode water-soluble ligand-binding proteins from other species or organisms, in particular orthologous water-soluble ligand-binding protein encoding genes from mammals. The term "orthologous" as used herein means homologous sequences in different species that arose from a common ancestor gene during speciation. Orthologous genes may or may not be responsible for a similar function; see, e.g., the glossary of the "Trends Guide to Bioinformatics", Trends Supplement 1998, Elsevier Science.

In a further aspect, the present invention provides a recombinant polynucleotide comprising a vector incorporating the polynucleotide of the present invention. Many suitable vectors are known to those skilled in molecular biology, the choice of which would depend on the function desired and include plasmids, cosmids, viruses, bacteriophages and other vectors used conventionally in genetic engineering. Methods which are well known to those skilled in the art can be used to construct

various plasmids and vectors; see, for example, the techniques described in Sambrook, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory (1989) N.Y. and Ausubel, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. (1989), (1994). Alternatively, the polynucleotides and vectors of the invention can be reconstituted into liposomes for delivery to target cells. As discussed in further details below, a cloning vector was used to isolate individual sequences of DNA. Relevant sequences can be transferred into expression vectors where expression of a particular polypeptide is required. Typical cloning vectors include pBscpt sk, pGEM, pUC9, pBR322 and pGBT9. Typical expression vectors include pTRE, pCAL-n-EK, pESP-1, pOP13CAT, pET, pGEX, pMALC, pPIC9, pBac.

Hence, in a preferred embodiment of the present invention the above-described polyncucleotides either alone or present in a vector are linked to control sequences which allow the expression of the polynucleotide in prokaryotic and/or eukaryotic cells.

The term "control sequence" refers to regulatory DNA sequences which are necessary to effect the expression of coding sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism. In prokaryotes, control sequences generally include promotor, ribosomal binding site, and terminators. In eukaryotes generally control sequences include promotors, terminators and, in some instances, enhancers, transactivators or transcription factors. The term "control sequence" is intended to include, at a minimum, all components the presence of which are necessary for expression, and may also include additional advantageous components.

The term "operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequences. In case the control sequence is a promotor, it is obvious for a skilled person that double-stranded nucleic acid is preferably used.

Thus, the vector of the invention is preferably an expression vector. An "expression vector" is a construct that can be used to transform a selected host cell and provides for expression of a coding sequence in the selected host. Expression vectors can for instance be cloning vectors, binary vectors or integrating vectors. Expression comprises transcription of the nucleic acid molecule preferably into a translatable mRNA. Regulatory elements ensuring expression in prokaryotic and/or eukaryotic

cells are well known to those skilled in the art. In the case of eukaryotic cells they comprise normally promotors ensuring initiation of transcription and optionally poly-A signals ensuring termination of transcription and stabilization of the transcript. Possible regulatory elements permitting expression in prokaryotic host cells comprise, e.g., the PL, lac, trp, T7 or tac promotor in E. coli, and examples of regulatory elements permitting expression in eukaryotic host cells are the AOX1 or GAL1 promotor in yeast or the CMV-, SV40-, RSV-promotor (Rous sarcoma virus), CMV-enhancer, SV40-enhancer or a globin intron in mammalian and other animal cells. In this context, suitable expression vectors are known in the art such as Okayama-Berg cDNA expression vector pcDV1 (Pharmacia), pCDM8, pRc/CMV, pcDNA1, pcDNA3 (In-vitrogene), pSPORT1 (GIBCO BRL). An alternative expression system which could be used to express the protein is an insect system. In one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in Spodoptera frugiperda cells or in Trichoplusia larvae. The coding sequence of a nucleic acid molecule of the invention may be cloned into a nonessential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promotor. Successful insertion of said coding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein coat. The recombinant viruses are then used to infect S. frugiperda cells or Trichoplusia larvae in which the protein of the invention is expressed (Smith, J. Virol. 46 (1983), 584; Engelhard, Proc. Nat. Acad. Sci. USA 91 (1994), 3224-3227).

In plants, promotors commonly used are the polyubiquitin promotor, and the actin promotor for ubiquitous expression. The termination signals usually employed are from the Nopaline Synthase promotor or from the CAMV 35S promotor. A plant translational enhancer often used is the TMV omega sequences, the inclusion of an intron (Intron-1 from the Shrunken gene of maize, for example) has been shown to increase expression levels by up to 100-fold. (Mait, Transgenic Research 6 (1997), 143-156; Ni, Plant Journal 7 (1995), 661-676). Additional regulatory elements may include transcriptional as well as translational enhancers. Advantageously, the above-described vectors of the invention comprises a selectable and/or scorable marker. Selectable marker genes useful for the selection of transformed cells and, e.g., plant tissue and plants are well known to those skilled in the art and comprise, for example, antimetabolite resistance as the basis of selection for dhfr, which confers resistance to methotrexate (Reiss, Plant Physiol. (Life Sci. Adv.) 13 (1994), 143-149); npt, which confers resistance to the aminoglycosides neomycin,

kanamycin and paromycin (Herrera-Estrella, EMBO J. 2 (1983), 987-995) and hygro, which confers resistance to hygromycin (Marsh, Gene 32 (1984), 481-485).

Useful scorable markers are also known to those skilled in the art and are commercially available. Advantageously, said marker is a gene encoding luciferase (Giacomin, Pl. Sci. 116 (1996), 59-72; Scikantha, J. Bact. 178 (1996), 121), green fluorescent protein (Gerdes, FEBS Lett. 389 (1996), 44-47) or ß-glucuronidase (Jefferson, EMBO J. 6 (1987), 3901-3907). This embodiment is particularly useful for simple and rapid screening of cells, tissues and organisms containing a vector of the invention.

The proteins can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, size exclusion chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") or FPLC is employed for purification.

The present invention furthermore relates to host cells produced by introducing a nucleic acid molecule into the host cell which upon its presence in the cell mediates the expression of a gene encoding water-soluble ligand-binding proteins or comprising a polynucleotide or a vector as described above or a polynucleotide according to the invention wherein the polynucleotides and/or nucleic acid molecule is foreign to the host cell. By "foreign" it is meant that the polynucleotide or nucleic acid molecule is either heterologous with respect to the host cell, this means derived from a cell or organism with a different genomic background, or is homologous with respect to the host cell but located in a different genomic environment than the naturally occurring counterpart of said nucleic acid molecule. This means that, if the nucleic acid molecule is homologous with respect to the host cell, it is not located in its natural location in the genome of said host cell, in particular it is surrounded by different genes. In this case the polynucleotide may be either under the control of its own promotor or under the control of a heterologous promotor. The vector or nucleic acid molecule according to the invention which is present in the host cell may either be integrated into the genome of the host cell or it may be maintained in some form extrachromosomally. In this respect, it is also to be understood that the nucleic acid molecule of the invention can be used to restore or create a mutant gene via homologous recombination.

The host cell can be any prokaryotic or eukaryotic cell, such as bacterial, insect, fungal, plant or animal cells.

The term "prokaryotic" is meant to include all bacteria which can be transformed or transfected with a DNA or RNA molecules for the expression of a protein of the invention. Prokaryotic hosts may include gram negative as well as gram positive bacteria such as, for example, E. coli, S. typhimurium, Serratia marcescens and Bacillus subtilis. The term "eukaryotic" is meant to include yeast, higher plant, insect and preferably mammalian cells. Depending upon the host employed in a recombinant production procedure, the protein encoded by the polynucleotide of the present invention may be glycosylated or may be non-glycosylated. The water-soluble ligand-binding protein of the invention may or may not also include an initial methionine amino acid residue. A polynucleotide of the invention can be used to transform or transfect the host using any of the techniques commonly known to those of ordinary skill in the art. Furthermore, methods for preparing fused, operably linked genes and expressing them in, e.g., mammalian cells and bacteria are well-known in the art (Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989).

Thus the present invention provides a cell capable of expressing a polypeptide as discussed herein. The cell comprises a recombinant host cell usually incorporating the polynucleotide. Preferably, the host cell incorporates the polynucleotide as the recombinant polynucleotide. Any suitable host cell may be chosen, again depending on the intended purpose. Suitable host cells include XLI-BLUE, B21(DE3)pLysS, HB101, SOLR and SP-Q01 (Saccharomyces pombe).

Using an appropriate combination of host cell, vector and polynucleotide, an expression system can be provided so as to obtain a polypeptide useful in the present invention. This may comprise a fusion polypeptide encoded by the recombinant polynucleotide, a part of which is encoded by the vector. Typically, the vector will have a promotor region, which is usually inducible, leading to 5' coding region associated with the promotor. By appropriate manipulation, the polynucleotide encoding the polypeptide can be attached to the 5' coding region in frame. In this way, expression of the nucleotide sequence downstream of the promotor region gives rise to the fusion polypeptide which includes the polypeptide of the present invention.

The present invention also relates to an antigen comprising an epitope of at least 5 continuous amino acids of the amino acid sequence depicted in any one of SEQ ID Nos. 2, 4, 6 or 8 and/or said epitope is detectable by a monoclonal or polyclonal

antibody which recognises, preferably with a binding affinity of at least 10^{-7}M, a protein of the invention as described above. In the present invention, "epitopes" refers to fragments of the AChBP of the invention having antigenic or immunogenic activity in an animal. A preferred embodiment of the present invention relates to antigens comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response; see, for instance, Geysen, Proc. Natl. Acad. Sci. USA 81 (1983); 3998-4002. Fragments which function as epitopes may be produced by any conventional means; see, e.g., Houghten, Proc. Natl. Acad. Sci. USA 82 (1985), 5131-5135 further described in U.S. Patent No. 4,631,211. In the present invention, antigenic epitopes preferably contain a sequence of at least five, six, seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope; see, for instance, Wilson, Cell 37 (1984), 767-778; Sutcliffe, Science 219 (1983), 660-666). Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art; see, for instance, Sutcliffe, supra; Wilson, supra; Chow, Proc. Natl. Acad. Sci. USA 82 (1985), 910-914; and Bittle, J. Gen. Virol. 66 (1985); 2347-2354. A preferred immunogenic epitope includes the soluble protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

The present invention also relates to antibodies specifically recognizing the water-soluble ligand-binding protein and ligand-gated ion channels of the present invention, in particular recognizing the above described antigen or epitope. As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and $F(ab')_2$ fragments) which are capable of specifically binding to protein. Fab and $F(ab')_2$ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody; see, e.g., Wahl, J. Nucl. Med. 24 (1983), 316-325. Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression

library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies; see also infra. Said antibody can be a monoclonal antibody, a polyclonal antibody, a single chain antibody, human or humanized antibody, primatized, chimerized or fragment thereof that specifically binds said peptide or polypeptide also including bispecific antibody, synthetic antibody, antibody fragment, such as Fab, Fv or scFv fragments etc., or a chemically modified derivative of any of these. The general methodology for producing antibodies is well-known and has been described in, for example, Köhler and Milstein, Nature 256 (1975), 494 and reviewed in J.G.R. Hurrel, ed., "Monoclonal Hybridoma Antibodies: Techniques and Applications", CRC Press Inc., Boco Raron, FL (1982), as well as that taught by L. T. Mimms et al., Virology 176 (1990), 604-619. Furthermore, antibodies or fragments thereof to the aforementioned peptides can be obtained by using methods which are described, e.g., in Harlow and Lane "Antibodies, A Laboratory Manual", CSH Press, Cold Spring Harbor, 1988. For the production of antibodies in experimental animals, various hosts including goats, rabbits, rats, mice, and others, may be immunized by injection with polypeptides of the present invention or any fragment or oligopeptide or derivative thereof which has immunogenic properties. Techniques for producing and processing polyclonal antibodies are known in the art and are described in, among others, Mayer and Walker, eds., "Immunochemical Methods in Cell and Molecular Biology", Academic Press, London (1987). Polyclonal antibodies also may be obtained from an animal, preferably a mammal, previously infected with the virus of the invention. Methods for purifying antibodies are known in the art and comprise, for example, immunoaffinity chromatography. Depending on the host species, various adjuvants or immunological carriers may be used to increase immunological responses. Such adjuvants include, but are not limited to, Freund's, complete or incomplete adjuvants, mineral gels such as aluminium hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions and dinitrophenol. An example of a carrier, to which, for instance, a peptide of the invention may be coupled, is keyhole limpet hemocyanin (KLH). When derivatives of said antibodies are obtained by the phage display technique, surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies which bind to an epitope of the peptide or polypeptide of the invention (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmborg, J. Immunol. Methods 183 (1995), 7-13). In many cases, the binding phenomena of antibodies to antigens is equivalent to other ligand/anti-ligand binding.

In another embodiment the present invention relates to an oligonucleotide probe comprising a nucleotide sequence having at least 15 continuous nucleotides of a polynucleotide of the invention and/or encoding the above described antigen. Such oligonucleotides will usually specifically hybridize to a polynucleotide encoding a water-soluble ligand-binding protein of the invention. Specific hybridization occurs preferably under stringent conditions and implies no or very little cross-hybridization with nucleotide sequences encoding no or substantially different proteins. Such nucleic acid molecules may be used as probes and/or for the control of gene expression. Nucleic acid probe technology is well known to those skilled in the art who will readily appreciate that such probes may vary in length. Preferred are nucleic acid probes of 17 to 35 nucleotides in length. Of course, it may also be appropriate to use nucleic acids of up to 100 and more nucleotides in length. The nucleic acid probes of the invention are useful for various applications. On the one hand, they may be used as PCR primers for amplification of polynucleotides according to the invention. Another application is the use as a hybridization probe to identify polynucleotides hybridizing to the polynucleotides of the invention by homology screening of genomic DNA libraries. Nucleic acid molecules according to this preferred embodiment of the invention which are complementary to a polynucleotide as described above may also be used for repression of expression of a gene comprising such a polynucleotide, for example due to an antisense or triple helix effect or for the construction of appropriate ribozymes (see, e.g., EP-B1 0 291 533, EP-A1 0 321 201, EP-A2 0 360 257) which specifically cleave the (pre)-mRNA of a gene comprising a polynucleotide of the invention. Selection of appropriate target sites and corresponding ribozymes can be done as described for example in Steinecke, Ribozymes, Methods in Cell Biology 50, Galbraith et al. eds Academic Press, Inc. (1995), 449-460. Standard methods relating to antisense technology have also been described (Melani, Cancer Res. 51 (1991), 2897-2901). Said nucleic acid molecules may be chemically synthesized or transcribed by an appropriate vector containing a chimeric gene which allows for the transcription of said nucleic acid molecule in the cell. Such nucleic acid molecules may further contain ribozyme sequences as described above.

In this respect, it is also to be understood that the polynucleotide of the invention can be used for "gene targeting" and/or "gene replacement", for restoring a mutant gene or for creating a mutant gene via homologous recombination; see for example Mouellic, Proc. Natl. Acad. Sci. USA, 87 (1990), 4712-4716; Joyner, Gene Targeting, A Practical Approach, Oxford University Press.

Furthermore, the person skilled in the art is well aware that it is also possible to label such a nucleic acid probe with an appropriate marker for specific applications, such as for the detection of the presence of a polynucleotide of the invention in a sample derived from an organism, in particular mammals, preferably human. A number of companies such as Pharmacia Biotech (Piscataway NJ), Promega (Madison WI), and US Biochemical Corp (Cleveland OH) supply commercial kits and protocols for these procedures. Suitable reporter molecules or labels include those radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles and the like. Patents teaching the use of such labels include US Patents US-A-3,817,837; US-A-3,850,752; US-A-3,939,350; US-A-3,996,345; US-A-4,227,437; US-A-4,275,149 and US-A-4,366,241. Also, recombinant immunoglobulins may be produced as shown in US-A-4,816,567 incorporated herein by reference.

Furthermore, the so-called "peptide nucleic acid" (PNA) technique can be used for the detection or inhibition of the expression of a polynucleotide of the invention. For example, the binding of PNAs to complementary as well as various single stranded RNA and DNA nucleic acid molecules can be systematically investigated using thermal denaturation and BIAcore surface-interaction techniques (Jensen, Biochemistry 36 (1997), 5072-5077).

The present invention also relates to a method for the production of a transgenic non-human animal, preferably transgenic mouse, comprising introduction of a polynucleotide or vector of the invention into a germ cell, an embryonic cell, stem cell or an egg or a cell derived therefrom. The non-human animal can be used in accordance with a screening method of the invention described herein. Production of transgenic embryos and screening of those can be performed, e.g., as described by A. L. Joyner Ed., Gene Targeting, A Practical Approach (1993), Oxford University Press. The DNA of the embryonal membranes of embryos can be analyzed using, e.g., Southern blots with an appropriate probe; see supra. The invention also relates to transgenic non-human animals such as transgenic mouse, rats, hamsters, dogs, monkeys, rabbits, pigs, C. elegans and fish such as Torpedo fish comprising a polynucleotide or vector of the invention or obtained by the method described above, preferably wherein said polynucleotide or vector is stably integrated into the genome of said non-human animal, preferably such that the presence of said polynucleotide or vector leads to the expression of the water-soluble protein of the present invention.

The present invention further relates to composition comprising any one of the above described water-soluble ligand-binding proteins, multimers such as dimers or pentamers thereof, ligand-gated ion channels, polynucleotides, vectors, host cells, antigens, antibodies, or oligonucleotide probes of the invention; and optionally suitable means for detection or performing a ligand-receptor binding assay. In this context, the present invention also relates to a method for identifying an agonist/activator or antagonist/inhibitor of a ligand-gated receptor comprising the steps of:

(a) contacting the water-soluble ligand-binding protein of the present invention, multimers such as dimers or pentamers thereof, or the ligand-gated ion channel of the invention or a cell expressing said protein in the presence of components capable of providing a detectable signal in response to ligand binding with a compound to be screened under conditions that permit binding of said compound to the ligand-binding protein; and

(b) detecting the presence or absence of a signal generated from the binding activity of the ligand-binding protein, wherein the presence/increase and absence/decrease of the signal is indicative for an agonist/activator and antagonist/inhibitor, respectively, of a ligand-gated receptor.

Since ligand-gated receptors are modulated allosterically by natural polyamines, such as spermine, and by polyamine derivatives, such as polyamine amides (e.g. philanthotoxin-343) and polymethylene tetraamines (e.g. methoctramine) (Usherwood, Farmaco. 55 (2000), 202-205) compounds comprising or based on such entities may be used as starting material for screening. An antagonist or agonist that "modulates the activity" of a polypeptide and causes an altered signal, for example response in the cell refers to a compound that alters the activity of the protein so that it behaves differently in the presence of the compound than in the absence of the compound. Typically, the effect of an antagonist is observed as a blocking of agonist-induced receptor activation. Antagonists include competitive as well as non-competitive antagonists. A competitive antagonist (or competitive blocker) interacts with or near the site specific for agonist binding. A non-competitive antagonist or blocker inactivates the function of the receptor by interacting with a site other than the agonist interaction site. As understood by those of skill in the art, bioassay methods for identifying compounds that modulate the activity of receptors such as proteins of the invention generally require comparison to a control. One type of "control" is a cell or culture that is treated substantially the same as the test cell or test culture exposed to the compound, with the distinction that the "control" cell or

culture is not exposed to the compound. For example, in methods that use voltage clamp electrophysiological procedures, the same cell can be tested in the presence or absence of compound, by merely changing the external solution bathing the cell. Accordingly, the response of the transfected cell to the "control" cell or culture to the same compound under the same reaction conditions. However, "control data" can also be used from the literature.

As described in Example 6 the 3-dimensional structure of AChBP could be solved by X-ray crystallography at 2.7Å resolution (current Rfactor = 27.9 %, Rfree = 30.0 %). In crystals, as in solution, AChBP forms a stable homo-pentamer with dimensions comparable to those of the ligand-binding domain of ligand-gated ion channels, in particular comparable to the nAChR, as determined in EM studies by Unwin and coworkers; see supra. The structural analysis revealed that In the AChBP homopentamer the monomers have immunoglobulin-like topology. At each of five subunit interfaces a ligand-binding site is located, with all residues consistent with biochemical data. In this site a buffer molecule (HERPES) stacks with cation-π interactions on a tryptophan, resembling acetylcholine binding. The AChBP structure is relevant for the development of drugs against, *e.g.,* Alzheimer's disease and nicotine addiction. The high-resolution crystal structure of AChBP, along with biochemical and pharmacological data, supports the teaching of the present invention that the water-soluble ligand-binding proteins of the invention such as AChBP are good mimics of ligand-binding domains of ligand-gated ion channels.

Thus, the present invention relates to a crystal of a water-soluble ligand-binding protein of the invention, preferably in a multimeric form such as dimer, pentamer or decamer. In one embodiment said crystal comprises a protein-ligand complex. Methods how to employ and analyze such crystals are known to the person skilled in the art; see for example US-A-5,872,011 which describes the crystal structure of a protein-ligand complex containing an N-terminal truncated eIF4E and uses thereof. The crystal structure of the ligand-gated receptor ligand-binding region in a complex with a ligand, preferably being an antagonist or agonist will reveal the determinants of receptor-antagonist/agonist interactions and how ligand-binding specificity and affinity are altered by remote residues and the redox state of the conserved disulphide bond. The structure may also indicate mechanisms for allosteric effector action and for ligand-induced channel gating. How the information on the crystal structure of a ligand-binding region in a complex with a ligand can be used for the development of agonists and antagonists has been described for the structure of a

glutamate-receptor ligand-binding core in complex with kainate (Armstrong et al., Nature 395 (1998), 913-917).

The crystal of the invention, in particular when comprising nAChR related proteins can be a complex of the protein with a ligand comprising an N-alkylated hydroxyalkyl and/or a quaternary ammonium ion. However, other ligands my be used as well. Preferred ligands comprise 4-(2-Hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES), B-bippinatin, lophotoxin, d-tubocurarine, nicotine, acetylcholine, conotoxin, carbamylcholine, galanthamine, epibatidine or alpha-bungarotoxin or derivatives thereof.

Different aspects of X-ray crystallography are such as data collection, structure solution, determining the molecular structure from X-ray diffraction, refinement, etc. are described in the prior art, see, e.g., Powell, Annu. Rep. Prog. Chem., Sect. C: Phys. Chem. 96 (2000), 139-175 and Methods in Enzymology, 276-277, edited by Carter and Sweet, Academic Press, 1997. Current methods and optimization algorithms for the refinement of X-ray crystal structures are described by Van Der Maelen Uria, Crystallogr. Rev. 7 (1999), 125-180.

The crystal of the invention effectively diffracts X-rays for the determination of the atomic coordinates of the protein or protein-ligand complex to a resolution of greater than 5.0, preferably greater than 4.0 Angstroms. In a preferred embodiment the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the protein-ligand complex to a resolution of greater than 3.0 Angstroms. In a more preferred embodiment the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the protein-ligand complex to a resolution of greater than 2.0 Angstroms. In one embodiment the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the protein-ligand complex to a resolution of about 2.7 Angstroms.

Preferably, the crystal of the invention is formed by a protein that has an amino acid sequence of amino acids 20 to 223 of SEQ ID No. 2, or an amino acid sequence that differs from amino acid 20 to 223 of SEQ ID No. 2 by only having conservative substitutions. As is described in the examples, the crystals of the AChBP comprise decameric forms of the protein. In order to ease the use of the AChBP protein for analysis and crystallography it is envisaged to create a mutation in residue Asp2 and Asp5 of the mature AChBP SEQ ID No. 2 or 4 to remove the calcium binding site, and prevent creation of a decamer. This deletion can be done for example by

oligonucleotide-directed mutagenesis. Alternatively crystals could be grown in a low calcium concentration or in the absence of calcium.

The crystal of the present invention preferably has (1) a space group of $P2_12_12_1$ and a unit cell of dimensions of a=120.6Å, b=137.0Å and c=161.5Å; (2) a space group of $P4_22_12$ and a unit cell of dimensions of a=b=141.6Å and c=120.8Å or (3) a space group of $P2_1$ and a unit cell of dimensions of a=121.1Å, b=162.1Å, c=139.4Å, ß=90.1°.

The crystal of the present invention is preferably from a protein that has secondary structural elements that include .alpha.-helix and antiparallel .beta.-sheets as shown in and described for Figures 7, 10, 11 and/or 12. Most preferably, the crystal of the invention has a three-dimensional structure as defined by atomic coordinates shown in Table 1. Those of skill in the art understand that a set of structure coordinates determined by X-ray crystallography is not without standard error. For the purpose of this invention, any set of structure coordinates for AChBP or AChBP mutants that have a root mean square deviation of protein backbone atoms (N, C.alpha., C and O) of less than 0.75 Angstrom when superimposed - using backbone atoms - on the structure coordinates listed in Table 1 shall be considered identical.

In a most preferred embodiment of the present invention, the crystal has a binding cavity as shown in Figures 6, 8, 9 and/or 13.

In accordance with the findings of the present invention, it is proposed to use the water-soluble ligand-binding proteins of molluscs as the blueprint for the receptor binding site of the ligand-gated ion channel superfamily including nACh, 5-HT3, glycine, $GABA_A$, and $GABA_C$, most preferably for the nAChR. The availability of X-ray structures, and the cloned sequences provide a unique opportunity to understand these receptors at the molecular level, possibly unravel the dynamic changes occurring upon ligand binding, and predict their tertiary and quaternary structure with a higher degree of confidence than possible for other protein modules. This should pave the way for designing ligands selective for any of the multiple subtypes in any of these receptor families. The AChBP-like structures can be used for computerized docking to homology models which leads to the *a priori* discovery of novel ligands before laboratory experiments begin to optimize the drug candidates.

Thus, the present invention also relates to a method of using the crystal of the invention in a drug screening assays, such as comprising:

(a) selecting a potential ligand by performing structure assisted drug design with the three-dimensional structure determined for the crystal,

wherein said selecting is performed in conjunction with computer modeling; optionally

(b) contacting the potential ligand with the ligand binding domain of the ligand-gated receptor in an in vitro or in vivo assay; and

(c) detecting the binding of the potential ligand for the ligand binding domain.

The use of macromolecular crystallography as a tool for investigating drug and receptor interactions, in particular structure-based drug design is reviewed in Oakley and Wilce, Clin. Exp. Pharmacol. Physiol. 27 (2000), 145-151. The desired drug could be an inhibitor or an agonist that mimics endogenous transmitters or ligands. Once the 3-D structure of the relevant target is known, computational processes can be used to search databases of compounds to identify ones that may interact strongly with the target. Lead compounds can be improved using the 3-D structure of the complex of the lead compound and its biological target. The activity of the selected compound can then be tested in a functional assay such as one of those described herein..

Preferably, the potential drug is selected on the basis of its having a greater affinity for the ligand binding domain of the ligand-gated receptor than that of a standard ligand for the ligand binding domain of the ligand-gated receptor. However, the affinity of the selected compound may also be less than that of a standard ligand. Such compounds are useful for example as a lead for the development of further analogues which in turn may have enhanced binding affinity or otherwise beneficial therapeutic properties. On the other hand, the selected compound may bind to a site of the ligand-gated receptor other than known ligands. In a preferred embodiment, the ligand-gated receptor is a nicotinic acetylcholine receptor.

In a further embodiment, the method of the present invention further comprises:

(d) forming a supplemental crystal of a protein-ligand complex by co-crystallization or soaking the crystal of the water-soluble ligand-binding protein with a potential drug, wherein the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the protein-ligand complex to a resolution of greater than 5.0, preferably greater than 4.0 Angstroms, more preferably greater than 3;

(e) determining the three-dimensional structure of the supplemental crystal;

(f) selecting a candidate drug by performing a structure assisted drug design with the three-dimensional structure determined for the supplemental crystal, wherein said selecting is performed in conjunction with computer modeling; optionally

(g) contacting the candidate drug with a cell that expresses the ligand-gated receptor; and

(h) detecting a cell response; wherein a candidate drug is identified as a drug when the cell response is altered compared to a cell that has not been contacted with the candidate compound.

The above described methods can further comprise an initial step that precedes step (a) wherein said initial step consists of determining the three-dimensional structure of a crystal comprising a protein-ligand complex formed between the water-soluble ligand-binding protein, and the ligand of the ligand-gated receptor, wherein the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the protein-ligand complex to a resolution of greater than 5.0, preferably greater than 4.0 Angstroms. Preferably, the resolution of crystal diffraction in the above described methods is at least 3.0, most preferably at least about 2.7 Angstroms.

In a still further embodiment, the present invention relates to a method of growing a crystal of a protein-ligand complex comprising:

(a) contacting the water-soluble ligand-binding protein described above with a ligand of a ligand-gated receptor, wherein the water-soluble ligand-binding protein forms a protein-ligand complex with the ligand; and

(b) growing the crystal of the protein-ligand complex; wherein the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the protein-ligand complex to a resolution of greater than 5.0, preferably greater than 4.0 Angstroms, more preferably at least 3.0, most preferably at least about 2.7 Angstroms.

The crystals of the present invention can also be used in X-ray crystallography–driven screening technique that combines the steps of lead identification, structural assessment, and optimization such as described for example in Nienaber et al., Nature Biotechnol. 18 (2000), 1105 - 1108. This crystallographic screening method (named CrystaLEAD) has been used to sample large compound libraries and detecting ligands by monitoring changes in the electron density map of the crystal relative to the unbound form. The electron density map yields a high- resolution picture of the ligand–protein complex that provides key information to a structure-

directed drug discovery process. The bound ligand is directly visualized in the electron density map. Ligands that bind away from the targeted site may be eliminated.

The above described methods can be coupled with state-of-the-art laboratory data collection facilities including CCD detectors and data acquisition robotics.

Further embodiments that may be used in accordance with the ligand-binding proteins and receptor of the present invention are described in the prior art, for example ligand screening and design by X-ray crystallography is disclosed in WO99/45379 and WO99/45389; WO00/14105 describes assaying a candidate compound for its ability to interact with a modified receptor tyrosine kinase including obtaining and applying crystallography coordinates to a computer algorithm for generating a model which is applied in an iterative process to various molecular structures in order to identify agonist and antagonists of the receptor. All these methods may be equally applied to the proteins and crystals of the present invention.

In one preferred embodiment, the present invention relates to a drug screening assay comprising soaking a crystal of the invention in a solution of compounds to be screened and detecting the binding of the compound to the ligand-binding protein. A possible procedure is also described in Example 9. Besides the detection methods of ligand-binding mentioned above, in the cited documents and in the examples, the detection can also be based on measuring the release of the ligand in the preformed crystal of a protein-ligand complex. As described herein before, said ligand preferably comprises an alkylated nitrogen and/or quaternary ammonium ion or may be one of those described above.

The structural information on the crystals of the present invention can also be used for increasing or decreasing the affinity of a drug to a ligand-gated receptor. Such a method can comprise performing structure assisted drug design with the three-dimensional structure determined for the crystal, wherein said drug design is performed in conjunction with computer modeling; and modifying said drug to alter or eliminate a portion thereof suspected of interacting with a binding site of the binding cavity or with a non-specific binding site of the protein in the crystal. This method can, of course, be combined with one or more steps of any of the above described screening methods or other screening methods well known in the art. Methods for clinical compound discovery comprises for example ultrahigh-throughput screening (Sundberg, Curr. Opin. Biotechnol. 11 (2000), 47–53) for lead identification, and structure-based drug design (Verlinde and Hol, Structure 2 (1994), 577–587) and

combinatorial chemistry (Salemme et al., Structure 15 (1997), 319–324) for lead optimization. Further information that could be taken into account for drug selection and design so far available for the localization of agonist and competitive antagonist binding sites on nicotinic acetylcholine receptors have recently been reviewed (Arias, Neurochem. Int. 36 (2000), 595-6450; Corringer et al., 1999). Once a drug has been selected, the method can have the additional step of repeating the method used to perform rational drug design using the modified drug and to assess whether said modified drug displays better affinity according to for example interaction/energy analysis.

A related method of the present invention for drug design comprises the step of using the structural coordinates of the water-soluble ligand-binding protein crystal comprising the coordinates of Table 1, to computationally evaluate a chemical entity for associating with the ligand-binding site or a non-specific binding site of a ligand-binding protein. This approach, made possible and enabled by this invention, is to screen computationally small molecule data bases for chemical entities or compounds that can bind in whole, or in part, to the AChBP. In this screening, the quality of fit of such entities or compounds to the binding site may be judged either by shape complementarity or by estimated interaction energy. Meng, et al., J. Coma. Chem. 13 (1992), 505-524. In addition, in accordance with this invention, AChBP mutants or chimerics may be crystallized in co-complex with known ligand-gated ion channel inhibitors. The crystal structures of a series of such complexes may then be solved by molecular replacement (for review see for example Brunger er al. Prog. Biophys. Mol. Biol. 72 (1999), 135-155; and references cited therein) and compared with that of wild-type AChBP. Potential sites for modification within the various binding sites of the ligand-binding domain may thus be identified. This information provides an additional tool for determining the most efficient binding interactions, for example, increased hydrophobic interactions, between AChPB and a chemical entity or compound.

The design of compounds that bind to or inhibit ligand-gated ion channels according to this invention generally involves consideration of two factors.

First, the compound must be capable of physically and structurally associating with the ligand-binding domain. Non-covalent molecular interactions important in the association of the ligand-binding domain with its ligand include hydrogen bonding, van der Waals and hydrophobic interactions.

Second, the compound must be able to assume a conformation that allows it to associate with the ligand-binding domain. Although certain portions of the compound

will not directly participate in this association, those portions may still influence the overall conformation of the molecule. This, in turn, may have a significant impact on potency. Such conformational requirements include the overall three-dimensional structure and orientation of the chemical entity or compound in relation to all or a portion of the binding site or the spacing between functional groups of a compound comprising several chemical entities that directly interact with the AChBP.

If the theoretical structure of the given compound suggests insufficient interaction and association between it and AChBP, synthesis and testing of the compound is obviated. However, if computer modelling indicates a strong interaction, the molecule may then be synthesized and tested for its ability to bind to AChPB or a ligand-gated ion channel and functionally tested according to the methods mentioned above. In this manner, synthesis of inoperative compounds may be avoided. Once suitable chemical entities or fragments have been selected, they can be assembled into a single compound or inhibitor. Assembly may be proceed by visual inspection of the relationship of the fragments to each other on the three-dimensional image displayed on a computer screen in relation to the structure coordinates of AChBP. This would be followed by manual model building using software such as Quanta or Sybyl. Useful programs to aid one of skill in the art in connecting the individual chemical entities or fragments include CAVEAT (Bartlett, et al, "CAVEAT: A Program to Facilitate the Structure-Derived Design of Biologically Active Molecules". In Molecular Recognition in Chemical and Biological Problems", Special Pub., Royal Chem. Soc. 78 (1989), 182-196); 3D Database systems such as MACCS-3D (Martin, J. Med. Chem. 35 (1992), 2145-2154) and HOOK (Molecular Simulations, Burlington, Mass.). Instead of proceeding to build an AChBP ligand in a step-wise fashion one fragment or chemical entity at a time as described above, AChBP binding compounds may be designed as a whole or "de novo" using either an empty active site or optionally including some portion(s) of a known ligand(s). These methods include LUDI (Bohm, J. ComR. Aid. Molec. Design 6 (1992), 61-78); LEGEND (Nishibata and Itai, Tetrahedron 47 (1991), 8985); and LeapFrog (Tripos Associates, St. Louis, Mo.). Other molecular modelling techniques may also be employed in accordance with this invention; see, e.g., Cohen, J. Med. Chem. 33 (1990), 883-894 and Navia and Murcko, Current Opinions in Structural Biology 2 (1992), 202-210.

Such computer modeling is preferably performed with a Docking program (Dunbrack et al., Protein Sci. 6 (1997), 1661-1681 and Folding Des. 2 (1997), R27-R42).

Methods for the identification of drugs or corresponding lead compounds in computational prescreen using X-ray crystal structures are described in the prior art

(Verlinde and Hol, Structure 2 (1994), 577–587; Kuntz, Science 257 (1992), 1078–1082; Shuker et al., Science 274 (1996), 1531–1534; Fejzo et al., Chem. Biol. 6 (1999), 755–769; WO 98/58961). The structural information can be consulted to efficiently optimize leads. Computational programs have been written to identify compounds ranging from very small molecules or functional groups (GRID: Goodford, J. Med. Chem. 28 (1985), 849–857; MCSS: Caflish et al., J. Med. Chem. 36 (1993), 2142–2167) to potential lead scaffolds (DOCK: Kuntz et al., Accounts Chem. Res. 27 (1994), 117–123) using solved X-ray crystal structures. Another method computationally prescreens compound libraries and experimentally tests the individual "hits" by X-ray crystallography (Verlinde et al., J. Comput. Aided Mol. Des. 6 (1992), 131–147) in order to decrease the size of the screening library. In addition, an experimental approach has been developed to find organic solvents that bind to active sites that may be recombined into a lead macromolecule (Allen et al., J. Phys. Chem. 100 (1996), 2605–2611).

Once a compound has been designed or selected by the above methods, the efficiency with which that compound may bind to the AChBP or a corresponding ligand-binding domain may be tested and optimized by computational evaluation. For example, a compound that has been designed or selected to function as an inhibitor must preferably demonstrate a relatively small difference in energy between its bound and free states (i.e., a small deformation energy of binding). Thus, the most efficient inhibitors should preferably be designed with a deformation energy of binding of not greater than about 10 kcal/mole, preferably, not greater than 7 kcal/mole. Inhibitors may interact with the ligand-binding domain in more than one conformation that is similar in overall binding energy. In those cases, the deformation energy of binding is taken to be the difference between the energy of the free compound and the average energy of the conformations observed when the inhibitor binds to the AChBP.

A compound designed or selected as binding to AChBP may be further computationally optimized so that in its bound state it would preferably lack repulsive electrostatic interaction with the target ligand-binding domain. Such non-complementary (e.g., electrostatic) interactions include repulsive charge-charge, dipole-dipole and charge-dipole interactions. Specifically, the sum of all electrostatic interactions between the ligand and the AChBP when the ligand is bound to AChBP, preferably make a neutral or favorable contribution to the enthalpy of binding. Specific computer software is available in the art to evaluate compound deformation

energy and electrostatic interaction. Examples of programs designed for such uses include Gaussian 92, revision C (Frisch, Gaussian, Inc., Pittsburgh, Pa.); AMBER, version 4.0 (Kollman, University of California at San Francisco); QUANTA/CHARMM (Molecular Simulations, Inc., Burlington, Mass.); and Insight II/Discover (Biosysm Technologies Inc., San Diego, Calif.). These programs may be implemented, for instance, using a Silicon Graphics workstation, IRIS 4D/35, IBM RISC/6000 workstation model 550 or better a Unix workstation (SGI, Alpha, Sun, etc.) or any Linux PC. Other hardware systems and software packages will be known to those skilled in the art.

Once an AChBP-binding compound has been optimally selected or designed, as described above, substitutions may then be made in some of its atoms or side groups in order to improve or modify its binding properties. Generally, initial substitutions are conservative, i.e., the replacement group will have approximately the same size, shape, hydrophobicity and charge as the original group. It should, of course, be understood that components known in the art to alter conformation should be avoided. Such substituted chemical compounds may then be analyzed for efficiency of fit to AChBP by the same computer methods described in detail, above.

As mentioned before, the above described methods of the present invention can also be used as an initial drug screening assay followed by a classical drug screening assay using the biochemical assays known in the art.

Methods for the preparation of compounds, chemical derivatives and analogues are well known to those skilled in the art and are described in, for example, Beilstein, Handbook of Organic Chemistry, Springer edition New York Inc., 175 Fifth Avenue, New York, N.Y.

In one embodiment of the method of the present invention the identified drug prevents or promotes correct assembly of a ligand-gated ion channel. Thus, the selected drug may for example either interfere with the contact regions of the monomers of the ligand-gated ion channel or may act as a scaffold for the assembly. In the latter case, the drug may be based for example on an antibody which binds to the contact regions of two or more monomers when assembled and thus facilitates the assembly process. Preferred contact regions with respect to the AChBP and the related nicotinic acetylcholine receptor are given below. In a still further embodiment of the above described methods, the drug can be selected such as to bind to a non-specific binding site of a ligand-gated ion channel. The non-specific binding site can for example include those contact regions that are highly conserved between the monomers of the ligand-gated ion channels.

Once a drug has been selected in accordance with any one of the above described methods of the present invention, the drug or a pro-drug thereof can be synthesized in a therapeutically effective amount. As used herein, the term "therapeutically effective amount" means the total amount of the drug or pro-drug that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of a condition related to an ligand-gated ion channel, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. In addition or alternatively, in particular with respect to pre-clinical testing of the drug the term "therapeutically effective amount" includes the total amount of the drug or pro-drug that is sufficient to elicit a physiological response upon its binding to its target ligand-gated ion channel in an non-human animal test.

The present invention also relates to a drug produced by any one of the above described methods of the present invention, or a pro-drug thereof. Preferably, the drug or pro-drug thereof is present either alone or in a composition in a therapeutically effective amount.

The drug obtained by a method of the present invention may be characterized by its interaction with the binding sites in the binding cavity defined by the coordinates of crystal structure of the protein-ligand complex; for examples of such characterization see, e.g., US-A-5,798,247. Preferably, the drug, for example a potential inhibitor will form non-covalent bonds with one or more amino acids in the active site based upon the crystal structure. On the other hand, the drug may bind to a contact region of the individual monomers of the pentameric ligand-gated receptor. For example, multimer contact regions in *Lymnaea stagnalis* AChBP (SEQ ID No. 2) have been identified. Consecutive regions have at least every second residue involved in contacts with the other monomer. Contacts have been defined as 2 atoms within 4.2 angstrom distance in 2.7 Angstrom structure. The primary contact regions in mature AChBP (residues from A contacting B) are 15-21, 44-47, 85-87, 91-94, 122-124,143-146, 149, 185-187 and the complementary contact regions (from B contacting A, (identical to residues on A contacting E) are 3-4, 7-8, 11, 37-39, 53, 75-77, 96-104, 114-118, 163-170; see also Figure 14.

Thus, in one preferred embodiment the drug of the present invention interacts with a ligand-gated receptor comprising a pentamer with monomers A to E, wherein the drug binds to one or more primary contact regions of a monomer (residues from A contacting B) defined by amino acid residues 15 to 21, 44 to 47, 85 to 87, 91 to 94, 122 to 124, 143 to 146, 149, 185 to 187 of SEQ ID No. 2 and/or to one or more of the

complementary contact regions of the other monomer (from B contacting A, (identical to residues on A contacting E) defined by amino acid residues 3 to 4, 7 to 8, 11, 37 to 39, 53, 75 to 77, 96 to 104, 114 to 118 and 163-170 of SEQ ID No. 2; or to one of the contact regions identified in Figure 14; or to the corresponding contact regions of the monomers of a ligand-gated ion channel. Preferably, the ligand-gated ion channel is the nicotinic acetylcholine receptor and the order of the monomers is $\alpha\gamma\alpha\delta\beta$.

Any available method may be used to construct such model from the crystallographic and/or amino acid sequence data disclosed herein or obtained from independent analysis of crystalline AChBP proteins or other water-soluble ligand-binding proteins of the present invention. Such a model can be constructed from available analytical data points using known software packages such as HKL, MOSFILM, XDS, CCP4, SHARP, PHASES, HEAVY, XPLOR, TNT, NMRCOMPASS, NMRPIPE, DIANA, NMRDRAW, FELIX, VNMR, MADIGRAS, QUANTA, BUSTER, SOLVE, O, FRODO, RASMOL, CNS , REFMAC, ARP/WARP, XTALVIEW and CHAIN. The model constructed from these data can then be visualized using available systems, including, for example, Silicon Graphics, Evans and Sutherland, SUN, Hewlett Packard, Apple Macintosh, DEC, IBM, and Compaq. The present invention also provides for devices such as a computer system which comprises the model of the invention and hardware used for construction, processing and/or visualization of the model of the invention. Further embodiments provide a computer system comprising computer hardware and the model of the present invention. The study of the interaction of the candidate species with the model can be performed using available software platforms, including QUANTA, RASMOL, O, CHAIN, FRODO, INSIGHT, DOCK, MCSS/HOOK, CHARMM, LEAPFROG, CAVEAT (UC Berkley), CAVEAT (MSI), MODELLER, CATALYST, XTALVIEW and ISIS. Computer readable media such as floppy discs, CD ROMs, tapes, and any other storage or processing means comprising crystallographic and/or nucleotide/amino acid sequence data disclosed herein or obtained from independent analysis of crystalline AChBP proteins or other water-soluble ligand-binding proteins of the present invention are subject of the present invention as well. Any one of the mentioned means and devices can advantageously be used for modeling an antagonist/inhibitor or agonist/activator of a ligand-gated receptor.

Furthermore, the present invention relates to the construction of theoretical three dimensional (3D) models of ligand-binding domains of ligand-gated ion channels by computer-assisted molecular modeling using the X-ray coordinates of the water-soluble ligand-binding proteins of the invention. These 3D models can correspond

either to the entire ligand-binding domain (~220 to 240 extracellular amino acids) or may be limited to the ligand-binding site.

The concept of using 3D structures of the mollusc ligand-binding proteins for molecular modeling and tool for structure prediction of for example mammalian, in particular human ligand-gated ion channels gains support from the observation that the ligand-binding domain of vertebrate glutamate receptor channels and bacterial periplasmic substrate-binding proteins (PBPs) share similar 3D structures despite the very low sequence similarity between ionotropic glutamate receptor subunits and the PBPs that were used as templates (12%); for review see Paas et al. TiPS 21 (2000), 87- 92 and refernces cited therein

Thus, on the basis of a computer-assisted molecular modeling, optionally supplemented by for example functional studies of site-specific mutants, the crystal structure of the ligand-binding domain of ligand-gated ion channels and theoretical 3D models of these domains can be predicted. In turn, these models can be used for structure assisted drug design. The predicted models may be further refined, for example by monitoring the effects of mutations of amino acid residues that are probably located in the ligand-binding site on (1) agonist-elicited channel activation and desensitization, (2) inhibition of channel activity by various competitive receptor antagonists; or (3) the binding of various ligands. Experimental setups for analyzing such effects are known to the person skilled in the art, see also the documents cited for functional assay systems of ligand-gated ion channels.

Thus, the embodiments of the present invention enable various possibilities for identification and modeling new ligands of ligand-gated ion channels as well as modifying the ion channels themselves. Accordingly, the present invention relates to the use of the above described polynucleotides, proteins, dimers and pentamers, ligand-gated ion channels, vectors, host cells, antigens, antibodies, oligonucleotide probes, crystals, their structural coordinates and methods for screening or profiling putative ligands of ligand-gated receptors.

Methods for the lead generation in drug discovery using proteins and detection methods such as mass spectrometry (Cheng et al. J. Am. Chem. Soc. 117 (1995), 8859–8860) and some nuclear magnetic resonance (NMR) methods (Fejzo et al., Chem. Biol. 6 (1999), 755–769; Lin et al., J. Org. Chem. 62 (1997), 8930–8931).

The newly identified drug obtained by a method of the present invention, i.e. an antagonist/inhibitor or agonist/activator can be used for the preparation of a pharmaceutical composition for the treatment of a ligand-gated ion channel mediated or related disorder. Such disorders are well know to the person skilled in the art. For

example, possible applications of agonist and antagonists to nAChRs are based on their participation in complex functions such as attention, memory, and cognition, and their involvement in the pathogenesis of certain neuropsychiatric disorders (Alzheimer's and Parkinson's diseases, Tourette's syndrome, schizophrenia, depression, etc). For the majority of these disorders, the use of nAChRs' agonists may represent either a prophylactic (esp. for Alzheimer's and Parkinson's diseases) or a symptomatic treatment; for review see for example Mihailescu and Drucker-Colin, Arch. Med. Res. 31 (2000), 131-144.

The medicinal chemistry and molecular biology of GABA-activated ligand-gated ion channels also in terms of agonist and antagonist structural profiles is described in Chebib et al., J. Med. Chem. 43 (2000), 1427-1447.

Glycine receptors and disorders of glycinergic neurotransmission are extensively reviewed in Rajendra et al., Pharmacol. Ther. 73 (1997), 121-146 and Barry et al., Clin. Exp. Pharmacol. Physiol. 26 (1999), 935-936.

The central role of 5-HT3 receptor in CNS disorders and 5-HT3 receptor antagonists are described in Bloom and Morales, Neurochemical Research 23 (1998), 653-659 and Higgins and Kilpatrick, Expert Opin. Invest. Drugs 8 (1999), 2183-2188.

In one embodiment, the antagonist/inhibitor is or is derived from a protein, an antigen, antibody or from a toxin of the ligand-gated ion channel. Likewise, the agonist/activator can be derived from a protein, an antigen, antibody or from a toxin of the ligand-gated ion channel. Possible starting points comprise for example peptide toxins, e.g., conotoxin (IMI) and alpha bungarotoxin, lophotoxins (Bippinatins), tubocurarine, decamethonium, alpha-cobratoxin, epibatidine, acetylcholine, choline, nicotine, carbachol, serotonin or GABA. The structure of these molecules together with that of the crystal of the target ligand-binding domain can be used to model the compound and elucidate side chains, functional groups etc. which may be added, deleted or modified in order to improve for example affinity and/or specificty of the drug or for example make a drug which acts on a different target non-reactive with a certain ligand-gated ion channel.

In a preferred embodiment for the uses according to the present invention, the ligand-gated ion channel is the nicotinic acetylcholine receptor and said mediated or related disorder is Tourette's syndrome, Alzheimer's disease, addiction to nicotine or schizophrenia.

As mentioned herein before, this is the first time it could be shown that water-soluble ligand-binding proteins exists in molluscs, which closely resemble the ligand-binding

domain of ligand-gated ion channel of higher mammals. It is expected that similar ligand-binding proteins exist in other molluscan species or even in the lineage the Mollusca, Protostomia, Coelomata, Bilateria, Eumetazoa, Metazoa, Fungi/Metazoa group. Accordingly, the present invention also relates to the use of a ligand of a ligand-gated ion channel for identifying and isolating a water-soluble ligand-binding protein from such species, preferably from a mollusc. Preferably, the ligand used for the isolation of the protein is α-bungarotoxin. The water-soluble ligand binding proteins obtainable from these organisms as well as derivatives that can be made in accordance with the teaching present herein are also subject of the present invention.

Furthermore, for the first time the crystal structure of a nicotinic binding site has been revealed. This crystal structure shows that the molluscan AChBP is a homolog of the LGIC superfamily ligand binding domains. It reveals the Ig-topology, the location of the binding site at the subunit interface, the position of the MIR and the extensive data on the nicotinic ligand binding residues. Importantly, it gives important new information about the exact fold and the arrangement of the nicotinic ligand-binding site in three dimensions. It shows the presence of a second pocket that has been noticed by EM analysis. Furthermore, it clarifies the arrangement of subunits by showing the relative positioning of the principal and complementary part of the ligand-binding site. It provides an explanation of the role of the LGIC superfamily conserved residues in stabilizing the monomer structure by the formation of hydrophobic cores and packing of secondary structure elements and it makes clear how the pentamers are built up, and how weakly the pentamer interfaces are conserved between LGICs.

This structure can be used for the numerous drug-design studies that are targeting the LGIC superfamily. The general structural knowledge on its folding will be applicable to the GABA, serotonin ($5HT_3$) and glycine receptor fields. It will help to understand their ligand-binding characteristics and could thus have impact on development of *e.g.* anti-emetics aimed at the $5HT_3$ receptor or the mood-defining drugs that target the GABA receptors. However, the availability of a three-dimensional description of the nicotinic ligand-binding site will be especially relevant for the design of new drugs against Alzheimers' disease, epilepsy and the addiction to smoking which have the neuronal nicotinic receptors as their targets.

Many embodiments and the examples feature the acetylcholine-binding protein (AChBP) of the invention and the embodiments generally described herein are

preferably related to the nicotinic acetylcholine receptor (nAChR), more preferably to the alpha subunit, and most preferably to the alpha 7 subunit. However, it should be understood that all embodiments equally apply to the other water-soluble ligand-binding proteins and generally to the ligand-gated ion channels mentioned herein. For example, the crystal structure of the AChBP can be used to model new ligands for the acetylcholine receptor, preferably such with inhibiting or stimulating action on the acetylcholine receptor. Likewise, it is possible to identify and model new ligands for other ligand-gated ion channels (including glycine, GABA and serotonin receptor) with inhibiting action. Such ligands may for example prevent correct assembly of ligand gated ion channels. Preferably such ligands prevent correct assembly of specific sub types of ligand gated ion channels. On the other hand, ligands can be identified and modeled that promote correct assembly of ligand gated ion channels, preferably of specific sub types of ligand gated ion channels. As mentioned before, the methods of the present invention also allow modeling inhibitors for the non-specific binding site of ligand gated ion channels.

In addition, it is possible to predict and create mutants and chimeras of AChBP with modified assembly behaviour, modified ligand binding behavior such as with increased resemblance of the binding site to the acetylcholine receptor subtype on the primary binding site and generally with increased resemblance to particular ligand-gated ion channels in activity and conformational changes. In view of the closest relationship between AChBP and the acetylcholine receptor it is particular preferred to create mutants and chimeras with increased resemblance of the binding site to the acetylcholine receptor subtype on the secondary binding site. However, the prediction and creation of mutants and chimeras with increased resemblance of the binding site to other ligand gated ion channels subtype on the primary binding site or on the secondary binding site are envisaged as well.

These and other embodiments are disclosed and encompassed by the description and Examples of the present invention. Further literature concerning any one of the antibodies, methods, uses and compounds to be employed in accordance with the present invention may be retrieved from public libraries and databases, using for example electronic devices. For example the public database "Medline" may be utilized which is available on the Internet, for example under http://www.ncbi.nlm.nih.gov/PubMed/medline.html. Further databases and addresses, such as http://www.ncbi.nlm.nih.gov/, http://www.infobiogen.fr/, http://www.fmi.ch/biology/research_tools.html, http://www.tigr.org/, are known to the person skilled in the art and can also be obtained using, e.g., http://www.lycos.com.

An overview of patent information in biotechnology and a survey of relevant sources of patent information useful for retrospective searching and for current awareness is given in Berks, TIBTECH 12 (1994), 352-364.

This disclosure may best be understood in conjunction with the accompanying drawings, incorporated herein by references. Furthermore, a better understanding of the present invention and of its many advantages will be had from the following examples, given by way of illustration and which are not intended as limiting.

Unless stated otherwise in the examples, all recombinant DNA techniques are performed according to protocols as described in Sambrook et al. (1989), Molecular Cloning : A Laboratory Manual. Cold Spring Harbor Laboratory Press, NY or in Volumes 1 and 2 of Ausubel et al. (1994), Current Protocols in Molecular Biology, Current Protocols. Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfase (1993) by R.D.D. Croy, jointly published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK).

Brief description of the drawings

Figure 1: Clustal X (1.8) multiple sequence alignment of AChBP amino acid sequences. The AChBP alignment was made using "ClustalX_1.8" (Thompson et al., Nucleic Acids Research 24 (1997), 4876-4882. The subsequent alignment was further processed using "Genedoc" version 2.5.000 (Nicholas et al. (1997) Genedoc a tool for editing and annotating multiple sequence alignments). Identical amino acids are indicated with "*", equivalent amino acid with ":", and similar amino acids with ".". Glycosylation sites are Asn 66 for L-AChBP and Asn 21 and 26 for B-AChBP in the amino acid sequence of the respective mature AChBP SEQ ID No. 2 and 4, and 6 and 8, respectively.

Figure 2: Hydrophobicity plots of the mature AChBP amino acid sequences. The B&L-AChBP hydrophobicity plots were made using "Protein sequence analyses" according to the method described in Kyte and Doolite (J. Mol. Biol. 157 (1982), 105-132). **2A:** L-AChBP_T1 (SEQ ID No. 2), **2B:** L-AChBP_T2 (SEQ ID No. 4), **2C:** B-AChBP_T1 (SEQ ID No. 6), **2D:** B-AChBP_T2 (SEQ ID No. 8).

Figure 3: Clustal X (1.8) multiple sequence alignment of AChBP amino acid sequences with the amino acid sequences of the ligand-binding domains of the ligand-gated receptors nAChR-α7, $GABA_AR$-β1, 5-HT3R and GlyR-α1. Sequence alignment and processing was performed as described for Figure 1. The accession numbers of the amino acid sequences used for the alignment are as follows: Human alpha1: Human alpha7: Y08420; Human 5HT3: CAA06442; Human GlyR_alpha1: S12382; Human $GABA_A$_b1: NP_000797. A similar sequence alignment can be performed with the corresponding rat sequences (ratnAChRa7_Q05941, rat5HT3R_P35563, ratGABARb1_P15431, ratGlyRa1_p24524) which will give substantially similar if not identical results.

Figure 4: Clustal X (1.8) multiple sequence alignment of AChBP amino acid sequences with the amino acid sequences of nAChRs. Sequence alignment and processing was performed as described for Figure 1. The accession numbers of the amino acid sequences used for the alignment are as follows: Human alpha1: ACHUA1; Human alpha2: AAG23253; Human alpha3: A53956; Human alpha4: P43681; Human alpha5: P30532; Human alpha6: Q15825; Human alpha7: Y08420; Human alpha9: CAB65091. A similar sequence alignment can be performed with the corresponding rat sequences (ratnAChRa7_Q05941, rnAChRa9_P43144, rnAChR2_P1238, rnAChRa3_P04757, rnAChRa4_P09483) which will give substantially similar if not identical results.

Figure 5: Clustal X (1.8) multiple sequence alignment of AChBP amino acid sequences with the amino acid sequences of nAChRs alpha 1 and 7. Sequence alignment and processing was performed as described for Figure 1. The accession numbers of the amino acid sequences used for the alignment are as follows: Human alpha1: ACHUA1; Human alpha7: Y08420. A similar sequence alignment can be performed with

the corresponding rat sequence ratnAChRa7_Q05941 which will give substantially similar if not identical results.

Figure 6: The pentameric structure of AChBP. **a** In this schematic representation each monomer has a different grey level. Subunits are labeled anti-clockwise, with A-B, B-C, C-D, D-E and E-A forming the plus and minus interface side, with the principal and complementary ligand-binding sites respectively (ball-and-stick representation). **b** Viewing the AChBP pentamer perpendicular to the five-fold axis. The equatorially located ligand-binding site (ball-and-stick representation) is highlighted only in the A (light) and B (dark) interface.

Figure 7: The AChBP monomer. Ribbon representation of the AChBP monomer. The secondary structure starting from the N-terminus (top) towards the C-terminus (bottom). The monomer is viewed towards the center of the pentamer. In the nAChR, the top would correspond to the N-terminus of the ligand binding domain, pointing towards the synaptic cleft, while the C-terminus would be entering the membrane at the bottom, continuing into the transmembrane domain. The AChBP monomer is built up mainly of ß-strands, except for an N-terminal ⟨-helix. It contains 14 ß-strands that are organized in the two antiparallel ß-sheets, with an immunoglobulin topology. However, in contrast to the classical immunoglobulin fold, the AChBP ß-sheets are rotated against each other, forming a small pocket, as visible in Figure 6.

Figure 8: The ligand-binding site at dimer interface. Ribbon representation of two neighboring AChBP monomers. Monomer A is shown in grey and monomer B in dark grey. The ligand-binding site is located at the interface between two monomers. As predicted for the nAChRs, the acetylcholine binding site in AChBP occurs at the interface between two neighboring subunits. Similar to the model proposed for the nAChRs, the ligand-binding site is asymmetric, formed mainly by aromatic residues. Residues from mature AChBP monomer A (TyrA89, TrpA143, TyrA185, CysA187, CysA188 and TyrA192) form the principal component, while residue TrpB53 from monomer B

creates the complementary part of the ligand-binding site. There are five identical ligand-binding sites in the AChBP pentamer, similar to the homomeric α7 neuronal receptor.

Figure 9: The ligand binding site. Stereo figure showing the ligand binding site in AChBP, at the interface of two monomers. Residues from mature AChBP monomer A (TyrA89, TrpA143, TyrA185, CysA187, CysA188 and TyrA192) form the principal component, while residue TrpB53 from monomer B creates the complementary part of the ligand-binding site with with additional residues ArgB104, LeuB112 and MetB114. There are five identical ligand-binding sites in the AChBP pentamer, similar to the homomeric α7 neuronal receptor.

Figure 10: Multiple sequence alignment of AChBP amino acid sequences with indication of secondary structure and solvent accessibility derived from the crystal structure. Alignment of the four molluscan AChBP sequences, with secondary structure and solvent accessibility of the Lymnea stagnalis AChBP-1 indicated from the crystal structure. The Figure was prepared with ESPript (Gouet et al., Bioinformatics. 15 (1999), 305-308), using DSSP (Kabsch and Sander, Biopolymers. 22 (1983), 2577-2637). Under the alignment the solvent accessibility is indicated, white most buried, dark blue most exposed, according to ESPript defaults (blue A> 0.4, cyan 0.1<A<0.4, white A<0.1).

Figure 11: Sequence alignment of AChBP with LGICs. The alignment shows only the N-terminal domain of the LGIC subunits and is based on a multi-sequence alignment of 92 full-length LGIC sequences. Abbreviations used, H and Tca, stand for human and *Torpedo californica*. Secondary structure elements (α:α-helix, β: β-strand, η: 3_{10}-helix) are indicated above the sequence, in accordance with Fig 12a. AChBP shares 23% sequence identity with the ligand-binding domain of human α_7. The LGIC conserved residues (bold, grey background) are displayed. Beginning and end of the Cys-loop are indicated by a "*". Nicotinic receptor ligand-binding residues on the principal and complementary side are indicated.

Figure 12: Overview of the AChBP monomer structure. **a** Stereo representation of the AChBP monomer as viewed from outside the pentameric ring. Disulfide bridges are indicated in ball-and-stick representation. In a complete ion-channel the N-terminus would be pointing towards the synaptic cleft, while the C-terminus would enter the membrane at the bottom, continuing into the first transmembrane domain. **b** Topology diagram of the AChBP monomer. For comparison with Ig-folds the strands have been labeled a-g, showing the additional strand (b') and hairpin (f'-f"). In this structure, strands have been labeled β1-β10 with loops (or turns) L1-L10 preceding each strand with the same number. The β5 strand is broken (β5-β5') with internal loop L5', β6 also has a small break, but is shown continuously; (see Fig. 11). The precise beginnings and ends of strands may change slightly with increasing resolution, but the topology seen here will be highly conserved across the entire family of LGICs.

Figure 13: The ligand-binding site. **a** Stereo representation of the ligand-binding site in ball-and-stick representation, showing the contribution of the principal A (TyrA89/α_1Tyr93), B (TrpA143/α_1Trp149) and C (TyrA185/α_1Tyr190, CysA187/α_1Cys192, CysA188/α_1Cys193, TyrA192 /α_1Tyr198) and the complementary D (TrpB53/γTrp55, GlnB55/γGlu57) , E (ArgB104/γLeu109, ValB106/γTyr111, LeuB112/γTyr117, MetB114 /γLeu119) and F (TyrB164) 'loops'. **b** Stereo view of the electron density map displaying a HEPES buffer molecule in the ligand-binding site. This experimental density (contoured at 1 σ) is derived from cross-crystal averaging. **c** Location of the principal ligand-binding residues on the monomer. **d** Location of the complementary ligand-binding residues on the monomer. (orientation as in Figure 6b)

Figure 14: Dimer interface **a** Stereo figure of the dimer interface. Representation of the interface residues (ball-and-stick) on a schematic secondary structure figure. The figure shows the plus face of subunit A and the minus minus face of subunit B **b** Dimer interface interactions. Note that due to the low conservation of these interfaces (Fig. 11) the actual interactions will not be conserved in any LGIC interface, but that in all receptors the topological regions are likely to form the interface.

Figure 15: Conservation in the LGIC superfamily. Conserved residues are indicated on the top, middle and bottom respectively on the monomer as viewed from the central pore. The hydrophilic conserved residues are indicated in dark. Conserved residues are indicated as viewed from the central pore. Hydrophobic Cluster I: residues 6, 10, 63, 65, 71, 81, 105, 111; Cluster II: residues 20, 27, 29, 31, 58, 82, 84, 86, 140, 150, 152, 195; Cluster III: residues 33, 35, 38, 41, 48, 52, 125, 138, 171, 173, 199, 201. The hydrophilic conserved residues: Asp60, Asp85, Asn90, Gly109, Cys123, Cys136, Lys203. Conserved residues in the ligand binding site: 106, 145, 192. These three and Lys203 are the only conserved residues without structural role in the monomer. Note how very few conserved residues are at the surface. Within the LGIC family the Cys-loop residues are also highly conserved; see bottom, left.

EXAMPLES

EXAMPLE 1: Isolation of Lymnaea AChBP from the CNS, determination of mass and N-terminal protein sequence

Isolation: 80 CNS of Lymnaea were homogenized in lysis buffer (PBS [16 mM Na_2HPO_4, 4 mM NaH_2PO_4, pH 7.4; 150 mM NaCl] 0.5% Nonidet P-40; 0.1% triton, 0.2% tween-20) containing 1 ug/ml aprotinin, 10 ug/ml benzamidine, 0.5 ug/ml leupeptin, 24 ug/ml pefabloc. The CNS lysate was cleared by triplicate centrifugation at 12,000x g for 5 min. Streptavidin-coated magnetic beads (Dynal, Oslo), 5 mg, were saturated with α-bungarotoxin conjugated to Biotin (4 ug) (Molecular Probes, Oxford, UK). These beads were washed in PBS to remove excess α-bungarotoxin, then added to the cleared CNS lysate, and incubated for 1 h. After this, beads were washed 3 times in PBS to remove unbound protein. A control reaction without α-bungarotoxin was performed. Proteins bound to α-bungarotoxin were allowed to elute off in 10 µl of PBS containing 10-4 M nicotine for 1h.

Mass determination: The eluent was separated on a microcolumn LC system was similar to that described previously (Hsieh et al.; Anal. Chem. 70; 1998; 1847-1852). A commercial syringe pump (Perkin-Elmer /ABI, model 140B) was used to deliver a flow rate of 20 µl /min to the column. After loading of sample to the column the flow rate was dropped to 10 µl /min. The eluent was then switched from 0.2% acetic acid to 0.2% acetic acid/ 60% acetonitril in 1 min. Electrospray mass spectra in MS mode were acquired on a Micromass Q-TOF quadropole time-of-flight mass spectrometer equipped with a Z-spray atmospheric pressure ionization source.

Protein sequence analysis: For sequence analysis α-bungarotoxin binding protein was extracted using the same procedure, now followed by SDS-PAGE and Western Blotting on PDVF membrane. Sequence analysis was performed with Edman degradation of the 24 kDa blotted protein (apparent MW) using a protein sequencer (ABI, Perkin Elmer).

EXAMPLE 2: Cloning the Lymnaea AChBP cDNA sequence: PCR and screening of a cDNA library

PCR cloning: A degenerate oligonucleotide was synthesized based on the amino acid sequence LDRADILYNI (SEQ ID No. 10), residues 1-10, of AChBP, (5'-CGGATCCGA(TC)(AC)GIGC(GATC)GA(TC)AT(ATC)(TC)T(GATC)TA(TC)AA(TC)AT-3'; SEQ ID No. 11), containing a BamHI restriction site, and used in combination with a primer on the lZAPII lambda vector. PCR was performed on a lZAP II cDNA

library of the Lymnaea CNS, in a 100 µl reaction volume with 1.0 unit of Super Taq DNA polymerase (Boehringer Mannheim, Germany) in a DNA thermal cycler (Perkin-Elmer Cetus, CT) using 45 cycles of (94 °C, 20 sec; 53 °C, 30 sec; and 72 °C, 1 min. Amplified cDNA was digested with *Bam*HI and *Eco*RI, separated on agarose gel, and a product of ~900 bp was cloned and sequenced.

Library screening: Approximately 20,000 clones of the amplified lambda ZAP II CNS cDNA library were plated at a density of 10^5 pfu/400 cm^2 and absorbed to charged Nylon membranes (Boehringer Mannheim, Germany). The AChBP PCR product was used as a random primed probe, labeled with [alfa^{32}P]dATP (specific activity >10^9 cpm/mg). Membranes were hybridized in 6x SSC (1x SSC: 0.15 M NaCl and 0.015 M Na-citrate), 0.2% SDS, 5x Denhardts and 10 ug/ml herring sperm DNA at 65 °C for 18 h. The filters were washed in 0.2x SSC, 0.2% SDS, at 65 °C for 30 min, and autoradiographed. Four individual cDNA clones were *in vivo* excised, and sequenced using dideoxy chain termination in both orientations. Two types of sequence were obtained, named L-AChBP_T1 and L-AChBP_T2. The signal sequences were determined with "SMART", Simple Modular Architectur Research Tool (V3.1); see Schultz et al., Proc. natl. Acad. Sci. USA 95 (1998), 5857-5864 and Nucleic Acids Res. 28 (2000), 231-234. In case of L-AChBP_T1 (SEQ ID No. 2) the prediction could experimentally be confirmed.

EXAMPLE 3: Lymnaea AChBP-related sequences: cloning of the Bulinus truncatus cDNAs

Total RNA was isolated from Bulinus brain ganglia (CNS), and reverse transcribed into hexanucleotide primed cDNA. Two degenerate oligonucleotides, directed to the Lymnaea AChBP_T1 sequence, forward primer: 5'-GCGAATTCGAYACIGARWSIGGNGCNACNTG-3' (SEQ ID No. 12), reverse primer: 5'-GCGAAGCTTCRTCYTCRTAIGCYTCNGCRCARC-3' (SEQ ID No. 13), were used to amplify AChBP-related sequences. PCR was performed on one animal equivalent of CNS cDNA using 150 pmole of each primer under standard conditions for 45 cycles (94'C, 20 sec; 54' C, 30 sec; 72 'C, 1 min). Amplified cDNA was EcoRI/HindIII digested, cloned into EcoRI/HindIII digested pBluescript, and sequenced. The ORFs of the obtained sequences showed a Bulinus AChBP, sequence-related to Lymnaea AChBP, named B-AChBP_T1. This partial cDNA was used to screen a Bulinus brain cDNA library using the same hybridization protocol as described for the cloning of the Lymnaea cDNAs, and yielded two cDNA clones, encoding B-AChBP_T1 and B-AChBP_T2. Sequencing of the cDNAs was performed in both orientations.

EXAMPLE 4: The production of L-AChBP-T1 and -T2 and B-AChBP-T1 and -T2 in the yeast Pichia pastoris and functional characterization

Production of recombinant AChBP:

In order to produce L-AChBP_T1 and T2 and B-AChBP_T1 and T2 as recombinant proteins in the Pichia pastoris expression system (Pichia Expression Kit version 3.0, Invitrogen), the DNA sequence encoding the mature form of these proteins (see sequence files) was cloned into the pPIC9 expression vector (Invitrogen). The mature sequences of L-AChBP_T1, T2 and B-AChBP_T1 and T2 were PCR amplified (using Pfu-taq DNA polymerase (Stratagene) in order to avoid introduction of errors into the sequence due to PCR) and restriction sites were added to the primers to allow rapid pPIC9 compatible cloning. The amplified sequence of mature AChBP L-AChBP_T1 was EcoRI inserted into pPIC9, whereas L-AChBP_T2 and B-AChBP_T1 and T2 were XhoI/EcoRI inserted into pPIC9 (the alpha-mating factor cleavage site was fully reconstructed after XhoI digestion).

Constructs with and without an additional C-terminal His-tag (SRGHHHHHH (SEQ ID No. 14) in the case of L-AChBP_T1, EFKDDDDKHHHHHH (SEQ ID No. 15) otherwise) were generated for each of the AChBP (sub)types. The AChBP/pPIC9 constructs were amplified in E. coli DH5αF and isolated and purified using the plasmid Maxi Kit (Qiagen). Due to the engineered cleavage site at the N-terminus of the amino acid sequence four additional amino acids (EAEA, SEQ ID No. 16) will precede the N-terminus of the original mature protein. Prior to transfection into Pichia pastoris the constructs were linearised (for protocol see supplier's manual; Pichia Expression Kit version 3.0, Invitrogen) and subsequently purified by phenol/chloroform extraction, and ethanol precipitation. Approximately 5 µg of each of the linearised constructs was transformed into freshly prepared electro-competent Pichia pastoris cells and plated onto MD plates (for protocol see supplier's manual; Pichia Expression Kit version 3.0, Invitrogen corporation). Electrocompetent Pichia pastoris cells were aquired according to the protocol provided by Invitrogen. Plates were incubated at 30°C until the appearance of Pichia colonies, which were subsequently analysed for the presence of the correct insert by PCR amplification (for protocol see supplier's manual; Pichia Expression Kit version 3.0, Invitrogen). Colonies containing an homologous recombination with the Pichia genome, carrying the AChBP sequence, were grown in 25 ml of BMGY for 1-2 days (30°C; rotation at 250rpm), after which the cells were centrifuged (10 min., 1500g) and the cell pellet was resuspended into 10 ml of BMMY. Growth (30°C, 250rpm) was continued for an

additional 4 days (day 3-6), during which the expression of AChBP was induced by the addition of 100% methanol (1% of total culture volume) once every 24 hours. At day seven the culture was centrifuged (15 min.; 2000g; 4°C) and the medium was collected. The AChBP expression level of the various cultures was determined by the analyses of a fraction of the collected medium with SDS-polyacrylamide gel electrophoresis (see suppliers manual; Pichia Expression Kit version 3.0, Invitrogen). The cultures that yielded the highest level of AChBP expression were selected and stored as glycerol stocks.

Recombinant AChBP that contained a C-terminal His-tag was isolated and purified from the Picha pastoris medium using Talon metal affinity resin (according to protocol as described within the user manual; Clontech laboratories Inc.). The protein concentration was subsequently analysed using SDS-polyacrylamide gel electrophoresis and reference marker proteins. Polyclonal antibodies have been raised succesfully to the recombinant L-AChBP_T1 and B-AChBP_T1 proteins in Balb-C mice. Immune-sera were obtained without crosslinking of the proteins.

Binding characteristics of AChBP:

First the binding curve of α-Bungarotoxin to His-tagged AChBP was determined, and an affinity of 3.5 nM was calculated. Using α-Bungarotoxin in a competitive binding assay ligands of several types of ligand-gated ion channels were then tested on His-tagged AChBP, i.e., ACh, serotonin, GABA, glycine, and glutamate. Both ACh and serotonin did compete with α-Bungarotoxin binding at 4.2 mM and 269 mM, IC50s respectively. GABA, Glycine and glutamate did not compete for binding with α-Bungarotoxin. Thus, as predicted by the primary sequence and by subunit structure also the ligand-binding characteristics of AChBP resembled that of a nAChR.

In a second series of competitive binding assays the ligand binding characteristics of AChBP were studied in more detail, now using various agonists and antagonists of the AChRs. Nicotine a classical agonist of the nAChRs, is a high affinity ligand of His-tagged AChBP (IC50 98 nM). Epibatidine, a high affinity agonist of the nAChRs, also binds with high affinity to His-tagged AChBP (IC50 1.4 nM), which is even higher than the 58 pM affinity of epibatidine reported for the nAChR (Badio, Mol. Pharmacol. 45 (1994), 563-569). Other cholinergic agonists bind with a lower affinity e.g., decamethonium, carbachol, and choline respectively with IC50s of 4.1 μM, 43 μM. and 190 μM. Summary of affinities indicated in Table 2.

Table 2

	IC50 (μM)	nHill		IC50 (μM)	nHill
serotonin	269 ± 67	0.65 ± 0.03	α-cobratoxin	16.2 ± 0.1	4.08 ± 0.30
choline	190 ± 32	0.91 ± 0.20	atropine	5.25 ± 0.49	1.91 ± 0.23
carbachol	43 ± 2.7	0.67 ± 0.05	decamethonium	4.1 ± 0.3	1.13 ± 0.09
acetylcholine	4.2 ± 1.1	0.72 ± 0.09	physostigmine	1.25 ± 0.04	0.66 ± 0.07
nicotine	0.098 ± 0.025	0.78 ± 0.05	d-tubocurarine	0.093 ± 0.003	0.83 ± 0.04
epibatidine	0.0014 ± 0.0001	0.66 ± 0.04	gallamine	0.039 ± 0.007	0.71 ± 0.14
			α-bungarotoxin	0.0026 ± 0.0006	0.80 ± 0.18

Competition-binding of typical antagonists of the nAChRs, e.g., tubocurarine and α-Bungarotoxin, have a high affinity for His-tagged AChBP, respectively IC50s of 93 nM and 2.6 nM. The cholinergic antagonist succinylcholine has a very low affinity for His-tagged AChBP (IC50 7.9 mM). Interestingly, also muscarinic receptor antagonists bind to His-tagged AChBP with relatively high affinity, e.g., the muscarinic allosteric modulator gallamine (IC50 39 nM), and the muscarinic antagonist atropine (IC50 5.3 mM). Physotigmine which is a known blocker of acetylcholinesterase and is also an antagonist of the nAChR, binds to His-tagged AChBP with an IC50 of 1.3 mM.

Finally, Bipinnatin-B was tested, a synthetic form of the coral lophotoxin on AChBP (Groebe and Abramson, J. Biol. Chem. 270 (1995), 281-286). Bipinnatin-B is a general blocker of nAChRs and is known to covalently bind to Tyr-190 of the α subunits (Abramson, J. Biol. Chem. 263 (1988), 18568-18573). His-tagged AChBP was incubated with the toxin, and the mass of the protein increased with 430.1 Da, corresponding well to the calculated mass of Bipinnatin-B of 431 Da, indicating that the toxin also binds to Tyr-184 in His-tagged AChBP.

EXAMPLE 5: Expression and purification of recombinant AChBP for crystallization

The AChBP_T1 protein from Lymnea stagnalis (AChBP) was overexpressed in Pichia pastoris GS115 strain using the AOX1 gene expression system from Invitrogen. Media and methods used for AChBP expression are also described in Invitrogen manual Pichia Expression Kit. For long term storage the transformants were grown overnight in YPD medium at 30°C.

YPD or Yeast Extract Peptone Dextrose medium

1% yeast extract (Difco)

2% peptone (Difco)

2% dextrose (glucose) (Merck)

The cells were harvested and suspended in YPD medium containing 15% glycerol at final OD600 of ~50. The cells were frozen in a dry ice/ethanol bath and stored in the freezer (Revco) at –80°C. Normally, the expression of AChBP started with plating the cells from the glycerol stock on MD plate.

MD or Minimal Dextrose Medium

1.34% YNB (yeast nitrogen base w/o amino-acids) (Difco)

4x10-5 % d-biotin (Sigma)

1% dextrose

For plates add 15g of agar (Difco)

The plate was stored in the incubator (Heraeus) for 3-4 days at 30°C. A single colony was picked from the plate and inoculated in 150 ml baffled flask (Nalgene) containing 25 ml of BMGY medium.

BMGY or Buffered Glycerol-complex Medium

1% yeast extract

2% peptone

100 mM potassium phosphate (pH 6.0) (Merck)

1.34% YNB

4x10-5 % d-biotin

1% glycerol (Merck)

The culture was placed into the shaker (New Brunswick) and left to grow overnight rotating at 250 rpm at 30°C. The following day 12.5 ml of the culture was inoculated into 225 ml of BMGY medium in a 1000 ml baffled flask. In order to increase the yield of expressed AChBP a larger number of flasks were used, usually 16. The flasks were placed in the shaker and start-cultures were rotated at 250 rpm at 30°C. After two days the start-cultures were centrifuged for 15 min at 2500 rpm (Sorvall RC3B+, rotor H-6000A) at room temperature. In order to increase the cell mass for bigger protein production, cell pellets of two start-culture flasks were pooled together and resuspended in 200 ml of BMMY medium containing 1% (w/v) casamino acids.

BMMY of Buffered Methanol-complex Medium + 1% casamino acids

1% yeast extract

2% peptone

100 mM potassium phosphate (pH 6.0)

1.34% YNB

4x10-5 % d-biotin

0.5% methanol (Merck)

1% casamino acids (Difco)

The cultures were put back into the shaker (250 rpm, 30°C) and induced for the following 4 days. The concentration of methanol in the medium was kept constant by adding 1% (v/v) methanol to the cultures every 24 hours. After 4 days 100 ml of culture was harvested and the original volume of 200 ml was readjusted by adding fresh BMMY medium with 1% casamino acids. The remaining cultures were induced for another 4 days. The harvested cultures were centrifuged for 15 min at 4000 rpm (Sorvall RC3B+, rotor H-6000A) and the cell pellet was discarded. The supernatant was first filtered through a 0.22 µm filter (Millipore) to remove any remaining cells and it was concentrated using a Minitan system (Waters/Millipore) with 30kDa cutoff filter (Waters/Millipore). Both the filtration and concentration and were performed at 4°C. Finally, centrifugation at 16000 rpm was done (Sorvall RC5C, rotor SS-34) in order to remove any debris left after the first two steps. The final volume of concentrated sample was ~80 ml and it was dialyzed overnight against 2 x 5 l (20 mM Tris [pH 8.0], 150 mM NaCl and 0.02% NaN_3) using 15kDa cutoff dialysis membrane (Spectra/Por) at 4°C. The dialyzed protein solution (~100 ml) was loaded onto an anion-exchange column (POROS 50 HQ, Pharmacia, column volume 8 ml). After the initial wash step of ~15 column volumes using loading buffer, a salt gradient of 30 column volumes was run from 150 mM to 1000 mM NaCl. Both solutions contained also 20 mM Tris (pH 8.0) and 0.02% NaN_3. The peak of interest eluted at ~300 mM NaCl (conductivity range 16-24 mS/cm). The presence of AChBP was checked by Bio-Rad Protein Assay (Bio-Rad) and SDS-PAGE and the fractions of interested were pooled and concentrated using a Centriprep with a 30kDa cutoff membrane (Amicon). The concentrated sample (volume of 5 ml) was loaded onto a gel filtration column (Superdex 200 HR 16/60, Pharmacia, column volume 120 ml) using 20mM Tris (pH 8.0), 150 mM NaCl and 0.02% NaN_3. The protein eluted starting from 60 to 71 ml with peak at ~66 ml. The final purification step of the protein was done on an anion-exchange column (MonoQ HR10/10, Pharmacia, column volume 6 ml). The protein was loaded onto the column in the same buffer as eluted from the gel filtration column. The salt gradient used for the column was the identical to the one used for the POROS 50 HQ column. The fractions in the conductivity range 25-27.5 mS/cm were pooled together and dialyzed against buffer containing 50 mM HEPES (pH 7.0) and 0.02% NaN_3. The protein was concentrated up to ~20 mg/ml using a Centricon with a 30kDa cutoff membrane (Amicon). The total yield was about 2 mg purified

protein per liter of expressed medium. The concentrated protein was stored at 4°C and used for crystallization experiments and biochemical characterization. N-terminal sequencing revealed the presence of EAEAYVEF residues that are part of the pIC9-encoded signal sequence, before residue 2. The experimental mass was determined to be 26544 Da (MALDI), which is ~2kDa more than calculated mass based on amino-acid sequence (24649 Da). The difference is assigned to glycosylation of AChBP at position Asn66 in the mature sequence, confirmed by deglycosylation experiments with N-glycosidase F (Boehringer).

The purification of the first harvest was done separately from the full harvest. They were pooled together prior to the last purification step (anion-exchange chromatography step on MonoQ column). All above mentioned chromatography columns were mounted on an FPLC system (Pharmacia) controlled by the UNICORN system (Pharmacia). All solutions used in the FPLC system were prepared with MilliQ UF+ water, filtered through 0.22 µm filter (Millipore) and degassed.

EXAMPLE 6: Crystallization of the AChBP

All the crystallization experiments were done by vapor diffusion technique in a hanging drop mode using 12 well tray (Nelipak) and siliconized cover slides (Hampton Research). Trays were placed in a sandwich box (Semadeni) and stored at 19°C temperature conditioned room. The initial crystallization attempts were performed using Hampton Crystal Screen I and II (Hampton Research). Drops contained 2 µl of protein (10 mg/ml in 50 mM HEPES [pH 7.0] and 0.02% NaN_3) and 2 µl of reservoir solution. From the first screen it became clear that AChBP makes crystalline precipitate in the presence of $CaCl_2$ salt. A more detailed screen was made which produced crystals suitable for X-ray analysis. The AChBP crystals appeared in the following conditions: 9-11% (w/v) PEG 4000 (Hampton Research), 100 mM HEPES (pH 7.0), 50-200 mM $CaCl_2$ x $6H_2O$ and 0.02% NaN_3 or or PEG MME 550 10-18% in the same conditions, with 0.3 mM ZnAcetate as additive. Depending on the batch of the protein used and the $CaCl_2$ concentration three different crystal forms were found: orthorhombic, tetragonal and monoclinic. Both orthorhombic and monoclinic crystal forms are frequently twinned. Orthorhombic rod-like crystals appeared immediately upon setting up the crystallization experiments (in between first few hours) under high [$CaCl_2$]. The size of the crystals varied from 0.05x0.05x0.15 to 0.25x0.25x1.0 mm. The crystals diffract X-ray up to 3 Å resolution and show high degree of mosaicity (~05-1.2°). They have the symmetry of space group $P2_12_12_1$ with cell constants of a= 120.62Å, b=137.01Å, c=161.54Å with 2 pentamer molecules per asymmetric unit. Tetragonal crystals, squared in shape,

grew at lower $CaCl_2$ concentration, reaching 0.2x0.3x0.35 mm in size. The maximal resolution obtained was 2.7 Å with a lower mosaicity (0.5°). They belong to space group $P4_22_12$ space group with cell dimensions of a=b=141.66Å, c=120.83Å with one pentamer molecule per asymmetric unit. The exact crystallization condition for the tetragonal crystal which was used for refinement of the crystal structure: 11.5% (w/v) PEG 4000, 100 mM HEPES (pH 7.0), 150 mM $CaCl_2$ and 0.02% NaN_3. The third crystal form, monoclinic $P2_1$, is very similar in morphology to the orthorhombic crystals with cell dimensions of a=121.1Å, b=162.1Å, c=139.4Å, β=90.13°, containing 4 pentamers per asymmetric unit. This crystals were gave lower resolution data (~ 3.3Å resolution). All three crystal forms were used in the structure determination of AChBP.

The resolution limit of diffraction depended very much on the size of the crystals. And the largest crystals diffracted weakly to ~4Å resolution when exposed to a conventional rotating anode X-ray source. Therefore, the use of synchrotron radiation was critical for the structure determination. The crystals had to be cryo-protected in order to slow down the damage caused by high intensity synchrotron radiation. The cryo-protection of the AChBP crystal was done in multiple steps. The first steps included the stabilization of crystal by adding the 2 µl of mother liquor (equilibrated reservoir solution) to the drop with the crystal. After 5 minutes 3 µl of stabilizing solution was added to the drop. Normally, the stabilizing solution contained slightly higher concentrations (1-5%) of the components of the original crystallization buffer. As protectant glycerol (Merck) was added, increasing the concentration stepwise from 0% to 30% (v/v). For example, the starting solution contained 15% PEG 4000, 100 mM HEPES (pH 7.0), 150 mM $CaCl_2$ and 0.02% NaN_3 and the final solution contained 30% (v/v) glycerol in addition to the components just mentioned. The AChBP crystals do not tolerate drastic increase in the glycerol concentrations therefore a gentle but more time consuming approach has to be adopted. The solution around the crystal has to be stepwise exchanged (usually 5% increase of glycerol concentrations) allowing crystals to equilibrate for at least 5 minutes in each glycerol concentration. Once the crystals were equilibrated in stabilizing solution with 30% glycerol they were flash-cooled in liquid nitrogen or in the cryo-stream. In all three space groups AChBP forms a decamer structure with perfect 52 symmetry, where two pentamers contact each other through a calcium-binding site, at the 'top' of the α1 helix. This binding site (Asp2 and Asp5 from two monomers) is not conserved in the LGIC family. In the tetragonal space group the 2-fold of the decamer coincides with a crystallographic two-fold, which leads to

pseudocentrosymmetric behavior of the phases at low resolution. In solution the AChBP protein acts as pentamer.

Those of skill in the art will appreciate that the aforesaid crystallization conditions can be varied. Such variations may be used alone or in combination, and include final protein (optionally in complex with a ligand) concentrations between 1 mg/ml and 30 mg/ml; all combinations of AChPB/ligand to precipitant ratios; use of citrate concentrations between 0 mM and 200 mM; DTT concentrations between 0 mM and 10 mM; and any concentration of beta-mercaptoethanol; pH ranges between 5.5 and 9.5; PEG concentrations between 5% and 25% (w/v); PEG weights between 2000 and 8000; HEPES concentrations between 5 and 500 mM; use of TRIS or other solutions instead of HEPES, and any concentration or type of detergent; any other type of precipitating agent; any other buffer; any temperature between –50 ºC and 30 ºC; and crystallization of AChBP or complexes thereof by batch, liquid bridge, or dialysis method using these conditions or variations thereof.

EXAMPLE 7: Structure determination

The crystal structure was determined using the multiwave anomalous dispersion (MAD) technique on a Pb derivative, but non-crystallographic symmetry (NCS) averaging was necessary to obtain interpretable electron density. Collection of native data and heavy-atom derivatives were carried out at the synchrotron beam-lines in Grenoble (ESRF/BM14 and ID14) and Hamburg (DESY/BW7A, BW7B and X11). The AChBP orthorhombic crystal was soaked in stabilizing solution containing 5 mM trimethylleadacetate (MePb) for 5 days. Data sets were collected at four different wavelengths (0.9492Å, 0.8610Å, 0.9507Å and 0.9499Å) and data were integrated and reduced using DENZO/SCALEPACK (Otwinowski and Minor (1997) Processing of X-ray diffraction data collected in oscillation mode. In Methods in Enzymology, Volume 276: Macromolecular Crystallography, part A. C.W. Carter and R.M. Sweet, eds. (New York: Academic Press), pp. 307-326). The program SOLVE (Terwilliger (1997) SOLVE: An automated structure solution for MAD and MIR. Edition 1.16) found 5 Pb sites which were situated on the interface between two pentamers. The Pb parameters were refined and phases calculated with SHARP (La Fortelle et al. (1997) Advances in MIR and MAD phasing: Maximum-likelihood refinement in a graphical environment, with SHARP. Proceedings of the CCP4 study weekend). Mean figure of merit (FOM) value for 4 wavelengths was 0.45. Search and optimization of 5-fold NCS operators were done using programs NCS6D and IMP (Kleywegt and Jones (1999) Software for handling macromolecular envelopes. Acta

Crystallo., D55, 941-944). 10-fold averaging using refined NCS operators in conjunction with density modification by DM (Cowtan (1994) DM: An automated procedure for phase improvement by density modification. In Joint CCP4 and ESF-EACBM Newsletter on Protein Crystallography 31, 34-38) yielded an interpretable electron density map. However, some parts of the pentamers were still not clearly defined. Therefore, a second MAD experiment was performed on the monoclinic crystals soaked in 10 mM MePb for 5 days. Data were collected for only two wavelengths, at the Pb peak (0.9479Å) and remote (0.9498Å) wavelength. The processing of the two collected data sets was done with MOSFLM (Leslie (1992) Recent changes to the MOSFLM package for processing film and image plate data. In Joint CCP4 and ESF-EACBM Newsletter on Protein Crystallography, Number 26) and data were scaled with SCALA (CCP4. The CCP4 suite: programs for protein crystallography. Acta Crystallog. D50, 760-763). 10 Pb sites were identified with Solve. The Pb parameters were refined and phases calculated with SHARP in single anomalous dispersion (SAD) mode using data collected at the Pb absorption peak The NCS operators needed for 20-fold averaging were found by NCS6D and improved with IMP. 20-fold averaging and density modification by program DM further improved electron density. The initial model tracing and sequence assignment were done based on the 20-fold averaged electron density with program O (Jones et al., 1991). However, parts of the molecules were not clearly defined. The electron density was further improved doing multi-crystal averaging with DMMULTI (Cowtan, 1994) using amplitudes of tetragonal, orthorhombic and native data sets and experimental phases of the orthorhombic and monoclinic MAD experiments. Initially missing parts became clearly defined and a complete model could be built. The initial atomic model was refined with the program CNS (Brünger et al. (1998) Acta Crystallogr. D 54, 905-921) against a maximum-likelihood target without experimental phases contribution using tetragonal native data which extend to 2.7Å resolution. Refinement included five-fold NCS restraints, an overall anisotropic B factor and bulk solvent correction. The five-fold NCS restraints were released for the parts of the pentamer that clearly do not follow the five-fold symmetry. The current model contains one pentamer of AChBP consisting of 1035 residues, 14 well-ordered solvent molecules, 5 Ca^{2+} ions, 5 Cl^- ions and 5 Hepes molecules, well-ordered solvent molecules and 5 HEPES molecules. The following residues are not well defined in the electron density: -8-0 (part of α-mating S. cerevisiae signal sequence not native to AChBP EAEAYVEF; SEQ ID No. 21), 125-135, 155-165, 186-191 and 206-210.

Electron density is detectable in the ligand-binding site of AChBP. It is presumed that a HEPES molecule could account for this extra electron density based on its chemical properties. HEPES or N-2-Hydroxyethylpiperazine-N'-2-ethanesulfonic acid contains a quaternary ammonium ion similar to ligand such as acetylcholine (ACh) and d-tubocurarine. It has been proposed that the binding of ACh would be mediated by cation-π interaction involving N^+ and π-systems of aromatic residues present in the binding site of nicotinic acetylcholine receptor. Without intending to be bound by theory it is suggested in accordance with the observation of the present invention that the observed HEPES molecule mimics ligand binding analogous to the binding of natural ligands like ACh in the ligand-binding site.

EXAMPLE 8: More detailed description of the structure determined in Example 7

As described in the previous example, the crystal structure of AChBP was solved using weak Pb MAD data in two crystal forms. The electron density map was improved substantially by cross-crystal averaging of three crystal forms with 20, 10 and 5 copies of the monomer in the asymmetric unit respectively (Table 3).

Table 1: Data collection statistics

Data set	λ_1 peak	λ_2 remote	λ_3 infl.	λ_1 peak	λ_2 infl.	Native
Space group	$P2_12_12_1$			$P2_1$		$P4_22_12$
Resol. (Å)	3.3/3.4-3.3			3.0/3.1-3.0		2.7/2.8-2.7
λ (Å)	0.9492	0.8610	0.9507	0.9479	0.9498	0.943
Compl. (%)	99.7/99.7	99.6/99.6	99.7/99.7	99.9/99.9	99.5/99.5	97.8/96.5
Mosaicity (°)	0.62			0.43		0.78
Redundancy	3.7/3.8	3.8/3.9	3.7/3.8	3.5/2.2	3.2/2.0	6.5
R_{merge} (%)	7.7/46.8	7.8/45.2	8.3/55.0	5.9/26.1	6.0/32.9	5.9/67.4
$I/\sigma I$	8.7/1.6	8.4/1.7	8.3/1.4	7.7/2.7	6.8/1.5	27.4/2.3

Phasing	ISO/ANO	ISO/ANO	ISO/ANO	ISO/ANO	ISO/ANO
R_{cullis} (%)	0.74/0.89	n.a./0.92	0.54/0.94	n.a./0.74	0.66/0.77
Phasing power	0.57/1.2	n.a./1.06	2.3/0.91	n.a./1.1	0.37/1.22
FOM (overall)	0.45			0.28	

The structure was refined at 2.7 Å in space group $P4_22_12$, with one AChBP pentamer in the asymmetric unit. Thus, native data (X11) were collected and the Pb-1 data sets (BW7A) at the EMBL/DESY synchrotron in Hamburg and the Pb-2 data sets (BM14) at the ESRF, Grenoble (Table 3). Data were processed with DENZO/SCALEPACK (Otwinowski & Minor, Methods Enzymol. 276, 307-326 1997) (native) or MOSFLM (Leslie, Acta Crystallogr. D. Biol. Crystallogr. 55, 1696-1702, 1999)/SCALA (CCP4) (Pb-1, Pb-2). The Pb sites, located at the interface of two pentamers, were found for both MAD sets by SOLVE (Terwilliger, Acta Crystallogr. 55, 849-861, 1999) and heavy atom parameters were optimized with SHARP (La Fortelle et al., Methods Enzymol. 276, 472-494, 1997). NCS operators were found and refined with NCS6D and IMP (Kleywegt and Jones, SERC Daresbury Laboratory, Warrington, pp. 59-66, 1994). DM-multi (Cowtan, Joint CCP4 and ESF-EACBM Newsletter on Protein Crystallography, 31, 34-38, 1994) multi-crystal averaging used amplitudes of monoclinic, orthorhombic and native (tetragonal) data sets and experimental phases of the orthorhombic and monoclinic MAD experiments. The model was built in O (Jones et al., Acta Crystallogr. A47, 110-119, 1991) and refined with the program CNS (Brünger et al., Acta Crystallogr. D54, 905-921, 1998), against the tetragonal data to 2.7 Å resolution. Refinement included partial 5-fold NCS restraints, an overall anisotropic B factor and bulk solvent correction. The unusual double cysteine Cys187-Cys188 formed a clear disulfide bridge. Because of the limited resolution it was refined with standard parameters. The final model contains 1025 residues of AChBP pentamer, 5 HEPES molecules, 10 Ca^{2+} ions and 15 water molecules. The entire AChBP pentamer is well ordered, except for the N-terminal 7 residues (part of the signal sequence) and the last five C-terminal residues. In addition, the HEPES, the loop region 155-160 and the sugar residues attached to residue Asn66 are not well resolved in the electron density. R.m.s deviations from ideal geometry for bond distances and angles are 0.01 Å and 1.6°, respectively. The sequence alignment was calculated by CLUSTALX (Thompson et al., Nucleic. Acids. Res. 25, 4876-4882,

1997) and the corresponding figure with Espript (Gouet et al., Bioinformatics. 15, 305-308, 1999). Figures 2-5 were done using programs MOLSCRIPT (Kraulis, P.J., J. Appl. Cryst. 24, 946-950, 1991), BOBSCRIPT (Esnouf, Acta Crystallogr. D55, 938-940, 1999) and RASTER3D (Merritt and Bacon, Methods Enzymol. 277, 505-524, 1997). Refinement took place with partial five-fold NCS restraints, resulting in an R-factor of 26.4% (R_{free} = 30%).

The AChBP pentamer:

The AChBP homopentamer, when viewed along the five-fold axis, resembles a windmill toy, with petal-like monomers (Fig. 6a). When viewed perpendicular to the five-fold axis it has a disc-like appearance (Fig. 6b). The overall proportions of the pentamer are ~80x80x62 Å, and the diameter of the central hole is ~18 Å. These dimensions are in good agreement with the *Torpedo* nAChR N-terminal domain EM data (Miyazawa et al., J. Mol. Biol. 288, 765-786, 1999). The only subunit contacts in the AChBP pentamer are dimer interfaces, of which each monomer has two, one called the plus side and one called the minus side. We refer to the A (plus)-B (minus) interface, as example for the five equivalent interfaces AB, BC, CD, DE and EA (Fig 6).

The AChBP monomer:

Each AChBP monomer is a single domain protein, asymmetric in shape, with a size of ~50x21x27 Å (Fig. 12a). It consists of an N-terminal β-helix, two short 3_{10} helices and a core of 10 β-strands forming a β-sandwich. The order of β-strands conforms to a modified immunoglobulin (Ig) topology (Fig. 12b) with an extra β-hairpin (f'-f") and an extra strand (b') (Bork et al., J. Mol. Biol. 242, 309-320, 1994). These additional strands introduce two so-called "Greek key" folding motifs. The Ig-based structure prediction (Le Novère et al., 1999; Corringer et al., Biophys. J. 76, 2329-2345, 1999) agrees well with the AChBP structure, although location of the binding site was missed due to the presence of extra β-strands (Fig. 12b). Compared to the classical Ig-fold, the AChBP β-strands are considerably twisted, with the β-sheets rotated against each other, resulting in two separate hydrophobic cores. Thus the three-dimensional fold does not resemble other Ig-like proteins and comparison to the protein database (Holm and Sander, Nucleic. Acids. Res. 25, 231-234, 1997) did not result in a significant match to any known structure.

Positioning of functional regions:

Couple of regions that are important to receptor function can be localized in the AChBP structure. In muscle type nAChRs the main immunogenic region (MIR), comprising residues $\alpha_1$67-$\alpha_1$76, acts as an epitope in the autoimmune disease myasthenia gravis (Tzartos et al., Mol. Neurobiol. 5, 1-29, 1991). Although the MIR-related region in AChBP (residues 65-72) shows no sequence homology to the α_1-subunit, its location in loop L3 at the top of the pentamer in a highly accessible position agrees well with the expected accessibility for this region. It also fits with EM studies that located the MIR at the distal end of the receptor relative to the membrane (Beroukhim and Unwin, Neuron 15, 323-331, 1995).

On each AChBP monomer, a large cavity that is accessible from the central pore of the pentameric ring can be seen. The cavity is framed at the entrance by β-strands (β3, β4, β5 and β5') (Fig 12a) and is uncharged, mainly hydrophobic, in character. This region probably corresponds to the tunnel framed by twisted β-strands that was observed in the α_1-subunit of *Torpedo* receptor at 4.6 Å resolution (Miyazawa et al., J. Mol. Biol. 288, 765-786, 1999). However, this cavity is not in contact with another large pocket observed at each interface between subunits. These latter pockets are lined by residues shown to be involved in ligand binding in nAChR (Arias, Neurochem. Int. 36, 595-645, 2000; Corringer et al., Annu. Rev. Pharmacol. Toxicol. 40, 431-458, 2000). They are buried from the solvent, and located close to the outside of the pentameric ring. When viewed perpendicular to the five-fold axis they are roughly equatorially positioned, ~30 Å away from the C-termini (Fig. 6b), conforming to the expected location of the *Torpedo* receptor ligand-binding site, as determined by labeling (Fernando Valenzuela et al., Biophys. J. 66, 674-682, 1994) and EM studies (Unwin, J. Mol. Biol. 229, 1101-1124, 1993).

The ligand-binding site:

Each ligand-binding site is found in a cleft formed by a series of loops from the principal face of one subunit and a series of β-strands from the complementary face of an adjacent subunit. It is a large cavity buried by a series of loops from the principal side and by a β-strands from the complementary side (Fig. 13). The principal side on the plus side of the AB interface consists of residues coming from 'loop A' (TyrA89), 'loop B' (TrpA143, A145) and 'loop C' (TyrA185, the double cysteine A187-A188, and TyrA192) (Fig 13c). The complementary part of this binding

site is contributed by monomer B and made of 'loop D' (TrpB53, GlnB55), 'loop E' (ArgB104, ValB106, LeuB112 and MetB114) and 'loop F' (TyrB164) (Fig 13d). In this pocket four of the aromatic residues form the bottom half of the cavity (TyrA89, TyrA185, TyrB164 and TrpB53). The pocket walls are formed by the TyrA192, TrpA143, main chain of A145 Met B114, the side-chain of GlnB55 and the double cysteine (CysA187-CysA188). The hydrophobic parts of ArgB104, ValB106 and LeuB112 form the top of the pocket (Fig 13a).

All residues in the pocket had been successfully identified by photoaffinity labeling and mutagenesis studies (Arias, Neurochem. Int. 36, 595-645, 2000; Corringer et al., Annu. Rev. Pharmacol. Toxicol. 40, 2000). Although the side chain of HisA145 is pointing away from the cavity, its main chain is involved. One residue identified by labeling studies, TrpA82 (α_1Trp86) (Galzi et al., J. Biol. Chem. 265, 10430-10437, 1990; Dennis et al., Biochemistry 27, 2346-2357, 1988) is involved in hydrophobic core formation and located far from the pocket, thus not participating in ligand binding. Otherwise, the AChBP ligand-binding site confirms the available biochemical and mutational data on nAChR completely.

The structure, however, shows for the first time how these residues are positioned with respect to each other and therefore provide a valuable tool for drug design as described in the above description of the present invention.

All observed residues are conserved between known nicotinic ligand-binding subunits except the 'loop F' TyrB164 residue. The 'loop F' region has an unusual conformation, but since it is relatively weakly resolved, its precise analysis is difficult. The 'loop F' region is stabilized in the structure by a calcium binding site formed by AspB161, AspB175 and the main chain of B176. This Ca^{2+} ion is structurally important for TyrB164 orientation and could therefore be important for proper ligand binding. The present findings are supported by labeling studies on muscle/*Torpedo* subunits showing that residues homologous to AspB161, γAsp174/δAsp180 play a role in ligand binding (Czajkowski et al., Proc. Natl. Acad. Sci. U.S.A. 90, 6285-6289, 1993; Czajkowski and Karlin, J. Biol. Chem. 270, 3160-3164, 1995; Martin et al., J. Biol. Chem. 271, 13497-13503, 1996). Additionally, calcium binding sites that enhance the response to agonist binding have been identified in the homologous region (residue range 161-172) of neuronal α_7 receptor (Galzi et al., EMBO J. 15, 5824-5832, 1996). The 'loop F' region has low sequence conservation in the nicotinic family (Fig. 11) and in other superfamily members it may well have a different conformation, even to the extent of forming a β-strand that connects the two sheets

into a β-barrel. Such changes could well lead to variations in affinity, *e.g.* by changing the size of the ligand-binding site or its access route.

The most likely access routes to the ligand binding sites are from above or below the double-cysteine-containing 'loop C' (Fig. 13a). This region buries the pocket from the solvent and therefore prevents access from the outside. Access from the central pore has been suggested in the literature (Miyazawa, J. Mol. Biol. 288, 765-786, 1999), but this would require major structural rearrangements at the interface, which makes it less likely.

Ligand binding:

Surprisingly, features of bulky electron density were found that stacked onto Trp143 in each ligand-binding site in the experimental cross-crystal averaged electron density (Fig 13b). Upon consideration we have assigned this to a HEPES (N-2-Hydroxyethylpiperazine-N'-2-ethanesulfonic acid) buffer molecule, that contains a positively charged quaternary ammonium group and therefore has some similarity to known nicotinic receptor ligands. Its EC50 is 100 mM, indicating that its binding under crystallization conditions (100-150 mM) is possible. Although HEPES molecule does not make any specific contacts with the protein, it stacks with its quaternary ammonium onto Trp143, making cation-π interactions as expected for nicotinic agonists (Dougherty, Science 271, 163-168, 1996) (Fig. 13b). However, due to limited resolution of the present data and probable low occupancy, the precise orientation of the HEPES molecule should be taken with some degree of reservation.

It has been suggested (Changeux and Edelstein, Neuron 21, 959-980, 1998) that the ligand-binding site of nAChRs could be similar to that of acetylcholinesterase (AChE). Although the size of the binding site is roughly similar in AChBP and AChE, the observed arrangement of aromatic residues is quite different. However, the stacking of the quaternary ammonium of HEPES, as far as it has been refined in the current AChBP structure, is similar to that of the quaternary ammonium of the decamezonium in AChE on the Trp84 residue (Harel et al., Proc. Natl. Acad. Sci. U.S.A. 90, 9031-9035, 1993).

Subunit arrangement:

From the location of the ligand-binding site conclusions can be drawn about the relative arrangement of subunits in the *Torpedo* and muscle receptors. It has been suggested that the $\alpha_1\gamma$ and $\alpha_1\delta$ interfaces occur in a clockwise $\alpha_1\gamma\alpha_1\delta\beta_1$ arrangement

when looking towards the membrane (Machold et al., Eur. J. Biochem. 234, 427-430, 1995). Such a clockwise arrangement disagrees with the structure determined in accordance with the present invention, because the relative arrangement of the principal binding site and its complementary partner is anticlockwise when looking towards the 'bottom' (membrane) side of the pentamer (Fig. 6).

Pentamer interface:

The subunit interface consists on the plus side entirely of loop regions (L1, L2, L4, L5, L7, L8 and L10), whereas the minus side mostly presents secondary structure elements to the interface (α1, β1, β2, β3, β5, β6 and L9) (Fig. 14). Several residues are important for both ligand-binding and pentamer formation. The interface buries a considerably surface area (2700 $Å^2$), with a mainly uncharged character including only a single bifurcated salt bridge (GluA149-ArgB3 and ArgB104). Most intriguing about the interface residues is the lack of conservation of these particular residues in the entire superfamily, not only with AChBP, but also amongst each other (Fig. 11). These changes involve major changes in character, including changes from hydrophobic to charged. Even when a residue is conserved in any particular subunit, its expected counterpart is missing (either in the same subunit, as in the α_7 homopentamers, or in contacts such as muscle $\alpha_1\delta$ or $\alpha_1\gamma$ or neuronal $\alpha_4\beta_2$) with the sole exception of the ligand-binding site. The high level of structural conservation however, determines involvement of the same topological regions in these contacts in all family members (Fig 14b). This indicates that shape complementarity must play a major role in determining the conservation of the pentamer structure. It also indicates that different combinations of subunits will have different interfaces, creating variations in the precise allosteric contacts and movements in the various subclasses of these Ion channels.

Ligand-gated ion channels:

The lack of conservation of the interface residues seems a general feature in the superfamily of LGICs, as the residues that form the interface are among the least conserved regions of the domains (Fig. 11). Apparently pentamer formation does not impose very stringent evolutionary requirements in this case. However, there is clear sequence conservation within the superfamily (Fig. 11) and it is interesting to analyze this in the light of the structure.

In the AChBP monomer structure the conserved hydrophobic residues can be grouped into three clusters (Fig. 15). In AChBP, as in other proteins with Ig-like fold, the packing of the β-sheets is promoted mainly by hydrophobic and to a lesser extent by electrostatic interactions. The first cluster is involved in packing of the N-terminal helix α1 against the main framework of the monomer and it involves residues 6, 10, 63, 65, 71, 81, 105 and 111. The second cluster, comprising residues 20, 27, 29, 31, 58, 82, 84, 86, 140, 150, 152 and 195, is situated in the upper half of the β-core region. The third cluster, including residues 33, 35, 38, 41, 48, 52, 125, 138, 171, 173, 199 and 201, is located at the lower end of the structure (Fig 15). The only non-hydrophobic residues that are highly conserved in the superfamily are Asp60, Asp85, Asn90 and Gly109. Asp60 and Gly109 are involved stabilizing the turns of a Greek key motif connecting strands β3, β5, β6 and β2, where Asp60 stabilizes the N-terminus of a small 3_{10} helix and Gly109 enables tight turn formation. Conserved residues Asp85 and Asn90 are involved in packing of the β-sheets. Asp85 forms hydrogen bonds to the highly conserved Ser142 and Thr144 and residue Asn90 brings together the main-chain oxygens of Ser122 and Arg137, enabling disulfide bond formation of the nearby absolutely conserved disulfide bond (123-136). This disulphide bond is topologically equivalent to so-called 'tyrosine cornerstone' (Hemmingsen et al., Protein Sci. 3, 1927-1937, 1994), which links the two β-sheets together in Ig-like proteins. This explains why in the *Torpedo* receptor the Cys128-Cys142 bond is important for both preservation of subunit conformational stability (Mishina et al., Nature 313, 364-369, 1985) and complete nAChR assembly (Green & Wanamaker, J. Neurosci. 18, 5555-5564, 1998). Since the observed overall structural conservation is high, it is clear that all LGIC N-terminal domains will have the same three-dimensional structure.

In contrast to the above residues, the Cys-loop is a highly conserved hydrophobic region in the LGIC family but presents a totally different character in AChBP (Fig. 11).

In AChBP, this loop is hydrophilic and is found at the bottom (membrane) side of the protein, at the dimer interface. This location and its hydrophobicity in the LGIC family implies that this loop could interact with the membrane or with the transmembrane region of the receptors, functions that are absent in AChBP.

Since all ligand gated ion channels have intrinsically the same function, opening of a membrane pore, it is likely that the conserved regions of the protein determine this function. That also indicates that it is unlikely that the interface of the pentamer has a major role in opening the channel. It is possible that the conserved Cys-loop is

directly involved in transmitting this kind of information to the membrane part of the LGICs. Another option is that large structural changes in the β-sheet regions play a role in opening the channel. Indeed, the movement observed at 9 Å for *Torpedo* nAChR upon agonist binding (Unwin, Nature 373, 37-43, 1995), fits well with such a suggestion. In accordance with the present invention a twisted β-sandwich would be observed, with two distinct hydrophobic cores and it is entirely possible that these cores move with respect to each other upon ligand binding. The effect of such movements will then be modulated by the varying subunit interfaces in the different subtypes of the receptor, allowing intricate specificity in the neuronal signal transmission.

EXAMPLE 9: Ligand-binding crystallization studies

AChBP was cocrystallized in complex with α-bungarotoxin (αBTX, Sigma). Prior to the crystallization experiments the stability of the complex has been investigated. Using gel-filtration chromatography (Superdex 200 HR 10/30, Pharmacia, column volume 24 ml) it has been found that it is possible to purify stable complex between AChBP and αBTX. The gel-filtration run was performed using 20 mM Tris (pH 8.0), 150 mM NaCl and 0.02% NaN_3. The stability of the complex was also confirmed with native PAGE. The crystallization experiments were done based on the same set of conditions found to work for AChBP alone; see Example 6. A small screen was set up with different precipitant concentrations and various AChBP:α BTX concentrations. Tiny crystals appeared in the conditions containing 10-12% PEG 4000, 100 mM HEPES (pH 7.0), 20-80 mM $CaCl_2$ and 0.02% NaN_3. The best looking crystals grew under above mentioned conditions when AChBP: ⟨BTX were mixed in 1:10 molar ratio. In order to check if complex indeed crystallized, crystals were thoroughly washed, dissolved in denaturing buffer and checked on SDS-PAGE that clearly showed that they contained both proteins.

In addition, a number of small ligands were bound to AChBP in soaking experiments. These include: B-bippinatin (a synthetic analog of lophotoxin), acetylcholine (ACh, Sigma), d-tubocurarine chloride (Sigma), carbamylcholine chloride (CCh, Sigma), galanthamine hydrobromide (Sigma), epibatidine (Sigma) and nicotine (Sigma). The soaking solutions were made of stabilizing solutions (see Example 6) and together with dissolved ligands (ligands were normally dissolved in 20 mM HEPES [pH 7.0]). The ligand concentrations used were dependent on its binding constants, as determined by ligand-binding studies. The soaking times were different depending on the ligand used. After the soaking step the crystals were flash-cooled in liquid nitrogen.

EXAMPLE 10: Generating human alpha7 nAChR / AChBP chimeras

The chimeric proteins of nAChR subunits and AChBP can be used as tools in the development of novel, nAChR subtype specific ligands. As a first step in developing these tools chimeric proteins have been designed and constructed in which part(s) of the human alpha7 nAChR were grafted into AChBP. Previous studies on the molecular determinants of ligand-binding by the alpha7 nAChR have identified three amino acid domains that compose the primary part of the ligand-binding site, further referred to as "loops A, B, and C". Within each of the three loops amino acid residues are present that are thought to directly interact with the ligand. Based on sequence conservation of the nAChR and AChBP the three possible ligand-binding loops of AChBP have been pin-pointed in accordance with the present invention as follows: loop A, Trp-101 -> Tyr-108; loop B, Trp-162 -> His-164; loop C, Tyr-204 -> Tyr-211. The chimeric proteins that were constructed replace either one (A, B or C) or multiple (A&B, A&C, B&C and A&B&C) of the ligand-binding loops of AChBP with the corresponding human alpha7 nAChR sequence.

The loop-A domain of AChBP was replaced by the corresponding domain of the human alpha7 nAChR using a two-step polymerase chain reaction (PCR). In the first step two separate PCR amplifications (35 cycles: 94 ºC;30 sec., 58 ºC; 30 sec and 72 ºC; 60 sec.) yielded two halves of the chimera construct. AChBP cDNA (wild type) was used as template, and outer primers located either just before the start codon (gcgctcgagaaaagaggctgaagctttggaccgggcagacatctt; SEQ ID No. 17) or just before the stop codon (cgcgaattcaagaatttcggagcgtccctt; SEQ ID No. 18) were each used in combination with two internal primers gtggaaaccagacattctcctctacaacgccatctcgaaacc (SEQ ID No. 19) and gaggagaatgtctggtttccacaaagagcttattggcac (SEQ ID No. 20), respectively. The internal primers contained a 5'-tag-sequence that encoded for the introduced alpha7 nAChR domain. As such the two generated chimeric PCR products share a common tag containing a part of the alpha7 nAChR subunit. In the second step, the two PCR products from the first round were pooled and, in the absence of primers, went through 5 rounds of PCR amplification (94 ºC; 30 sec., 54 ºC; 3 mm. and 72 ºC; 90 sec.). This allowed the two halves of the chimera to anneal to each other at the common alpha7 nAChR tag. The subsequent addition of the two outer primers and another 35 cycles of 25 PCR amplification (94 ºC; 30 sec., 58 ºC; 30 sec. and 72 ºC; 90 sec.) yielded the final chimera construct. All PCR amplifications were hot-started and performed using PFU DNA-polymerase (Invitrogen). The loop-A AChBP/alpha7 chimera was cloned, using XhoI/EcoRI restriction sites in the outer primers, into the His-tag containing yeast expression

vector pPIC9 (Invitrogen). Validation of the construct was achieved by DNA sequencing. Expression of the chimera construct was achieved according to the Pichia pastoris protein expression protocol of Invitrogen.

As described in the examples and the description, the present invention provides water-soluble ligand-binding proteins derived from molluscs and analogs of ligand-gated ion channels, crystals thereof and their use for screening ligands of ligand-gated ion channels. In particular, ligand-binding proteins have been identified that are capable of forming multimers and are amenable to crystallization. The crystall structure of one these proteins, an acetylcholine binding protein (AChBP) is provided, which can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and thus for screening of drugs that act on these ion channels. Furthermore, chimeric proteins are provided that are capable of binding a ligand of a ligand-gated receptor, and comprising at least the amino acids of the AChBP determining solubility of the AChBP, in the same positions as in the AChBP, and furthermore comprising amino acids determining binding to said ligand.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Description, and Examples is hereby incorporated herein by reference. Moreover, the sequence listing is herein incorporated by reference.

Table 1

```
REMARK Written by O version 7.0.1
CRYST1  141.660  141.660  120.870  90.00  90.00  90.00
ORIGX1      1.000000  0.000000  0.000000        0.00000
ORIGX2      0.000000  1.000000  0.000000        0.00000
ORIGX3      0.000000  0.000000  1.000000        0.00000
SCALE1      0.007059  0.000000  0.000000        0.00000
SCALE2      0.000000  0.007059  0.000000        0.00000
SCALE3      0.000000  0.000000  0.008273        0.00000
ATOM      1  CB  PHE A   1      65.468  25.127   1.161  1.00 73.24    6
ATOM      2  CG  PHE A   1      64.224  24.803   0.370  1.00 76.49    6
ATOM      3  CD1 PHE A   1      63.433  25.819  -0.178  1.00 77.52    6
ATOM      4  CD2 PHE A   1      63.798  23.471   0.244  1.00 78.15    6
ATOM      5  CE1 PHE A   1      62.224  25.522  -0.840  1.00 79.11    6
ATOM      6  CE2 PHE A   1      62.590  23.148  -0.412  1.00 79.82    6
ATOM      7  CZ  PHE A   1      61.797  24.179  -0.958  1.00 79.89    6
ATOM      8  C   PHE A   1      66.638  27.146   1.923  1.00 69.89    6
ATOM      9  O   PHE A   1      67.034  26.519   2.903  1.00 70.26    8
ATOM     10  N   PHE A   1      67.407  25.990  -0.118  1.00 71.31    7
ATOM     11  CA  PHE A   1      66.214  26.375   0.689  1.00 70.93    6
ATOM     12  N   ASP A   2      66.562  28.478   1.909  1.00 68.78    7
ATOM     13  CA  ASP A   2      66.958  29.233   3.105  1.00 68.57    6
ATOM     14  CB  ASP A   2      67.577  30.615   2.739  1.00 69.98    6
ATOM     15  CG  ASP A   2      66.639  31.523   1.914  1.00 73.55    6
ATOM     16  OD1 ASP A   2      67.059  32.068   0.844  1.00 73.75    8
ATOM     17  OD2 ASP A   2      65.485  31.714   2.349  1.00 75.27    8
ATOM     18  C   ASP A   2      65.794  29.374   4.102  1.00 67.66    6
ATOM     19  O   ASP A   2      64.622  29.273   3.719  1.00 68.25    8
ATOM     20  N   ARG A   3      66.126  29.560   5.386  1.00 65.60    7
ATOM     21  CA  ARG A   3      65.131  29.703   6.453  1.00 60.77    6
ATOM     22  CB  ARG A   3      65.765  30.222   7.737  1.00 60.30    6
ATOM     23  CG  ARG A   3      66.393  29.174   8.604  1.00 59.51    6
ATOM     24  CD  ARG A   3      66.375  29.629  10.048  1.00 61.41    6
ATOM     25  NE  ARG A   3      66.440  28.471  10.927  1.00 61.03    7
ATOM     26  CZ  ARG A   3      67.550  27.787  11.159  1.00 62.03    6
ATOM     27  NH1 ARG A   3      68.692  28.169  10.586  1.00 60.01    7
ATOM     28  NH2 ARG A   3      67.509  26.694  11.918  1.00 62.76    7
ATOM     29  C   ARG A   3      64.034  30.659   6.055  1.00 59.92    6
ATOM     30  O   ARG A   3      62.883  30.487   6.454  1.00 59.64    8
ATOM     31  N   ALA A   4      64.395  31.685   5.291  1.00 57.25    7
ATOM     32  CA  ALA A   4      63.404  32.641   4.836  1.00 55.16    6
ATOM     33  CB  ALA A   4      64.065  33.782   4.088  1.00 53.78    6
ATOM     34  C   ALA A   4      62.421  31.917   3.927  1.00 54.69    6
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ATOM     36  N   ASP A   5      62.942  31.127   2.995  1.00 54.79    7
ATOM     37  CA  ASP A   5      62.097  30.392   2.060  1.00 55.84    6
ATOM     38  CB  ASP A   5      62.937  29.580   1.058  1.00 56.83    6
ATOM     39  CG  ASP A   5      63.918  30.437   0.278  1.00 59.97    6
ATOM     40  OD1 ASP A   5      63.519  31.519  -0.213  1.00 61.60    8
ATOM     41  OD2 ASP A   5      65.095  30.025   0.148  1.00 62.19    8
ATOM     42  C   ASP A   5      61.176  29.443   2.815  1.00 55.90    6
ATOM     43  O   ASP A   5      60.011  29.268   2.445  1.00 53.57    8
ATOM     44  N   ILE A   6      61.695  28.832   3.877  1.00 55.26    7
ATOM     45  CA  ILE A   6      60.890  27.889   4.650  1.00 55.12    6
ATOM     46  CB  ILE A   6      61.743  27.107   5.657  1.00 55.82    6
ATOM     47  CG2 ILE A   6      60.878  26.056   6.354  1.00 53.18    6
ATOM     48  CG1 ILE A   6      62.924  26.455   4.933  1.00 56.24    6
ATOM     49  CD1 ILE A   6      63.802  25.568   5.816  1.00 59.65    6
ATOM     50  C   ILE A   6      59.742  28.561   5.396  1.00 54.71    6
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ATOM	51	O	ILE	A	6	58.589	28.159	5.256	1.00	55.75	8
ATOM	52	N	LEU	A	7	60.058	29.583	6.182	1.00	52.58	7
ATOM	53	CA	LEU	A	7	59.041	30.299	6.929	1.00	51.88	6
ATOM	54	CB	LEU	A	7	59.697	31.387	7.784	1.00	51.65	6
ATOM	55	CG	LEU	A	7	60.589	30.828	8.895	1.00	51.59	6
ATOM	56	CD1	LEU	A	7	61.484	31.902	9.480	1.00	51.45	6
ATOM	57	CD2	LEU	A	7	59.700	30.225	9.953	1.00	51.32	6
ATOM	58	C	LEU	A	7	58.048	30.915	5.961	1.00	51.46	6
ATOM	59	O	LEU	A	7	56.846	30.921	6.204	1.00	51.87	8
ATOM	60	N	TYR	A	8	58.561	31.417	4.848	1.00	51.83	7
ATOM	61	CA	TYR	A	8	57.727	32.041	3.832	1.00	53.61	6
ATOM	62	CB	TYR	A	8	58.601	32.520	2.672	1.00	55.43	6
ATOM	63	CG	TYR	A	8	57.806	33.119	1.543	1.00	57.65	6
ATOM	64	CD1	TYR	A	8	57.217	34.379	1.668	1.00	58.24	6
ATOM	65	CE1	TYR	A	8	56.439	34.914	0.644	1.00	58.94	6
ATOM	66	CD2	TYR	A	8	57.601	32.407	0.366	1.00	58.93	6
ATOM	67	CE2	TYR	A	8	56.825	32.930	-0.665	1.00	60.13	6
ATOM	68	CZ	TYR	A	8	56.244	34.183	-0.518	1.00	60.03	6
ATOM	69	OH	TYR	A	8	55.453	34.699	-1.527	1.00	63.97	8
ATOM	70	C	TYR	A	8	56.636	31.114	3.296	1.00	52.67	6
ATOM	71	O	TYR	A	8	55.483	31.511	3.143	1.00	52.13	8
ATOM	72	N	ASN	A	9	57.009	29.880	2.997	1.00	53.39	7
ATOM	73	CA	ASN	A	9	56.051	28.918	2.488	1.00	53.87	6
ATOM	74	CB	ASN	A	9	56.750	27.613	2.096	1.00	58.21	6
ATOM	75	CG	ASN	A	9	57.646	27.772	0.860	1.00	62.45	6
ATOM	76	OD1	ASN	A	9	57.647	28.824	0.209	1.00	64.72	8
ATOM	77	ND2	ASN	A	9	58.405	26.724	0.530	1.00	62.99	7
ATOM	78	C	ASN	A	9	54.987	28.638	3.526	1.00	53.31	6
ATOM	79	O	ASN	A	9	53.794	28.725	3.239	1.00	52.02	8
ATOM	80	N	ILE	A	10	55.420	28.300	4.736	1.00	53.77	7
ATOM	81	CA	ILE	A	10	54.489	28.018	5.829	1.00	55.18	6
ATOM	82	CB	ILE	A	10	55.229	27.788	7.150	1.00	53.51	6
ATOM	83	CG2	ILE	A	10	54.220	27.639	8.272	1.00	53.99	6
ATOM	84	CG1	ILE	A	10	56.109	26.541	7.044	1.00	50.48	6
ATOM	85	CD1	ILE	A	10	57.043	26.346	8.202	1.00	47.68	6
ATOM	86	C	ILE	A	10	53.523	29.183	6.032	1.00	57.42	6
ATOM	87	O	ILE	A	10	52.319	28.997	6.221	1.00	57.74	8
ATOM	88	N	ARG	A	11	54.070	30.390	5.997	1.00	58.29	7
ATOM	89	CA	ARG	A	11	53.283	31.600	6.156	1.00	60.48	6
ATOM	90	CB	ARG	A	11	54.199	32.810	6.042	1.00	64.72	6
ATOM	91	CG	ARG	A	11	53.513	34.134	6.270	1.00	70.99	6
ATOM	92	CD	ARG	A	11	53.241	34.337	7.757	1.00	79.75	6
ATOM	93	NE	ARG	A	11	53.059	35.751	8.105	1.00	86.33	7
ATOM	94	CZ	ARG	A	11	53.848	36.733	7.665	1.00	89.85	6
ATOM	95	NH1	ARG	A	11	54.871	36.451	6.845	1.00	92.68	7
ATOM	96	NH2	ARG	A	11	53.636	37.992	8.056	1.00	90.02	7
ATOM	97	C	ARG	A	11	52.204	31.701	5.082	1.00	59.54	6
ATOM	98	O	ARG	A	11	51.038	31.954	5.363	1.00	59.64	8
ATOM	99	N	GLN	A	12	52.614	31.489	3.841	1.00	59.22	7
ATOM	100	CA	GLN	A	12	51.718	31.595	2.705	1.00	58.15	6
ATOM	101	CB	GLN	A	12	52.542	31.776	1.441	1.00	59.05	6
ATOM	102	CG	GLN	A	12	52.118	32.961	0.629	1.00	60.64	6
ATOM	103	CD	GLN	A	12	52.674	34.226	1.192	1.00	61.53	6
ATOM	104	OE1	GLN	A	12	53.879	34.345	1.360	1.00	65.50	8
ATOM	105	NE2	GLN	A	12	51.811	35.182	1.489	1.00	62.18	7
ATOM	106	C	GLN	A	12	50.732	30.460	2.472	1.00	57.30	6
ATOM	107	O	GLN	A	12	49.714	30.651	1.814	1.00	57.03	8
ATOM	108	N	THR	A	13	51.029	29.280	2.987	1.00	56.84	7
ATOM	109	CA	THR	A	13	50.142	28.147	2.773	1.00	57.26	6
ATOM	110	CB	THR	A	13	50.922	26.964	2.186	1.00	57.29	6
ATOM	111	OG1	THR	A	13	52.000	26.616	3.071	1.00	55.40	8

ATOM	112	CG2	THR	A	13	51.477	27.326	0.813	1.00	58.15	6
ATOM	113	C	THR	A	13	49.411	27.650	4.013	1.00	58.45	6
ATOM	114	O	THR	A	13	48.423	26.932	3.905	1.00	58.36	8
ATOM	115	N	SER	A	14	49.892	28.034	5.187	1.00	60.01	7
ATOM	116	CA	SER	A	14	49.290	27.584	6.424	1.00	60.03	6
ATOM	117	CB	SER	A	14	50.198	27.930	7.601	1.00	61.46	6
ATOM	118	OG	SER	A	14	49.813	27.207	8.758	1.00	65.18	8
ATOM	119	C	SER	A	14	47.899	28.147	6.664	1.00	59.50	6
ATOM	120	O	SER	A	14	47.560	29.240	6.189	1.00	58.72	8
ATOM	121	N	ARG	A	15	47.102	27.377	7.407	1.00	58.04	7
ATOM	122	CA	ARG	A	15	45.740	27.753	7.755	1.00	55.62	6
ATOM	123	CB	ARG	A	15	44.744	26.996	6.877	1.00	56.74	6
ATOM	124	CG	ARG	A	15	44.925	27.253	5.385	1.00	59.62	6
ATOM	125	CD	ARG	A	15	43.688	26.851	4.614	1.00	61.99	6
ATOM	126	NE	ARG	A	15	42.519	27.540	5.151	1.00	64.02	7
ATOM	127	CZ	ARG	A	15	41.261	27.216	4.870	1.00	65.48	6
ATOM	128	NH1	ARG	A	15	41.007	26.201	4.050	1.00	67.33	7
ATOM	129	NH2	ARG	A	15	40.256	27.908	5.408	1.00	64.23	7
ATOM	130	C	ARG	A	15	45.516	27.420	9.219	1.00	52.12	6
ATOM	131	O	ARG	A	15	45.135	26.310	9.562	1.00	53.25	8
ATOM	132	N	PRO	A	16	45.751	28.392	10.104	1.00	50.04	7
ATOM	133	CD	PRO	A	16	46.198	29.750	9.773	1.00	48.52	6
ATOM	134	CA	PRO	A	16	45.597	28.249	11.551	1.00	49.56	6
ATOM	135	CB	PRO	A	16	45.959	29.634	12.073	1.00	49.66	6
ATOM	136	CG	PRO	A	16	46.870	30.165	11.041	1.00	49.57	6
ATOM	137	C	PRO	A	16	44.215	27.816	12.016	1.00	50.11	6
ATOM	138	O	PRO	A	16	44.060	27.322	13.131	1.00	51.27	8
ATOM	139	N	ASP	A	17	43.208	28.013	11.176	1.00	50.70	7
ATOM	140	CA	ASP	A	17	41.856	27.640	11.548	1.00	50.64	6
ATOM	141	CB	ASP	A	17	40.850	28.609	10.931	1.00	54.16	6
ATOM	142	CG	ASP	A	17	40.873	29.974	11.592	1.00	59.76	6
ATOM	143	OD1	ASP	A	17	41.245	30.060	12.791	1.00	60.67	8
ATOM	144	OD2	ASP	A	17	40.500	30.965	10.920	1.00	62.99	8
ATOM	145	C	ASP	A	17	41.482	26.218	11.157	1.00	50.71	6
ATOM	146	O	ASP	A	17	40.353	25.783	11.390	1.00	48.36	8
ATOM	147	N	VAL	A	18	42.429	25.484	10.583	1.00	51.85	7
ATOM	148	CA	VAL	A	18	42.143	24.128	10.148	1.00	52.53	6
ATOM	149	CB	VAL	A	18	42.262	24.011	8.622	1.00	53.05	6
ATOM	150	CG1	VAL	A	18	41.834	22.618	8.169	1.00	51.38	6
ATOM	151	CG2	VAL	A	18	41.396	25.077	7.963	1.00	51.76	6
ATOM	152	C	VAL	A	18	42.993	23.050	10.779	1.00	52.56	6
ATOM	153	O	VAL	A	18	44.199	23.006	10.588	1.00	52.64	8
ATOM	154	N	ILE	A	19	42.327	22.172	11.519	1.00	53.41	7
ATOM	155	CA	ILE	A	19	42.954	21.042	12.202	1.00	52.70	6
ATOM	156	CB	ILE	A	19	41.871	20.319	13.072	1.00	52.71	6
ATOM	157	CG2	ILE	A	19	40.819	19.671	12.190	1.00	52.40	6
ATOM	158	CG1	ILE	A	19	42.504	19.290	13.992	1.00	53.50	6
ATOM	159	CD1	ILE	A	19	41.546	18.811	15.056	1.00	50.39	6
ATOM	160	C	ILE	A	19	43.596	20.097	11.164	1.00	52.96	6
ATOM	161	O	ILE	A	19	42.957	19.687	10.193	1.00	51.39	8
ATOM	162	N	PRO	A	20	44.878	19.757	11.355	1.00	53.70	7
ATOM	163	CD	PRO	A	20	45.711	20.210	12.472	1.00	54.14	6
ATOM	164	CA	PRO	A	20	45.644	18.876	10.461	1.00	56.34	6
ATOM	165	CB	PRO	A	20	47.078	18.996	10.981	1.00	56.60	6
ATOM	166	CG	PRO	A	20	47.060	20.235	11.840	1.00	58.05	6
ATOM	167	C	PRO	A	20	45.177	17.432	10.474	1.00	58.61	6
ATOM	168	O	PRO	A	20	45.974	16.523	10.682	1.00	59.22	8
ATOM	169	N	THR	A	21	43.886	17.231	10.246	1.00	62.30	7
ATOM	170	CA	THR	A	21	43.283	15.900	10.236	1.00	66.91	6
ATOM	171	CB	THR	A	21	41.765	16.020	10.495	1.00	65.83	6
ATOM	172	OG1	THR	A	21	41.516	15.813	11.883	1.00	67.19	8

ATOM	173	CG2	THR	A	21	40.975	15.010	9.687	1.00	68.42	6
ATOM	174	C	THR	A	21	43.522	15.060	8.967	1.00	70.65	6
ATOM	175	O	THR	A	21	43.365	15.538	7.832	1.00	70.53	8
ATOM	176	N	GLN	A	22	43.899	13.802	9.179	1.00	74.54	7
ATOM	177	CA	GLN	A	22	44.152	12.844	8.096	1.00	78.38	6
ATOM	178	CB	GLN	A	22	45.513	12.180	8.296	1.00	79.92	6
ATOM	179	CG	GLN	A	22	46.668	13.174	8.402	1.00	83.40	6
ATOM	180	CD	GLN	A	22	47.836	12.640	9.244	1.00	84.08	6
ATOM	181	OE1	GLN	A	22	47.709	12.451	10.467	1.00	82.79	8
ATOM	182	NE2	GLN	A	22	48.976	12.397	8.592	1.00	83.48	7
ATOM	183	C	GLN	A	22	43.055	11.779	8.158	1.00	80.25	6
ATOM	184	O	GLN	A	22	43.050	10.929	9.058	1.00	80.25	8
ATOM	185	N	ARG	A	23	42.133	11.825	7.199	1.00	82.59	7
ATOM	186	CA	ARG	A	23	40.999	10.896	7.162	1.00	84.29	6
ATOM	187	CB	ARG	A	23	41.478	9.447	7.095	1.00	85.05	6
ATOM	188	CG	ARG	A	23	41.983	9.032	5.717	1.00	87.64	6
ATOM	189	CD	ARG	A	23	43.517	8.991	5.617	1.00	90.14	6
ATOM	190	NE	ARG	A	23	43.958	8.775	4.231	1.00	92.92	7
ATOM	191	CZ	ARG	A	23	43.557	7.768	3.447	1.00	94.10	6
ATOM	192	NH1	ARG	A	23	42.700	6.854	3.901	1.00	94.07	7
ATOM	193	NH2	ARG	A	23	44.000	7.687	2.195	1.00	93.77	7
ATOM	194	C	ARG	A	23	40.130	11.099	8.399	1.00	85.22	6
ATOM	195	O	ARG	A	23	39.979	12.237	8.881	1.00	84.91	8
ATOM	196	N	ASP	A	24	39.549	10.011	8.908	1.00	86.21	7
ATOM	197	CA	ASP	A	24	38.705	10.105	10.105	1.00	86.07	6
ATOM	198	CB	ASP	A	24	37.689	8.952	10.194	1.00	89.13	6
ATOM	199	CG	ASP	A	24	37.418	8.289	8.847	1.00	91.57	6
ATOM	200	OD1	ASP	A	24	36.945	8.994	7.900	1.00	92.21	8
ATOM	201	OD2	ASP	A	24	37.680	7.058	8.756	1.00	91.67	8
ATOM	202	C	ASP	A	24	39.631	10.021	11.305	1.00	84.31	6
ATOM	203	O	ASP	A	24	39.173	9.975	12.458	1.00	84.64	8
ATOM	204	N	ARG	A	25	40.935	9.981	11.029	1.00	81.75	7
ATOM	205	CA	ARG	A	25	41.936	9.898	12.091	1.00	79.08	6
ATOM	206	CB	ARG	A	25	43.309	9.539	11.527	1.00	81.87	6
ATOM	207	CG	ARG	A	25	43.471	8.100	11.087	1.00	86.55	6
ATOM	208	CD	ARG	A	25	44.960	7.785	10.851	1.00	90.81	6
ATOM	209	NE	ARG	A	25	45.187	6.380	10.489	1.00	95.61	7
ATOM	210	CZ	ARG	A	25	46.388	5.815	10.345	1.00	96.85	6
ATOM	211	NH1	ARG	A	25	47.495	6.537	10.530	1.00	97.46	7
ATOM	212	NH2	ARG	A	25	46.487	4.522	10.023	1.00	97.32	7
ATOM	213	C	ARG	A	25	42.059	11.201	12.870	1.00	75.12	6
ATOM	214	O	ARG	A	25	42.158	12.283	12.281	1.00	75.55	8
ATOM	215	N	PRO	A	26	42.034	11.112	14.212	1.00	70.63	7
ATOM	216	CD	PRO	A	26	41.636	9.933	14.999	1.00	69.09	6
ATOM	217	CA	PRO	A	26	42.152	12.281	15.083	1.00	67.24	6
ATOM	218	CB	PRO	A	26	41.802	11.723	16.460	1.00	67.68	6
ATOM	219	CG	PRO	A	26	40.930	10.565	16.158	1.00	68.06	6
ATOM	220	C	PRO	A	26	43.593	12.762	15.053	1.00	64.53	6
ATOM	221	O	PRO	A	26	44.491	12.000	14.694	1.00	63.60	8
ATOM	222	N	VAL	A	27	43.816	14.020	15.420	1.00	61.16	7
ATOM	223	CA	VAL	A	27	45.168	14.544	15.476	1.00	57.20	6
ATOM	224	CB	VAL	A	27	45.197	16.079	15.374	1.00	56.96	6
ATOM	225	CG1	VAL	A	27	46.535	16.615	15.872	1.00	54.60	6
ATOM	226	CG2	VAL	A	27	44.986	16.496	13.930	1.00	55.09	6
ATOM	227	C	VAL	A	27	45.685	14.114	16.835	1.00	55.33	6
ATOM	228	O	VAL	A	27	45.026	14.328	17.849	1.00	53.70	8
ATOM	229	N	ALA	A	28	46.852	13.484	16.858	1.00	54.55	7
ATOM	230	CA	ALA	A	28	47.405	13.023	18.118	1.00	53.25	6
ATOM	231	CB	ALA	A	28	48.250	11.785	17.907	1.00	52.00	6
ATOM	232	C	ALA	A	28	48.230	14.117	18.761	1.00	52.77	6
ATOM	233	O	ALA	A	28	49.324	14.451	18.294	1.00	52.53	8

ATOM	234	N	VAL	A	29	47.683	14.672	19.837	1.00	51.33	7
ATOM	235	CA	VAL	A	29	48.332	15.730	20.590	1.00	49.28	6
ATOM	236	CB	VAL	A	29	47.367	16.921	20.845	1.00	47.59	6
ATOM	237	CG1	VAL	A	29	48.056	17.985	21.676	1.00	44.30	6
ATOM	238	CG2	VAL	A	29	46.891	17.497	19.527	1.00	44.21	6
ATOM	239	C	VAL	A	29	48.782	15.171	21.930	1.00	49.54	6
ATOM	240	O	VAL	A	29	48.014	14.524	22.635	1.00	49.14	8
ATOM	241	N	SER	A	30	50.043	15.402	22.261	1.00	49.54	7
ATOM	242	CA	SER	A	30	50.574	14.946	23.523	1.00	52.38	6
ATOM	243	CB	SER	A	30	51.869	14.163	23.309	1.00	51.50	6
ATOM	244	OG	SER	A	30	52.846	14.945	22.645	1.00	56.10	8
ATOM	245	C	SER	A	30	50.819	16.187	24.362	1.00	54.25	6
ATOM	246	O	SER	A	30	51.360	17.174	23.880	1.00	56.41	8
ATOM	247	N	VAL	A	31	50.396	16.134	25.618	1.00	56.86	7
ATOM	248	CA	VAL	A	31	50.543	17.258	26.531	1.00	58.42	6
ATOM	249	CB	VAL	A	31	49.170	17.768	27.012	1.00	58.48	6
ATOM	250	CG1	VAL	A	31	49.338	19.086	27.744	1.00	59.95	6
ATOM	251	CG2	VAL	A	31	48.219	17.910	25.835	1.00	56.73	6
ATOM	252	C	VAL	A	31	51.328	16.803	27.747	1.00	59.56	6
ATOM	253	O	VAL	A	31	51.073	15.729	28.281	1.00	60.85	8
ATOM	254	N	SER	A	32	52.271	17.631	28.185	1.00	61.06	7
ATOM	255	CA	SER	A	32	53.105	17.312	29.338	1.00	60.16	6
ATOM	256	CB	SER	A	32	54.388	16.619	28.868	1.00	59.88	6
ATOM	257	OG	SER	A	32	55.294	16.430	29.937	1.00	60.41	8
ATOM	258	C	SER	A	32	53.465	18.568	30.116	1.00	60.19	6
ATOM	259	O	SER	A	32	54.206	19.416	29.621	1.00	61.87	8
ATOM	260	N	LEU	A	33	52.946	18.689	31.333	1.00	58.89	7
ATOM	261	CA	LEU	A	33	53.256	19.847	32.170	1.00	57.23	6
ATOM	262	CB	LEU	A	33	52.112	20.142	33.142	1.00	55.20	6
ATOM	263	CG	LEU	A	33	50.740	20.363	32.511	1.00	54.66	6
ATOM	264	CD1	LEU	A	33	49.762	20.880	33.543	1.00	51.01	6
ATOM	265	CD2	LEU	A	33	50.880	21.342	31.373	1.00	55.39	6
ATOM	266	C	LEU	A	33	54.518	19.601	32.979	1.00	56.76	6
ATOM	267	O	LEU	A	33	54.697	18.526	33.533	1.00	58.14	8
ATOM	268	N	LYS	A	34	55.394	20.597	33.028	1.00	57.17	7
ATOM	269	CA	LYS	A	34	56.633	20.512	33.800	1.00	57.46	6
ATOM	270	CB	LYS	A	34	57.865	20.690	32.910	1.00	60.89	6
ATOM	271	CG	LYS	A	34	57.940	19.723	31.738	1.00	68.80	6
ATOM	272	CD	LYS	A	34	58.048	18.249	32.186	1.00	73.30	6
ATOM	273	CE	LYS	A	34	58.071	17.290	30.961	1.00	74.90	6
ATOM	274	NZ	LYS	A	34	58.210	15.842	31.340	1.00	75.55	7
ATOM	275	C	LYS	A	34	56.522	21.691	34.741	1.00	54.81	6
ATOM	276	O	LYS	A	34	56.567	22.834	34.308	1.00	55.33	8
ATOM	277	N	PHE	A	35	56.358	21.422	36.026	1.00	52.88	7
ATOM	278	CA	PHE	A	35	56.215	22.507	36.976	1.00	50.00	6
ATOM	279	CB	PHE	A	35	55.586	21.993	38.260	1.00	45.71	6
ATOM	280	CG	PHE	A	35	54.186	21.542	38.072	1.00	45.07	6
ATOM	281	CD1	PHE	A	35	53.912	20.256	37.634	1.00	45.46	6
ATOM	282	CD2	PHE	A	35	53.133	22.429	38.252	1.00	47.46	6
ATOM	283	CE1	PHE	A	35	52.612	19.848	37.372	1.00	45.03	6
ATOM	284	CE2	PHE	A	35	51.819	22.036	37.990	1.00	49.48	6
ATOM	285	CZ	PHE	A	35	51.560	20.735	37.547	1.00	48.14	6
ATOM	286	C	PHE	A	35	57.494	23.268	37.247	1.00	49.05	6
ATOM	287	O	PHE	A	35	58.549	22.687	37.480	1.00	48.49	8
ATOM	288	N	ILE	A	36	57.374	24.588	37.191	1.00	46.86	7
ATOM	289	CA	ILE	A	36	58.492	25.482	37.393	1.00	45.55	6
ATOM	290	CB	ILE	A	36	58.538	26.551	36.284	1.00	43.92	6
ATOM	291	CG2	ILE	A	36	59.771	27.411	36.433	1.00	39.03	6
ATOM	292	CG1	ILE	A	36	58.526	25.876	34.917	1.00	44.17	6
ATOM	293	CD1	ILE	A	36	59.671	24.916	34.699	1.00	46.33	6
ATOM	294	C	ILE	A	36	58.392	26.181	38.739	1.00	46.38	6

ATOM	295	O	ILE	A	36	59.405	26.580	39.318	1.00	45.40	8
ATOM	296	N	ASN	A	37	57.176	26.340	39.244	1.00	46.13	7
ATOM	297	CA	ASN	A	37	57.023	27.008	40.526	1.00	46.27	6
ATOM	298	CB	ASN	A	37	57.491	28.462	40.400	1.00	46.32	6
ATOM	299	CG	ASN	A	37	58.009	29.030	41.707	1.00	48.59	6
ATOM	300	OD1	ASN	A	37	57.408	28.844	42.759	1.00	49.38	8
ATOM	301	ND2	ASN	A	37	59.124	29.743	41.639	1.00	46.71	7
ATOM	302	C	ASN	A	37	55.595	26.975	41.046	1.00	46.17	6
ATOM	303	O	ASN	A	37	54.644	26.799	40.281	1.00	44.02	8
ATOM	304	N	ILE	A	38	55.465	27.117	42.362	1.00	46.64	7
ATOM	305	CA	ILE	A	38	54.173	27.158	43.033	1.00	48.46	6
ATOM	306	CB	ILE	A	38	53.988	25.951	43.923	1.00	47.34	6
ATOM	307	CG2	ILE	A	38	52.680	26.066	44.671	1.00	49.13	6
ATOM	308	CG1	ILE	A	38	53.983	24.697	43.050	1.00	48.40	6
ATOM	309	CD1	ILE	A	38	54.079	23.402	43.791	1.00	47.55	6
ATOM	310	C	ILE	A	38	54.245	28.433	43.847	1.00	50.74	6
ATOM	311	O	ILE	A	38	54.979	28.505	44.817	1.00	53.13	8
ATOM	312	N	LEU	A	39	53.485	29.438	43.433	1.00	53.46	7
ATOM	313	CA	LEU	A	39	53.527	30.757	44.045	1.00	55.16	6
ATOM	314	CB	LEU	A	39	53.350	31.806	42.952	1.00	54.91	6
ATOM	315	CG	LEU	A	39	54.330	31.591	41.800	1.00	57.26	6
ATOM	316	CD1	LEU	A	39	54.108	32.647	40.728	1.00	54.71	6
ATOM	317	CD2	LEU	A	39	55.757	31.623	42.341	1.00	54.68	6
ATOM	318	C	LEU	A	39	52.613	31.098	45.203	1.00	56.69	6
ATOM	319	O	LEU	A	39	53.043	31.750	46.157	1.00	59.24	8
ATOM	320	N	GLU	A	40	51.352	30.715	45.123	1.00	56.60	7
ATOM	321	CA	GLU	A	40	50.451	31.019	46.216	1.00	58.75	6
ATOM	322	CB	GLU	A	40	49.617	32.251	45.920	1.00	59.61	6
ATOM	323	CG	GLU	A	40	50.426	33.520	45.821	1.00	65.69	6
ATOM	324	CD	GLU	A	40	49.547	34.752	45.683	1.00	69.26	6
ATOM	325	OE1	GLU	A	40	48.747	34.812	44.715	1.00	72.53	8
ATOM	326	OE2	GLU	A	40	49.655	35.659	46.543	1.00	69.31	8
ATOM	327	C	GLU	A	40	49.534	29.863	46.448	1.00	60.49	6
ATOM	328	O	GLU	A	40	49.006	29.275	45.509	1.00	62.83	8
ATOM	329	N	VAL	A	41	49.348	29.525	47.710	1.00	60.13	7
ATOM	330	CA	VAL	A	41	48.474	28.431	48.049	1.00	60.14	6
ATOM	331	CB	VAL	A	41	49.292	27.230	48.576	1.00	59.98	6
ATOM	332	CG1	VAL	A	41	48.376	26.185	49.146	1.00	59.73	6
ATOM	333	CG2	VAL	A	41	50.118	26.632	47.444	1.00	59.26	6
ATOM	334	C	VAL	A	41	47.510	28.934	49.109	1.00	60.58	6
ATOM	335	O	VAL	A	41	47.864	29.793	49.934	1.00	61.24	8
ATOM	336	N	ASN	A	42	46.283	28.428	49.059	1.00	59.54	7
ATOM	337	CA	ASN	A	42	45.267	28.806	50.024	1.00	60.72	6
ATOM	338	CB	ASN	A	42	44.346	29.895	49.463	1.00	59.36	6
ATOM	339	CG	ASN	A	42	43.473	30.530	50.533	1.00	59.07	6
ATOM	340	OD1	ASN	A	42	42.811	29.835	51.303	1.00	60.43	8
ATOM	341	ND2	ASN	A	42	43.462	31.856	50.582	1.00	57.17	7
ATOM	342	C	ASN	A	42	44.474	27.535	50.286	1.00	62.57	6
ATOM	343	O	ASN	A	42	43.654	27.107	49.460	1.00	62.42	8
ATOM	344	N	GLU	A	43	44.731	26.921	51.435	1.00	63.02	7
ATOM	345	CA	GLU	A	43	44.045	25.695	51.792	1.00	62.62	6
ATOM	346	CB	GLU	A	43	44.772	25.004	52.942	1.00	65.20	6
ATOM	347	CG	GLU	A	43	44.206	23.642	53.253	1.00	67.62	6
ATOM	348	CD	GLU	A	43	45.088	22.827	54.174	1.00	69.40	6
ATOM	349	OE1	GLU	A	43	44.628	21.739	54.581	1.00	71.48	8
ATOM	350	OE2	GLU	A	43	46.228	23.256	54.479	1.00	67.83	8
ATOM	351	C	GLU	A	43	42.595	25.959	52.169	1.00	61.53	6
ATOM	352	O	GLU	A	43	41.755	25.058	52.086	1.00	59.68	8
ATOM	353	N	ILE	A	44	42.309	27.197	52.575	1.00	60.06	7
ATOM	354	CA	ILE	A	44	40.957	27.580	52.951	1.00	60.59	6
ATOM	355	CB	ILE	A	44	40.923	28.953	53.632	1.00	60.98	6

ATOM	356	CG2	ILE	A	44	39.469	29.343	53.943	1.00	61.06	6
ATOM	357	CG1	ILE	A	44	41.749	28.921	54.918	1.00	61.51	6
ATOM	358	CD1	ILE	A	44	41.119	28.117	56.022	1.00	61.37	6
ATOM	359	C	ILE	A	44	40.069	27.660	51.718	1.00	61.06	6
ATOM	360	O	ILE	A	44	38.942	27.148	51.708	1.00	61.53	8
ATOM	361	N	THR	A	45	40.581	28.302	50.674	1.00	60.25	7
ATOM	362	CA	THR	A	45	39.826	28.464	49.426	1.00	58.34	6
ATOM	363	CB	THR	A	45	40.086	29.844	48.805	1.00	58.12	6
ATOM	364	OG1	THR	A	45	41.492	29.992	48.535	1.00	58.85	8
ATOM	365	CG2	THR	A	45	39.632	30.934	49.762	1.00	56.98	6
ATOM	366	C	THR	A	45	40.139	27.407	48.374	1.00	56.43	6
ATOM	367	O	THR	A	45	39.465	27.328	47.349	1.00	54.64	8
ATOM	368	N	ASN	A	46	41.169	26.607	48.620	1.00	55.73	7
ATOM	369	CA	ASN	A	46	41.534	25.563	47.677	1.00	56.27	6
ATOM	370	CB	ASN	A	46	40.390	24.557	47.560	1.00	55.82	6
ATOM	371	CG	ASN	A	46	40.612	23.327	48.412	1.00	56.92	6
ATOM	372	OD1	ASN	A	46	39.671	22.621	48.746	1.00	55.85	8
ATOM	373	ND2	ASN	A	46	41.866	23.058	48.754	1.00	54.55	7
ATOM	374	C	ASN	A	46	41.869	26.127	46.299	1.00	56.62	6
ATOM	375	O	ASN	A	46	41.350	25.659	45.283	1.00	58.80	8
ATOM	376	N	GLU	A	47	42.744	27.130	46.275	1.00	54.91	7
ATOM	377	CA	GLU	A	47	43.156	27.766	45.044	1.00	52.39	6
ATOM	378	CB	GLU	A	47	42.606	29.183	44.999	1.00	50.63	6
ATOM	379	CG	GLU	A	47	41.107	29.247	44.938	1.00	48.77	6
ATOM	380	CD	GLU	A	47	40.601	30.675	44.951	1.00	53.28	6
ATOM	381	OE1	GLU	A	47	41.370	31.577	44.568	1.00	51.68	8
ATOM	382	OE2	GLU	A	47	39.429	30.902	45.333	1.00	58.43	8
ATOM	383	C	GLU	A	47	44.671	27.776	44.979	1.00	52.87	6
ATOM	384	O	GLU	A	47	45.347	28.009	45.981	1.00	53.20	8
ATOM	385	N	VAL	A	48	45.208	27.513	43.797	1.00	53.53	7
ATOM	386	CA	VAL	A	48	46.656	27.481	43.619	1.00	53.36	6
ATOM	387	CB	VAL	A	48	47.147	26.043	43.318	1.00	53.31	6
ATOM	388	CG1	VAL	A	48	48.646	26.029	43.122	1.00	55.73	6
ATOM	389	CG2	VAL	A	48	46.781	25.130	44.456	1.00	52.72	6
ATOM	390	C	VAL	A	48	47.108	28.390	42.484	1.00	52.90	6
ATOM	391	O	VAL	A	48	46.441	28.504	41.454	1.00	54.54	8
ATOM	392	N	ASP	A	49	48.242	29.046	42.691	1.00	52.21	7
ATOM	393	CA	ASP	A	49	48.818	29.928	41.692	1.00	51.57	6
ATOM	394	CB	ASP	A	49	49.084	31.291	42.304	1.00	52.64	6
ATOM	395	CG	ASP	A	49	49.264	32.352	41.268	1.00	53.86	6
ATOM	396	OD1	ASP	A	49	49.900	32.051	40.246	1.00	54.56	8
ATOM	397	OD2	ASP	A	49	48.779	33.482	41.474	1.00	57.00	8
ATOM	398	C	ASP	A	49	50.121	29.241	41.313	1.00	50.45	6
ATOM	399	O	ASP	A	49	51.074	29.254	42.075	1.00	52.15	8
ATOM	400	N	VAL	A	50	50.155	28.636	40.135	1.00	49.83	7
ATOM	401	CA	VAL	A	50	51.329	27.893	39.711	1.00	49.77	6
ATOM	402	CB	VAL	A	50	50.992	26.372	39.723	1.00	51.61	6
ATOM	403	CG1	VAL	A	50	50.095	26.015	38.531	1.00	51.90	6
ATOM	404	CG2	VAL	A	50	52.265	25.539	39.721	1.00	53.03	6
ATOM	405	C	VAL	A	50	51.890	28.290	38.335	1.00	49.01	6
ATOM	406	O	VAL	A	50	51.193	28.878	37.508	1.00	50.33	8
ATOM	407	N	VAL	A	51	53.163	27.974	38.117	1.00	46.39	7
ATOM	408	CA	VAL	A	51	53.863	28.245	36.861	1.00	45.41	6
ATOM	409	CB	VAL	A	51	55.111	29.134	37.083	1.00	43.93	6
ATOM	410	CG1	VAL	A	51	55.943	29.182	35.807	1.00	42.09	6
ATOM	411	CG2	VAL	A	51	54.696	30.536	37.497	1.00	41.05	6
ATOM	412	C	VAL	A	51	54.336	26.899	36.291	1.00	46.83	6
ATOM	413	O	VAL	A	51	54.879	26.063	37.016	1.00	47.95	8
ATOM	414	N	PHE	A	52	54.147	26.684	34.996	1.00	45.38	7
ATOM	415	CA	PHE	A	52	54.560	25.423	34.402	1.00	44.58	6
ATOM	416	CB	PHE	A	52	53.485	24.373	34.662	1.00	44.09	6

ATOM	417	CG	PHE	A	52	52.155	24.718	34.068	1.00	43.27	6
ATOM	418	CD1	PHE	A	52	51.857	24.393	32.758	1.00	42.79	6
ATOM	419	CD2	PHE	A	52	51.211	25.411	34.805	1.00	45.35	6
ATOM	420	CE1	PHE	A	52	50.643	24.755	32.194	1.00	41.86	6
ATOM	421	CE2	PHE	A	52	49.991	25.776	34.240	1.00	45.03	6
ATOM	422	CZ	PHE	A	52	49.712	25.445	32.933	1.00	41.04	6
ATOM	423	C	PHE	A	52	54.789	25.547	32.906	1.00	45.52	6
ATOM	424	O	PHE	A	52	54.403	26.536	32.288	1.00	46.49	8
ATOM	425	N	TRP	A	53	55.431	24.541	32.328	1.00	45.07	7
ATOM	426	CA	TRP	A	53	55.662	24.527	30.898	1.00	46.61	6
ATOM	427	CB	TRP	A	53	57.043	24.000	30.573	1.00	48.36	6
ATOM	428	CG	TRP	A	53	58.137	24.899	30.983	1.00	50.29	6
ATOM	429	CD2	TRP	A	53	59.531	24.604	30.942	1.00	50.34	6
ATOM	430	CE2	TRP	A	53	60.213	25.755	31.386	1.00	51.89	6
ATOM	431	CE3	TRP	A	53	60.274	23.473	30.570	1.00	52.05	6
ATOM	432	CD1	TRP	A	53	58.024	26.175	31.436	1.00	50.84	6
ATOM	433	NE1	TRP	A	53	59.267	26.700	31.682	1.00	52.12	7
ATOM	434	CZ2	TRP	A	53	61.605	25.817	31.470	1.00	53.79	6
ATOM	435	CZ3	TRP	A	53	61.660	23.527	30.649	1.00	53.82	6
ATOM	436	CH2	TRP	A	53	62.314	24.697	31.099	1.00	55.14	6
ATOM	437	C	TRP	A	53	54.644	23.599	30.285	1.00	47.55	6
ATOM	438	O	TRP	A	53	54.645	22.410	30.564	1.00	49.29	8
ATOM	439	N	GLN	A	54	53.765	24.139	29.457	1.00	47.91	7
ATOM	440	CA	GLN	A	54	52.765	23.312	28.825	1.00	48.38	6
ATOM	441	CB	GLN	A	54	51.517	24.132	28.529	1.00	47.98	6
ATOM	442	CG	GLN	A	54	50.322	23.309	28.095	1.00	50.36	6
ATOM	443	CD	GLN	A	54	49.001	24.016	28.375	1.00	54.00	6
ATOM	444	OE1	GLN	A	54	48.697	24.360	29.515	1.00	53.48	8
ATOM	445	NE2	GLN	A	54	48.209	24.231	27.335	1.00	57.12	7
ATOM	446	C	GLN	A	54	53.378	22.755	27.555	1.00	49.13	6
ATOM	447	O	GLN	A	54	53.095	23.203	26.453	1.00	50.86	8
ATOM	448	N	GLN	A	55	54.251	21.779	27.738	1.00	50.50	7
ATOM	449	CA	GLN	A	55	54.937	21.122	26.641	1.00	52.90	6
ATOM	450	CB	GLN	A	55	55.995	20.200	27.234	1.00	58.12	6
ATOM	451	CG	GLN	A	55	56.699	19.288	26.263	1.00	66.05	6
ATOM	452	CD	GLN	A	55	57.909	18.634	26.907	1.00	71.07	6
ATOM	453	OE1	GLN	A	55	57.890	18.307	28.107	1.00	73.93	8
ATOM	454	NE2	GLN	A	55	58.969	18.442	26.123	1.00	72.99	7
ATOM	455	C	GLN	A	55	53.939	20.353	25.774	1.00	51.30	6
ATOM	456	O	GLN	A	55	53.451	19.293	26.151	1.00	50.67	8
ATOM	457	N	THR	A	56	53.648	20.907	24.604	1.00	49.14	7
ATOM	458	CA	THR	A	56	52.690	20.325	23.684	1.00	46.69	6
ATOM	459	CB	THR	A	56	51.597	21.347	23.342	1.00	45.67	6
ATOM	460	OG1	THR	A	56	51.138	21.969	24.541	1.00	45.84	8
ATOM	461	CG2	THR	A	56	50.426	20.673	22.666	1.00	45.93	6
ATOM	462	C	THR	A	56	53.344	19.878	22.389	1.00	46.05	6
ATOM	463	O	THR	A	56	54.286	20.503	21.917	1.00	46.13	8
ATOM	464	N	THR	A	57	52.836	18.796	21.812	1.00	44.22	7
ATOM	465	CA	THR	A	57	53.384	18.286	20.569	1.00	44.65	6
ATOM	466	CB	THR	A	57	54.511	17.270	20.823	1.00	44.59	6
ATOM	467	OG1	THR	A	57	55.593	17.914	21.499	1.00	42.38	8
ATOM	468	CG2	THR	A	57	55.036	16.733	19.512	1.00	49.11	6
ATOM	469	C	THR	A	57	52.316	17.627	19.721	1.00	43.97	6
ATOM	470	O	THR	A	57	51.377	17.039	20.239	1.00	44.62	8
ATOM	471	N	TRP	A	58	52.452	17.753	18.410	1.00	42.72	7
ATOM	472	CA	TRP	A	58	51.502	17.153	17.489	1.00	44.75	6
ATOM	473	CB	TRP	A	58	50.139	17.883	17.529	1.00	42.24	6
ATOM	474	CG	TRP	A	58	50.130	19.267	16.967	1.00	40.43	6
ATOM	475	CD2	TRP	A	58	50.427	20.473	17.668	1.00	39.55	6
ATOM	476	CE2	TRP	A	58	50.354	21.521	16.735	1.00	41.08	6
ATOM	477	CE3	TRP	A	58	50.755	20.770	18.995	1.00	36.98	6

ATOM	478	CD1	TRP	A	58	49.887	19.624	15.677	1.00	39.98	6
ATOM	479	NE1	TRP	A	58	50.019	20.971	15.527	1.00	41.55	7
ATOM	480	CZ2	TRP	A	58	50.599	22.850	17.084	1.00	40.32	6
ATOM	481	CZ3	TRP	A	58	50.997	22.081	19.341	1.00	37.03	6
ATOM	482	CH2	TRP	A	58	50.919	23.109	18.389	1.00	38.53	6
ATOM	483	C	TRP	A	58	52.112	17.184	16.098	1.00	47.09	6
ATOM	484	O	TRP	A	58	53.226	17.675	15.915	1.00	47.06	8
ATOM	485	N	SER	A	59	51.390	16.670	15.115	1.00	48.64	7
ATOM	486	CA	SER	A	59	51.933	16.631	13.782	1.00	50.92	6
ATOM	487	CB	SER	A	59	52.245	15.187	13.435	1.00	53.25	6
ATOM	488	OG	SER	A	59	53.191	15.109	12.389	1.00	62.80	8
ATOM	489	C	SER	A	59	51.020	17.229	12.735	1.00	52.80	6
ATOM	490	O	SER	A	59	49.828	16.942	12.696	1.00	53.05	8
ATOM	491	N	ASP	A	60	51.602	18.065	11.881	1.00	55.45	7
ATOM	492	CA	ASP	A	60	50.881	18.721	10.792	1.00	57.44	6
ATOM	493	CB	ASP	A	60	50.741	20.221	11.071	1.00	57.33	6
ATOM	494	CG	ASP	A	60	49.856	20.936	10.058	1.00	57.43	6
ATOM	495	OD1	ASP	A	60	49.776	20.486	8.896	1.00	57.47	8
ATOM	496	OD2	ASP	A	60	49.256	21.967	10.424	1.00	56.76	8
ATOM	497	C	ASP	A	60	51.726	18.510	9.541	1.00	59.20	6
ATOM	498	O	ASP	A	60	52.679	19.245	9.304	1.00	58.82	8
ATOM	499	N	ARG	A	61	51.372	17.503	8.748	1.00	61.30	7
ATOM	500	CA	ARG	A	61	52.115	17.181	7.533	1.00	63.09	6
ATOM	501	CB	ARG	A	61	51.643	15.845	6.958	1.00	67.23	6
ATOM	502	CG	ARG	A	61	52.191	14.594	7.653	1.00	72.92	6
ATOM	503	CD	ARG	A	61	51.883	13.355	6.786	1.00	81.01	6
ATOM	504	NE	ARG	A	61	52.441	12.091	7.291	1.00	85.79	7
ATOM	505	CZ	ARG	A	61	52.320	10.917	6.660	1.00	87.50	6
ATOM	506	NH1	ARG	A	61	51.665	10.843	5.501	1.00	88.31	7
ATOM	507	NH2	ARG	A	61	52.852	9.815	7.179	1.00	87.74	7
ATOM	508	C	ARG	A	61	52.073	18.238	6.430	1.00	61.94	6
ATOM	509	O	ARG	A	61	52.927	18.225	5.550	1.00	61.39	8
ATOM	510	N	THR	A	62	51.095	19.141	6.461	1.00	60.78	7
ATOM	511	CA	THR	A	62	51.017	20.175	5.434	1.00	59.76	6
ATOM	512	CB	THR	A	62	49.666	20.952	5.483	1.00	60.01	6
ATOM	513	OG1	THR	A	62	49.582	21.720	6.689	1.00	62.71	8
ATOM	514	CG2	THR	A	62	48.500	20.000	5.442	1.00	59.86	6
ATOM	515	C	THR	A	62	52.172	21.171	5.616	1.00	58.73	6
ATOM	516	O	THR	A	62	52.400	22.044	4.774	1.00	59.33	8
ATOM	517	N	LEU	A	63	52.898	21.031	6.720	1.00	56.50	7
ATOM	518	CA	LEU	A	63	54.029	21.903	7.020	1.00	55.97	6
ATOM	519	CB	LEU	A	63	54.088	22.205	8.521	1.00	53.19	6
ATOM	520	CG	LEU	A	63	52.866	22.837	9.174	1.00	52.76	6
ATOM	521	CD1	LEU	A	63	53.074	22.909	10.672	1.00	51.73	6
ATOM	522	CD2	LEU	A	63	52.629	24.217	8.589	1.00	53.34	6
ATOM	523	C	LEU	A	63	55.351	21.264	6.603	1.00	55.80	6
ATOM	524	O	LEU	A	63	56.366	21.947	6.509	1.00	54.36	8
ATOM	525	N	ALA	A	64	55.332	19.952	6.368	1.00	56.30	7
ATOM	526	CA	ALA	A	64	56.532	19.207	5.987	1.00	56.99	6
ATOM	527	CB	ALA	A	64	56.194	17.744	5.810	1.00	54.20	6
ATOM	528	C	ALA	A	64	57.176	19.745	4.715	1.00	59.20	6
ATOM	529	O	ALA	A	64	56.487	20.224	3.816	1.00	60.08	8
ATOM	530	N	TRP	A	65	58.502	19.646	4.651	1.00	60.65	7
ATOM	531	CA	TRP	A	65	59.295	20.104	3.506	1.00	62.47	6
ATOM	532	CB	TRP	A	65	59.623	21.588	3.667	1.00	59.37	6
ATOM	533	CG	TRP	A	65	60.773	21.870	4.613	1.00	56.94	6
ATOM	534	CD2	TRP	A	65	60.685	22.167	6.020	1.00	56.89	6
ATOM	535	CE2	TRP	A	65	62.001	22.424	6.475	1.00	55.08	6
ATOM	536	CE3	TRP	A	65	59.622	22.245	6.938	1.00	54.01	6
ATOM	537	CD1	TRP	A	65	62.097	21.947	4.292	1.00	55.45	6
ATOM	538	NE1	TRP	A	65	62.838	22.282	5.400	1.00	53.98	7

ATOM	539	CZ2	TRP	A	65	62.286	22.757	7.808	1.00	52.03	6
ATOM	540	CZ3	TRP	A	65	59.910	22.577	8.266	1.00	53.82	6
ATOM	541	CH2	TRP	A	65	61.232	22.829	8.684	1.00	51.71	6
ATOM	542	C	TRP	A	65	60.603	19.297	3.445	1.00	65.72	6
ATOM	543	O	TRP	A	65	61.091	18.825	4.479	1.00	66.89	8
ATOM	544	N	ASN	A	66	61.181	19.138	2.255	1.00	68.69	7
ATOM	545	CA	ASN	A	66	62.431	18.371	2.149	1.00	71.84	6
ATOM	546	CB	ASN	A	66	62.735	17.983	0.689	1.00	73.23	6
ATOM	547	CG	ASN	A	66	63.968	17.084	0.568	1.00	76.18	6
ATOM	548	OD1	ASN	A	66	64.473	16.822	-0.541	1.00	76.68	8
ATOM	549	ND2	ASN	A	66	64.463	16.606	1.715	1.00	76.39	7
ATOM	550	C	ASN	A	66	63.581	19.199	2.723	1.00	71.96	6
ATOM	551	O	ASN	A	66	63.902	20.279	2.217	1.00	72.02	8
ATOM	552	N	SER	A	67	64.197	18.690	3.784	1.00	72.09	7
ATOM	553	CA	SER	A	67	65.292	19.403	4.435	1.00	72.65	6
ATOM	554	CB	SER	A	67	65.063	19.425	5.943	1.00	72.61	6
ATOM	555	OG	SER	A	67	64.969	18.105	6.449	1.00	70.09	8
ATOM	556	C	SER	A	67	66.655	18.794	4.177	1.00	73.27	6
ATOM	557	O	SER	A	67	67.576	19.031	4.961	1.00	72.43	8
ATOM	558	N	SER	A	68	66.799	18.026	3.097	1.00	74.60	7
ATOM	559	CA	SER	A	68	68.082	17.370	2.825	1.00	76.38	6
ATOM	560	CB	SER	A	68	68.006	16.490	1.564	1.00	75.57	6
ATOM	561	OG	SER	A	68	67.870	17.265	0.386	1.00	75.20	8
ATOM	562	C	SER	A	68	69.222	18.380	2.707	1.00	77.15	6
ATOM	563	O	SER	A	68	70.288	18.201	3.300	1.00	77.04	8
ATOM	564	N	HIS	A	69	68.992	19.451	1.962	1.00	78.21	7
ATOM	565	CA	HIS	A	69	70.015	20.479	1.804	1.00	79.62	6
ATOM	566	CB	HIS	A	69	70.445	20.578	0.341	1.00	84.04	6
ATOM	567	CG	HIS	A	69	71.007	19.302	-0.196	1.00	88.01	6
ATOM	568	CD2	HIS	A	69	72.208	19.022	-0.759	1.00	89.20	6
ATOM	569	ND1	HIS	A	69	70.332	18.100	-0.110	1.00	89.31	7
ATOM	570	CE1	HIS	A	69	71.096	17.133	-0.589	1.00	90.18	6
ATOM	571	NE2	HIS	A	69	72.240	17.666	-0.988	1.00	90.99	7
ATOM	572	C	HIS	A	69	69.441	21.799	2.279	1.00	77.78	6
ATOM	573	O	HIS	A	69	69.473	22.803	1.561	1.00	77.92	8
ATOM	574	N	SER	A	70	68.896	21.766	3.496	1.00	75.27	7
ATOM	575	CA	SER	A	70	68.300	22.931	4.141	1.00	72.21	6
ATOM	576	CB	SER	A	70	67.013	23.316	3.421	1.00	72.74	6
ATOM	577	OG	SER	A	70	66.368	22.158	2.919	1.00	74.05	8
ATOM	578	C	SER	A	70	68.031	22.563	5.595	1.00	69.35	6
ATOM	579	O	SER	A	70	68.138	21.384	5.962	1.00	70.38	8
ATOM	580	N	PRO	A	71	67.710	23.563	6.450	1.00	66.44	7
ATOM	581	CD	PRO	A	71	67.819	24.998	6.134	1.00	64.03	6
ATOM	582	CA	PRO	A	71	67.422	23.385	7.883	1.00	64.80	6
ATOM	583	CB	PRO	A	71	67.106	24.805	8.334	1.00	63.49	6
ATOM	584	CG	PRO	A	71	68.031	25.608	7.498	1.00	61.83	6
ATOM	585	C	PRO	A	71	66.295	22.395	8.223	1.00	63.99	6
ATOM	586	O	PRO	A	71	65.314	22.289	7.496	1.00	63.63	8
ATOM	587	N	ASP	A	72	66.434	21.679	9.333	1.00	63.39	7
ATOM	588	CA	ASP	A	72	65.424	20.701	9.734	1.00	63.43	6
ATOM	589	CB	ASP	A	72	66.056	19.634	10.617	1.00	65.69	6
ATOM	590	CG	ASP	A	72	67.229	18.974	9.959	1.00	70.53	6
ATOM	591	OD1	ASP	A	72	66.985	18.216	8.988	1.00	73.68	8
ATOM	592	OD2	ASP	A	72	68.389	19.218	10.390	1.00	71.00	8
ATOM	593	C	ASP	A	72	64.307	21.356	10.520	1.00	62.20	6
ATOM	594	O	ASP	A	72	63.164	20.878	10.520	1.00	61.88	8
ATOM	595	N	GLN	A	73	64.653	22.457	11.175	1.00	59.83	7
ATOM	596	CA	GLN	A	73	63.738	23.186	12.041	1.00	59.45	6
ATOM	597	CB	GLN	A	73	64.083	22.901	13.489	1.00	60.33	6
ATOM	598	CG	GLN	A	73	63.720	21.569	14.035	1.00	63.59	6
ATOM	599	CD	GLN	A	73	64.224	21.462	15.459	1.00	68.15	6

ATOM	600	OE1	GLN	A	73	65.425	21.595	15.699	1.00	70.61	8
ATOM	601	NE2	GLN	A	73	63.316	21.249	16.416	1.00	69.73	7
ATOM	602	C	GLN	A	73	63.779	24.703	11.886	1.00	57.04	6
ATOM	603	O	GLN	A	73	64.798	25.280	11.490	1.00	58.19	8
ATOM	604	N	VAL	A	74	62.670	25.336	12.243	1.00	52.68	7
ATOM	605	CA	VAL	A	74	62.557	26.782	12.211	1.00	50.24	6
ATOM	606	CB	VAL	A	74	62.036	27.279	10.859	1.00	48.70	6
ATOM	607	CG1	VAL	A	74	63.066	27.034	9.794	1.00	49.74	6
ATOM	608	CG2	VAL	A	74	60.738	26.584	10.515	1.00	47.98	6
ATOM	609	C	VAL	A	74	61.580	27.201	13.310	1.00	49.74	6
ATOM	610	O	VAL	A	74	60.756	26.401	13.754	1.00	48.96	8
ATOM	611	N	SER	A	75	61.691	28.442	13.769	1.00	47.62	7
ATOM	612	CA	SER	A	75	60.792	28.954	14.787	1.00	44.06	6
ATOM	613	CB	SER	A	75	61.525	29.902	15.728	1.00	44.67	6
ATOM	614	OG	SER	A	75	62.241	29.188	16.710	1.00	46.37	8
ATOM	615	C	SER	A	75	59.668	29.688	14.084	1.00	43.07	6
ATOM	616	O	SER	A	75	59.894	30.657	13.358	1.00	42.11	8
ATOM	617	N	VAL	A	76	58.451	29.214	14.307	1.00	42.71	7
ATOM	618	CA	VAL	A	76	57.272	29.792	13.687	1.00	43.33	6
ATOM	619	CB	VAL	A	76	56.482	28.711	12.936	1.00	44.34	6
ATOM	620	CG1	VAL	A	76	55.247	29.315	12.298	1.00	44.97	6
ATOM	621	CG2	VAL	A	76	57.359	28.058	11.894	1.00	43.12	6
ATOM	622	C	VAL	A	76	56.335	30.436	14.704	1.00	44.16	6
ATOM	623	O	VAL	A	76	56.093	29.882	15.773	1.00	45.89	8
ATOM	624	N	PRO	A	77	55.798	31.624	14.388	1.00	43.19	7
ATOM	625	CD	PRO	A	77	56.162	32.556	13.311	1.00	41.24	6
ATOM	626	CA	PRO	A	77	54.884	32.266	15.334	1.00	41.49	6
ATOM	627	CB	PRO	A	77	54.619	33.615	14.691	1.00	41.13	6
ATOM	628	CG	PRO	A	77	55.886	33.884	13.950	1.00	41.89	6
ATOM	629	C	PRO	A	77	53.617	31.439	15.453	1.00	40.82	6
ATOM	630	O	PRO	A	77	53.112	30.919	14.471	1.00	39.55	8
ATOM	631	N	ILE	A	78	53.116	31.318	16.671	1.00	42.42	7
ATOM	632	CA	ILE	A	78	51.908	30.556	16.959	1.00	42.14	6
ATOM	633	CB	ILE	A	78	51.526	30.751	18.441	1.00	42.09	6
ATOM	634	CG2	ILE	A	78	50.105	30.357	18.712	1.00	43.53	6
ATOM	635	CG1	ILE	A	78	52.464	29.921	19.285	1.00	43.22	6
ATOM	636	CD1	ILE	A	78	52.585	28.513	18.784	1.00	43.92	6
ATOM	637	C	ILE	A	78	50.749	30.942	16.057	1.00	43.58	6
ATOM	638	O	ILE	A	78	49.985	30.096	15.624	1.00	45.64	8
ATOM	639	N	SER	A	79	50.642	32.229	15.768	1.00	43.79	7
ATOM	640	CA	SER	A	79	49.588	32.767	14.918	1.00	44.38	6
ATOM	641	CB	SER	A	79	49.666	34.292	14.934	1.00	44.81	6
ATOM	642	OG	SER	A	79	50.972	34.732	14.584	1.00	45.88	8
ATOM	643	C	SER	A	79	49.590	32.295	13.465	1.00	43.50	6
ATOM	644	O	SER	A	79	48.607	32.498	12.758	1.00	42.80	8
ATOM	645	N	SER	A	80	50.685	31.683	13.016	1.00	42.62	7
ATOM	646	CA	SER	A	80	50.774	31.216	11.639	1.00	42.84	6
ATOM	647	CB	SER	A	80	52.137	31.555	11.043	1.00	44.68	6
ATOM	648	OG	SER	A	80	52.308	32.956	10.932	1.00	51.59	8
ATOM	649	C	SER	A	80	50.534	29.726	11.502	1.00	44.69	6
ATOM	650	O	SER	A	80	50.596	29.184	10.402	1.00	43.97	8
ATOM	651	N	LEU	A	81	50.248	29.068	12.620	1.00	45.13	7
ATOM	652	CA	LEU	A	81	50.003	27.631	12.631	1.00	41.19	6
ATOM	653	CB	LEU	A	81	51.061	26.926	13.467	1.00	39.92	6
ATOM	654	CG	LEU	A	81	52.534	27.167	13.185	1.00	41.52	6
ATOM	655	CD1	LEU	A	81	53.356	26.677	14.355	1.00	39.70	6
ATOM	656	CD2	LEU	A	81	52.922	26.464	11.918	1.00	42.52	6
ATOM	657	C	LEU	A	81	48.672	27.340	13.272	1.00	39.47	6
ATOM	658	O	LEU	A	81	48.089	28.197	13.921	1.00	40.21	8
ATOM	659	N	TRP	A	82	48.191	26.122	13.081	1.00	38.46	7
ATOM	660	CA	TRP	A	82	46.965	25.694	13.720	1.00	37.32	6

ATOM	661	CB	TRP	A	82	46.346	24.494	13.006	1.00	36.83	6
ATOM	662	CG	TRP	A	82	45.274	23.818	13.829	1.00	40.60	6
ATOM	663	CD2	TRP	A	82	45.459	22.741	14.757	1.00	39.63	6
ATOM	664	CE2	TRP	A	82	44.213	22.499	15.369	1.00	38.33	6
ATOM	665	CE3	TRP	A	82	46.560	21.961	15.132	1.00	40.54	6
ATOM	666	CD1	TRP	A	82	43.948	24.170	13.914	1.00	39.43	6
ATOM	667	NE1	TRP	A	82	43.311	23.383	14.839	1.00	39.00	7
ATOM	668	CZ2	TRP	A	82	44.040	21.511	16.332	1.00	38.94	6
ATOM	669	CZ3	TRP	A	82	46.388	20.982	16.088	1.00	39.99	6
ATOM	670	CH2	TRP	A	82	45.135	20.764	16.678	1.00	39.88	6
ATOM	671	C	TRP	A	82	47.485	25.241	15.064	1.00	36.99	6
ATOM	672	O	TRP	A	82	48.559	24.661	15.142	1.00	38.93	8
ATOM	673	N	VAL	A	83	46.744	25.503	16.123	1.00	37.43	7
ATOM	674	CA	VAL	A	83	47.179	25.086	17.437	1.00	37.48	6
ATOM	675	CB	VAL	A	83	47.729	26.300	18.209	1.00	37.40	6
ATOM	676	CG1	VAL	A	83	47.901	25.984	19.655	1.00	43.51	6
ATOM	677	CG2	VAL	A	83	49.054	26.688	17.644	1.00	37.34	6
ATOM	678	C	VAL	A	83	46.011	24.437	18.175	1.00	39.74	6
ATOM	679	O	VAL	A	83	44.858	24.823	17.997	1.00	42.50	8
ATOM	680	N	PRO	A	84	46.290	23.408	18.982	1.00	39.54	7
ATOM	681	CD	PRO	A	84	47.594	22.745	19.134	1.00	41.22	6
ATOM	682	CA	PRO	A	84	45.263	22.701	19.752	1.00	38.54	6
ATOM	683	CB	PRO	A	84	46.079	21.690	20.558	1.00	39.94	6
ATOM	684	CG	PRO	A	84	47.202	21.381	19.663	1.00	41.42	6
ATOM	685	C	PRO	A	84	44.509	23.663	20.658	1.00	36.09	6
ATOM	686	O	PRO	A	84	45.121	24.469	21.342	1.00	35.57	8
ATOM	687	N	ASP	A	85	43.186	23.576	20.668	1.00	32.88	7
ATOM	688	CA	ASP	A	85	42.397	24.458	21.505	1.00	34.36	6
ATOM	689	CB	ASP	A	85	41.014	24.668	20.898	1.00	35.14	6
ATOM	690	CG	ASP	A	85	40.268	23.381	20.696	1.00	37.78	6
ATOM	691	OD1	ASP	A	85	40.897	22.388	20.290	1.00	40.24	8
ATOM	692	OD2	ASP	A	85	39.050	23.367	20.927	1.00	37.65	8
ATOM	693	C	ASP	A	85	42.277	23.906	22.910	1.00	35.33	6
ATOM	694	O	ASP	A	85	41.180	23.726	23.420	1.00	38.82	8
ATOM	695	N	LEU	A	86	43.418	23.644	23.528	1.00	32.24	7
ATOM	696	CA	LEU	A	86	43.459	23.106	24.869	1.00	35.18	6
ATOM	697	CB	LEU	A	86	44.878	22.670	25.208	1.00	34.63	6
ATOM	698	CG	LEU	A	86	45.435	21.585	24.311	1.00	35.36	6
ATOM	699	CD1	LEU	A	86	46.842	21.241	24.749	1.00	34.84	6
ATOM	700	CD2	LEU	A	86	44.530	20.376	24.386	1.00	35.68	6
ATOM	701	C	LEU	A	86	42.973	24.086	25.925	1.00	36.01	6
ATOM	702	O	LEU	A	86	43.141	25.283	25.800	1.00	37.75	8
ATOM	703	N	ALA	A	87	42.378	23.556	26.979	1.00	38.03	7
ATOM	704	CA	ALA	A	87	41.870	24.369	28.060	1.00	38.29	6
ATOM	705	CB	ALA	A	87	40.428	24.674	27.811	1.00	36.17	6
ATOM	706	C	ALA	A	87	42.022	23.605	29.371	1.00	41.08	6
ATOM	707	O	ALA	A	87	41.798	22.399	29.407	1.00	43.90	8
ATOM	708	N	ALA	A	88	42.431	24.290	30.436	1.00	39.68	7
ATOM	709	CA	ALA	A	88	42.558	23.639	31.726	1.00	38.37	6
ATOM	710	CB	ALA	A	88	43.586	24.337	32.571	1.00	34.88	6
ATOM	711	C	ALA	A	88	41.180	23.729	32.376	1.00	40.65	6
ATOM	712	O	ALA	A	88	40.778	24.780	32.847	1.00	40.29	8
ATOM	713	N	TYR	A	89	40.460	22.613	32.371	1.00	42.49	7
ATOM	714	CA	TYR	A	89	39.116	22.502	32.934	1.00	44.24	6
ATOM	715	CB	TYR	A	89	38.727	21.023	33.052	1.00	46.70	6
ATOM	716	CG	TYR	A	89	38.641	20.286	31.725	1.00	51.62	6
ATOM	717	CD1	TYR	A	89	38.462	18.902	31.684	1.00	54.35	6
ATOM	718	CE1	TYR	A	89	38.353	18.222	30.466	1.00	56.33	6
ATOM	719	CD2	TYR	A	89	38.711	20.968	30.511	1.00	51.86	6
ATOM	720	CE2	TYR	A	89	38.604	20.297	29.302	1.00	53.71	6
ATOM	721	CZ	TYR	A	89	38.424	18.927	29.286	1.00	55.54	6

ATOM	722	OH	TYR	A	89	38.296	18.257	28.093	1.00	59.35	8
ATOM	723	C	TYR	A	89	38.888	23.185	34.280	1.00	43.81	6
ATOM	724	O	TYR	A	89	37.808	23.735	34.518	1.00	41.70	8
ATOM	725	N	ASN	A	90	39.880	23.149	35.167	1.00	43.90	7
ATOM	726	CA	ASN	A	90	39.709	23.781	36.473	1.00	43.12	6
ATOM	727	CB	ASN	A	90	39.976	22.770	37.598	1.00	40.92	6
ATOM	728	CG	ASN	A	90	41.340	22.156	37.517	1.00	42.04	6
ATOM	729	OD1	ASN	A	90	41.770	21.721	36.456	1.00	43.62	8
ATOM	730	ND2	ASN	A	90	42.033	22.102	38.646	1.00	43.25	7
ATOM	731	C	ASN	A	90	40.550	25.042	36.655	1.00	44.35	6
ATOM	732	O	ASN	A	90	40.881	25.434	37.769	1.00	46.42	8
ATOM	733	N	ALA	A	91	40.902	25.673	35.543	1.00	45.44	7
ATOM	734	CA	ALA	A	91	41.660	26.912	35.591	1.00	45.36	6
ATOM	735	CB	ALA	A	91	42.130	27.308	34.206	1.00	44.43	6
ATOM	736	C	ALA	A	91	40.680	27.940	36.136	1.00	45.00	6
ATOM	737	O	ALA	A	91	39.522	28.000	35.729	1.00	43.71	8
ATOM	738	N	ILE	A	92	41.164	28.750	37.064	1.00	46.47	7
ATOM	739	CA	ILE	A	92	40.359	29.753	37.734	1.00	46.18	6
ATOM	740	CB	ILE	A	92	40.674	29.673	39.232	1.00	47.56	6
ATOM	741	CG2	ILE	A	92	41.595	30.797	39.634	1.00	50.92	6
ATOM	742	CG1	ILE	A	92	39.409	29.713	40.055	1.00	50.52	6
ATOM	743	CD1	ILE	A	92	39.711	29.795	41.547	1.00	51.82	6
ATOM	744	C	ILE	A	92	40.659	31.157	37.177	1.00	45.80	6
ATOM	745	O	ILE	A	92	39.996	32.134	37.518	1.00	45.79	8
ATOM	746	N	SER	A	93	41.666	31.237	36.317	1.00	44.40	7
ATOM	747	CA	SER	A	93	42.076	32.483	35.687	1.00	41.89	6
ATOM	748	CB	SER	A	93	43.248	33.080	36.445	1.00	40.83	6
ATOM	749	OG	SER	A	93	44.400	32.275	36.274	1.00	37.97	8
ATOM	750	C	SER	A	93	42.541	32.112	34.295	1.00	42.18	6
ATOM	751	O	SER	A	93	42.762	30.942	34.023	1.00	41.06	8
ATOM	752	N	LYS	A	94	42.693	33.081	33.401	1.00	43.27	7
ATOM	753	CA	LYS	A	94	43.178	32.712	32.077	1.00	45.47	6
ATOM	754	CB	LYS	A	94	42.703	33.680	30.988	1.00	44.26	6
ATOM	755	CG	LYS	A	94	42.747	35.142	31.314	1.00	44.49	6
ATOM	756	CD	LYS	A	94	41.907	35.918	30.309	1.00	46.66	6
ATOM	757	CE	LYS	A	94	42.209	35.470	28.885	1.00	47.75	6
ATOM	758	NZ	LYS	A	94	41.443	36.237	27.873	1.00	49.19	7
ATOM	759	C	LYS	A	94	44.688	32.592	32.089	1.00	43.67	6
ATOM	760	O	LYS	A	94	45.359	33.102	32.980	1.00	44.46	8
ATOM	761	N	PRO	A	95	45.243	31.889	31.105	1.00	43.23	7
ATOM	762	CD	PRO	A	95	44.559	31.199	30.004	1.00	41.03	6
ATOM	763	CA	PRO	A	95	46.692	31.695	31.024	1.00	42.80	6
ATOM	764	CB	PRO	A	95	46.858	30.719	29.862	1.00	43.77	6
ATOM	765	CG	PRO	A	95	45.515	30.078	29.725	1.00	43.00	6
ATOM	766	C	PRO	A	95	47.480	32.962	30.783	1.00	41.84	6
ATOM	767	O	PRO	A	95	47.178	33.729	29.861	1.00	41.82	8
ATOM	768	N	GLU	A	96	48.483	33.183	31.627	1.00	40.74	7
ATOM	769	CA	GLU	A	96	49.350	34.322	31.472	1.00	39.25	6
ATOM	770	CB	GLU	A	96	49.704	34.960	32.817	1.00	41.50	6
ATOM	771	CG	GLU	A	96	50.548	36.235	32.682	1.00	46.46	6
ATOM	772	CD	GLU	A	96	50.864	36.910	34.014	1.00	51.10	6
ATOM	773	OE1	GLU	A	96	50.172	36.591	35.002	1.00	55.39	8
ATOM	774	OE2	GLU	A	96	51.784	37.772	34.079	1.00	51.01	8
ATOM	775	C	GLU	A	96	50.583	33.713	30.851	1.00	38.30	6
ATOM	776	O	GLU	A	96	51.424	33.169	31.548	1.00	37.33	8
ATOM	777	N	VAL	A	97	50.662	33.770	29.528	1.00	36.80	7
ATOM	778	CA	VAL	A	97	51.813	33.231	28.821	1.00	37.13	6
ATOM	779	CB	VAL	A	97	51.514	33.092	27.313	1.00	35.99	6
ATOM	780	CG1	VAL	A	97	52.704	32.480	26.600	1.00	34.96	6
ATOM	781	CG2	VAL	A	97	50.287	32.222	27.122	1.00	30.36	6
ATOM	782	C	VAL	A	97	53.002	34.160	29.061	1.00	37.37	6

ATOM	783	O	VAL	A	97	52.998	35.329	28.670	1.00	35.14	8
ATOM	784	N	LEU	A	98	54.022	33.619	29.715	1.00	37.54	7
ATOM	785	CA	LEU	A	98	55.203	34.389	30.070	1.00	39.37	6
ATOM	786	CB	LEU	A	98	55.773	33.851	31.374	1.00	38.96	6
ATOM	787	CG	LEU	A	98	54.848	33.662	32.568	1.00	39.17	6
ATOM	788	CD1	LEU	A	98	55.522	32.772	33.576	1.00	37.89	6
ATOM	789	CD2	LEU	A	98	54.501	34.997	33.169	1.00	38.95	6
ATOM	790	C	LEU	A	98	56.317	34.387	29.033	1.00	41.78	6
ATOM	791	O	LEU	A	98	57.310	35.114	29.177	1.00	42.77	8
ATOM	792	N	THR	A	99	56.162	33.579	27.992	1.00	39.65	7
ATOM	793	CA	THR	A	99	57.199	33.471	26.981	1.00	37.85	6
ATOM	794	CB	THR	A	99	57.793	32.063	27.004	1.00	39.36	6
ATOM	795	OG1	THR	A	99	56.745	31.102	26.822	1.00	40.29	8
ATOM	796	CG2	THR	A	99	58.490	31.812	28.325	1.00	36.68	6
ATOM	797	C	THR	A	99	56.762	33.784	25.559	1.00	37.27	6
ATOM	798	O	THR	A	99	55.571	33.809	25.260	1.00	37.48	8
ATOM	799	N	PRO	A	100	57.733	34.050	24.666	1.00	35.48	7
ATOM	800	CD	PRO	A	100	59.169	34.217	24.938	1.00	34.88	6
ATOM	801	CA	PRO	A	100	57.450	34.356	23.268	1.00	34.86	6
ATOM	802	CB	PRO	A	100	58.825	34.308	22.631	1.00	32.91	6
ATOM	803	CG	PRO	A	100	59.660	34.899	23.674	1.00	33.33	6
ATOM	804	C	PRO	A	100	56.535	33.287	22.735	1.00	34.32	6
ATOM	805	O	PRO	A	100	56.748	32.110	22.990	1.00	37.05	8
ATOM	806	N	GLN	A	101	55.508	33.684	22.005	1.00	35.52	7
ATOM	807	CA	GLN	A	101	54.591	32.698	21.483	1.00	38.08	6
ATOM	808	CB	GLN	A	101	53.181	33.271	21.452	1.00	39.02	6
ATOM	809	CG	GLN	A	101	52.557	33.223	22.836	1.00	42.77	6
ATOM	810	CD	GLN	A	101	51.356	34.102	22.965	1.00	46.68	6
ATOM	811	OE1	GLN	A	101	50.383	33.943	22.239	1.00	51.63	8
ATOM	812	NE2	GLN	A	101	51.408	35.045	23.900	1.00	48.84	7
ATOM	813	C	GLN	A	101	55.006	32.145	20.144	1.00	37.60	6
ATOM	814	O	GLN	A	101	54.331	32.329	19.136	1.00	36.16	8
ATOM	815	N	LEU	A	102	56.138	31.445	20.177	1.00	38.73	7
ATOM	816	CA	LEU	A	102	56.742	30.812	19.016	1.00	38.35	6
ATOM	817	CB	LEU	A	102	58.180	31.289	18.833	1.00	36.63	6
ATOM	818	CG	LEU	A	102	58.411	32.792	18.709	1.00	37.99	6
ATOM	819	CD1	LEU	A	102	59.890	33.054	18.550	1.00	39.54	6
ATOM	820	CD2	LEU	A	102	57.650	33.343	17.538	1.00	35.40	6
ATOM	821	C	LEU	A	102	56.763	29.311	19.200	1.00	39.23	6
ATOM	822	O	LEU	A	102	56.933	28.809	20.302	1.00	40.34	8
ATOM	823	N	ALA	A	103	56.574	28.595	18.104	1.00	40.83	7
ATOM	824	CA	ALA	A	103	56.603	27.142	18.125	1.00	41.49	6
ATOM	825	CB	ALA	A	103	55.334	26.569	17.497	1.00	41.49	6
ATOM	826	C	ALA	A	103	57.830	26.697	17.337	1.00	42.17	6
ATOM	827	O	ALA	A	103	58.472	27.484	16.645	1.00	43.45	8
ATOM	828	N	ARG	A	104	58.163	25.427	17.453	1.00	43.77	7
ATOM	829	CA	ARG	A	104	59.309	24.893	16.750	1.00	44.63	6
ATOM	830	CB	ARG	A	104	60.242	24.228	17.745	1.00	43.89	6
ATOM	831	CG	ARG	A	104	61.621	23.992	17.214	1.00	45.78	6
ATOM	832	CD	ARG	A	104	62.362	25.277	16.950	1.00	43.65	6
ATOM	833	NE	ARG	A	104	63.675	24.958	16.409	1.00	44.01	7
ATOM	834	CZ	ARG	A	104	64.618	25.848	16.124	1.00	46.53	6
ATOM	835	NH1	ARG	A	104	64.411	27.147	16.327	1.00	47.99	7
ATOM	836	NH2	ARG	A	104	65.775	25.432	15.632	1.00	47.13	7
ATOM	837	C	ARG	A	104	58.770	23.878	15.754	1.00	46.81	6
ATOM	838	O	ARG	A	104	58.042	22.961	16.124	1.00	49.12	8
ATOM	839	N	VAL	A	105	59.097	24.049	14.482	1.00	47.69	7
ATOM	840	CA	VAL	A	105	58.601	23.125	13.469	1.00	47.16	6
ATOM	841	CB	VAL	A	105	57.791	23.857	12.382	1.00	44.84	6
ATOM	842	CG1	VAL	A	105	57.198	22.861	11.421	1.00	41.16	6
ATOM	843	CG2	VAL	A	105	56.702	24.684	13.018	1.00	45.42	6

ATOM	844	C	VAL	A	105	59.731	22.355	12.799	1.00	49.71	6
ATOM	845	O	VAL	A	105	60.688	22.946	12.283	1.00	48.12	8
ATOM	846	N	VAL	A	106	59.597	21.030	12.821	1.00	50.55	7
ATOM	847	CA	VAL	A	106	60.571	20.123	12.232	1.00	51.43	6
ATOM	848	CB	VAL	A	106	60.648	18.816	13.037	1.00	52.44	6
ATOM	849	CG1	VAL	A	106	61.828	17.987	12.571	1.00	50.24	6
ATOM	850	CG2	VAL	A	106	60.762	19.128	14.521	1.00	52.53	6
ATOM	851	C	VAL	A	106	60.142	19.809	10.805	1.00	52.38	6
ATOM	852	O	VAL	A	106	58.961	19.644	10.536	1.00	52.65	8
ATOM	853	N	SER	A	107	61.101	19.718	9.895	1.00	52.34	7
ATOM	854	CA	SER	A	107	60.803	19.447	8.492	1.00	54.32	6
ATOM	855	CB	SER	A	107	62.111	19.185	7.735	1.00	55.62	6
ATOM	856	OG	SER	A	107	62.965	18.316	8.462	1.00	60.14	8
ATOM	857	C	SER	A	107	59.795	18.328	8.186	1.00	53.69	6
ATOM	858	O	SER	A	107	59.191	18.304	7.111	1.00	51.90	8
ATOM	859	N	ASP	A	108	59.598	17.412	9.122	1.00	54.61	7
ATOM	860	CA	ASP	A	108	58.667	16.318	8.890	1.00	57.15	6
ATOM	861	CB	ASP	A	108	59.164	15.046	9.580	1.00	58.72	6
ATOM	862	CG	ASP	A	108	59.114	15.134	11.097	1.00	61.68	6
ATOM	863	OD1	ASP	A	108	59.391	16.221	11.642	1.00	64.28	8
ATOM	864	OD2	ASP	A	108	58.816	14.105	11.747	1.00	62.23	8
ATOM	865	C	ASP	A	108	57.235	16.615	9.320	1.00	58.57	6
ATOM	866	O	ASP	A	108	56.379	15.725	9.301	1.00	58.30	8
ATOM	867	N	GLY	A	109	56.979	17.865	9.703	1.00	59.14	7
ATOM	868	CA	GLY	A	109	55.649	18.271	10.116	1.00	58.25	6
ATOM	869	C	GLY	A	109	55.397	18.166	11.602	1.00	58.69	6
ATOM	870	O	GLY	A	109	54.273	18.374	12.054	1.00	59.98	8
ATOM	871	N	GLU	A	110	56.423	17.821	12.369	1.00	58.71	7
ATOM	872	CA	GLU	A	110	56.255	17.713	13.813	1.00	58.33	6
ATOM	873	CB	GLU	A	110	57.380	16.871	14.425	1.00	61.59	6
ATOM	874	CG	GLU	A	110	57.062	16.242	15.797	1.00	66.10	6
ATOM	875	CD	GLU	A	110	55.913	15.218	15.728	1.00	70.89	6
ATOM	876	OE1	GLU	A	110	55.634	14.710	14.600	1.00	70.53	8
ATOM	877	OE2	GLU	A	110	55.303	14.916	16.800	1.00	70.77	8
ATOM	878	C	GLU	A	110	56.293	19.136	14.369	1.00	56.59	6
ATOM	879	O	GLU	A	110	57.114	19.955	13.941	1.00	54.81	8
ATOM	880	N	VAL	A	111	55.392	19.425	15.307	1.00	54.27	7
ATOM	881	CA	VAL	A	111	55.310	20.745	15.912	1.00	52.01	6
ATOM	882	CB	VAL	A	111	53.949	21.412	15.616	1.00	50.79	6
ATOM	883	CG1	VAL	A	111	53.902	22.795	16.242	1.00	47.90	6
ATOM	884	CG2	VAL	A	111	53.718	21.489	14.115	1.00	50.80	6
ATOM	885	C	VAL	A	111	55.465	20.666	17.418	1.00	51.33	6
ATOM	886	O	VAL	A	111	54.833	19.830	18.057	1.00	50.54	8
ATOM	887	N	LEU	A	112	56.300	21.539	17.979	1.00	49.64	7
ATOM	888	CA	LEU	A	112	56.501	21.569	19.418	1.00	50.36	6
ATOM	889	CB	LEU	A	112	57.911	21.107	19.791	1.00	54.86	6
ATOM	890	CG	LEU	A	112	58.651	20.020	18.989	1.00	59.01	6
ATOM	891	CD1	LEU	A	112	57.699	18.865	18.631	1.00	60.90	6
ATOM	892	CD2	LEU	A	112	59.248	20.632	17.727	1.00	57.28	6
ATOM	893	C	LEU	A	112	56.297	22.980	19.946	1.00	49.94	6
ATOM	894	O	LEU	A	112	57.004	23.893	19.553	1.00	49.38	8
ATOM	895	N	TYR	A	113	55.323	23.151	20.833	1.00	49.46	7
ATOM	896	CA	TYR	A	113	55.036	24.446	21.437	1.00	47.23	6
ATOM	897	CB	TYR	A	113	53.643	24.939	21.021	1.00	45.72	6
ATOM	898	CG	TYR	A	113	53.222	26.279	21.621	1.00	46.02	6
ATOM	899	CD1	TYR	A	113	54.092	27.364	21.654	1.00	42.86	6
ATOM	900	CE1	TYR	A	113	53.691	28.588	22.179	1.00	43.03	6
ATOM	901	CD2	TYR	A	113	51.936	26.462	22.131	1.00	45.25	6
ATOM	902	CE2	TYR	A	113	51.533	27.682	22.653	1.00	41.00	6
ATOM	903	CZ	TYR	A	113	52.410	28.740	22.677	1.00	42.42	6
ATOM	904	OH	TYR	A	113	52.008	29.952	23.211	1.00	42.79	8

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ATOM    905  C   TYR A 113      55.097  24.250  22.936  1.00 47.38   6
ATOM    906  O   TYR A 113      54.304  23.508  23.506  1.00 47.08   8
ATOM    907  N   MET A 114      56.047  24.916  23.577  1.00 48.38   7
ATOM    908  CA  MET A 114      56.205  24.788  25.015  1.00 48.39   6
ATOM    909  CB  MET A 114      57.485  24.020  25.304  1.00 52.09   6
ATOM    910  CG  MET A 114      57.675  23.679  26.739  1.00 59.10   6
ATOM    911  SD  MET A 114      59.383  23.282  26.925  1.00 67.20  16
ATOM    912  CE  MET A 114      59.324  21.518  26.416  1.00 67.26   6
ATOM    913  C   MET A 114      56.245  26.148  25.701  1.00 46.12   6
ATOM    914  O   MET A 114      57.308  26.660  26.027  1.00 46.76   8
ATOM    915  N   PRO A 115      55.076  26.754  25.922  1.00 44.80   7
ATOM    916  CD  PRO A 115      53.740  26.329  25.463  1.00 44.54   6
ATOM    917  CA  PRO A 115      55.005  28.059  26.575  1.00 44.08   6
ATOM    918  CB  PRO A 115      53.675  28.598  26.075  1.00 45.01   6
ATOM    919  CG  PRO A 115      52.831  27.366  26.077  1.00 43.44   6
ATOM    920  C   PRO A 115      55.030  27.935  28.102  1.00 43.24   6
ATOM    921  O   PRO A 115      54.552  26.947  28.664  1.00 40.79   8
ATOM    922  N   SER A 116      55.599  28.929  28.771  1.00 42.36   7
ATOM    923  CA  SER A 116      55.627  28.911  30.227  1.00 42.64   6
ATOM    924  CB  SER A 116      56.851  29.624  30.764  1.00 40.99   6
ATOM    925  OG  SER A 116      56.852  29.573  32.169  1.00 41.56   8
ATOM    926  C   SER A 116      54.382  29.658  30.653  1.00 42.71   6
ATOM    927  O   SER A 116      54.184  30.809  30.266  1.00 44.52   8
ATOM    928  N   ILE A 117      53.545  29.006  31.446  1.00 41.18   7
ATOM    929  CA  ILE A 117      52.303  29.616  31.879  1.00 40.12   6
ATOM    930  CB  ILE A 117      51.104  28.814  31.325  1.00 37.67   6
ATOM    931  CG2 ILE A 117      49.805  29.400  31.819  1.00 38.25   6
ATOM    932  CG1 ILE A 117      51.134  28.825  29.798  1.00 36.76   6
ATOM    933  CD1 ILE A 117      50.212  27.822  29.169  1.00 33.48   6
ATOM    934  C   ILE A 117      52.114  29.768  33.388  1.00 41.31   6
ATOM    935  O   ILE A 117      52.444  28.876  34.168  1.00 43.78   8
ATOM    936  N   ARG A 118      51.607  30.925  33.795  1.00 41.35   7
ATOM    937  CA  ARG A 118      51.283  31.153  35.194  1.00 41.26   6
ATOM    938  CB  ARG A 118      51.789  32.496  35.709  1.00 38.56   6
ATOM    939  CG  ARG A 118      51.290  32.758  37.113  1.00 37.29   6
ATOM    940  CD  ARG A 118      52.006  33.883  37.817  1.00 38.24   6
ATOM    941  NE  ARG A 118      51.453  34.066  39.150  1.00 41.49   7
ATOM    942  CZ  ARG A 118      52.006  34.794  40.107  1.00 43.10   6
ATOM    943  NH1 ARG A 118      53.148  35.423  39.892  1.00 46.98   7
ATOM    944  NH2 ARG A 118      51.417  34.890  41.282  1.00 43.21   7
ATOM    945  C   ARG A 118      49.765  31.156  35.179  1.00 41.21   6
ATOM    946  O   ARG A 118      49.144  31.842  34.374  1.00 41.57   8
ATOM    947  N   GLN A 119      49.152  30.394  36.063  1.00 41.94   7
ATOM    948  CA  GLN A 119      47.702  30.329  36.056  1.00 43.44   6
ATOM    949  CB  GLN A 119      47.292  29.433  34.895  1.00 41.21   6
ATOM    950  CG  GLN A 119      45.825  29.257  34.672  1.00 43.47   6
ATOM    951  CD  GLN A 119      45.552  28.554  33.364  1.00 41.25   6
ATOM    952  OE1 GLN A 119      46.333  27.721  32.931  1.00 42.28   8
ATOM    953  NE2 GLN A 119      44.439  28.877  32.736  1.00 42.81   7
ATOM    954  C   GLN A 119      47.183  29.801  37.385  1.00 44.09   6
ATOM    955  O   GLN A 119      47.866  29.041  38.062  1.00 43.59   8
ATOM    956  N   ARG A 120      45.990  30.228  37.778  1.00 46.26   7
ATOM    957  CA  ARG A 120      45.433  29.762  39.036  1.00 48.60   6
ATOM    958  CB  ARG A 120      44.780  30.900  39.797  1.00 51.27   6
ATOM    959  CG  ARG A 120      45.705  32.036  40.096  1.00 60.62   6
ATOM    960  CD  ARG A 120      45.261  32.728  41.362  1.00 67.20   6
ATOM    961  NE  ARG A 120      45.730  32.045  42.575  1.00 69.70   7
ATOM    962  CZ  ARG A 120      44.989  31.859  43.668  1.00 69.76   6
ATOM    963  NH1 ARG A 120      43.728  32.279  43.709  1.00 68.36   7
ATOM    964  NH2 ARG A 120      45.533  31.307  44.748  1.00 70.33   7
ATOM    965  C   ARG A 120      44.414  28.669  38.804  1.00 48.02   6
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ATOM	966	O	ARG	A	120	43.706	28.669	37.788	1.00	46.40	8
ATOM	967	N	PHE	A	121	44.341	27.739	39.753	1.00	46.74	7
ATOM	968	CA	PHE	A	121	43.406	26.628	39.648	1.00	48.15	6
ATOM	969	CB	PHE	A	121	44.129	25.330	39.301	1.00	45.72	6
ATOM	970	CG	PHE	A	121	44.973	25.415	38.074	1.00	44.95	6
ATOM	971	CD1	PHE	A	121	46.240	25.993	38.122	1.00	43.54	6
ATOM	972	CD2	PHE	A	121	44.495	24.944	36.866	1.00	41.66	6
ATOM	973	CE1	PHE	A	121	47.011	26.099	36.986	1.00	42.05	6
ATOM	974	CE2	PHE	A	121	45.257	25.047	35.733	1.00	41.56	6
ATOM	975	CZ	PHE	A	121	46.521	25.628	35.790	1.00	42.24	6
ATOM	976	C	PHE	A	121	42.622	26.376	40.908	1.00	49.43	6
ATOM	977	O	PHE	A	121	42.996	26.810	42.001	1.00	49.47	8
ATOM	978	N	SER	A	122	41.524	25.653	40.727	1.00	51.17	7
ATOM	979	CA	SER	A	122	40.657	25.250	41.823	1.00	52.06	6
ATOM	980	CB	SER	A	122	39.193	25.501	41.477	1.00	52.69	6
ATOM	981	OG	SER	A	122	38.354	25.046	42.520	1.00	51.12	8
ATOM	982	C	SER	A	122	40.896	23.754	41.978	1.00	52.70	6
ATOM	983	O	SER	A	122	40.529	22.966	41.103	1.00	51.13	8
ATOM	984	N	CYS	A	123	41.543	23.369	43.070	1.00	52.97	7
ATOM	985	CA	CYS	A	123	41.820	21.967	43.312	1.00	56.03	6
ATOM	986	C	CYS	A	123	42.017	21.693	44.803	1.00	59.48	6
ATOM	987	O	CYS	A	123	41.882	22.602	45.634	1.00	60.13	8
ATOM	988	CB	CYS	A	123	43.052	21.555	42.534	1.00	53.78	6
ATOM	989	SG	CYS	A	123	44.483	22.558	42.968	1.00	56.89	16
ATOM	990	N	ASP	A	124	42.342	20.443	45.143	1.00	61.91	7
ATOM	991	CA	ASP	A	124	42.525	20.084	46.542	1.00	63.81	6
ATOM	992	CB	ASP	A	124	42.391	18.571	46.749	1.00	65.05	6
ATOM	993	CG	ASP	A	124	41.828	18.226	48.128	1.00	66.74	6
ATOM	994	OD1	ASP	A	124	42.113	18.973	49.103	1.00	65.03	8
ATOM	995	OD2	ASP	A	124	41.101	17.209	48.234	1.00	67.39	8
ATOM	996	C	ASP	A	124	43.857	20.543	47.110	1.00	63.72	6
ATOM	997	O	ASP	A	124	44.910	20.036	46.745	1.00	64.11	8
ATOM	998	N	VAL	A	125	43.794	21.495	48.031	1.00	64.49	7
ATOM	999	CA	VAL	A	125	44.981	22.042	48.681	1.00	63.28	6
ATOM	1000	CB	VAL	A	125	44.861	23.578	48.804	1.00	62.29	6
ATOM	1001	CG1	VAL	A	125	46.058	24.135	49.539	1.00	61.76	6
ATOM	1002	CG2	VAL	A	125	44.735	24.194	47.429	1.00	61.51	6
ATOM	1003	C	VAL	A	125	45.190	21.449	50.078	1.00	63.42	6
ATOM	1004	O	VAL	A	125	46.283	21.534	50.632	1.00	63.08	8
ATOM	1005	N	SER	A	126	44.141	20.848	50.641	1.00	64.34	7
ATOM	1006	CA	SER	A	126	44.218	20.252	51.981	1.00	64.43	6
ATOM	1007	CB	SER	A	126	42.924	19.503	52.302	1.00	63.15	6
ATOM	1008	OG	SER	A	126	42.723	18.465	51.371	1.00	58.95	8
ATOM	1009	C	SER	A	126	45.414	19.306	52.128	1.00	64.40	6
ATOM	1010	O	SER	A	126	45.636	18.420	51.299	1.00	62.89	8
ATOM	1011	N	GLY	A	127	46.188	19.510	53.186	1.00	65.00	7
ATOM	1012	CA	GLY	A	127	47.343	18.676	53.416	1.00	67.55	6
ATOM	1013	C	GLY	A	127	48.647	19.293	52.939	1.00	71.25	6
ATOM	1014	O	GLY	A	127	49.725	18.717	53.130	1.00	72.65	8
ATOM	1015	N	VAL	A	128	48.572	20.463	52.317	1.00	72.58	7
ATOM	1016	CA	VAL	A	128	49.779	21.109	51.830	1.00	73.82	6
ATOM	1017	CB	VAL	A	128	49.505	22.482	51.162	1.00	73.07	6
ATOM	1018	CG1	VAL	A	128	48.855	22.272	49.837	1.00	75.57	6
ATOM	1019	CG2	VAL	A	128	48.625	23.359	52.065	1.00	72.32	6
ATOM	1020	C	VAL	A	128	50.792	21.376	52.912	1.00	75.60	6
ATOM	1021	O	VAL	A	128	51.984	21.102	52.727	1.00	76.00	8
ATOM	1022	N	ASP	A	129	50.324	21.907	54.041	1.00	77.55	7
ATOM	1023	CA	ASP	A	129	51.241	22.287	55.107	1.00	79.65	6
ATOM	1024	CB	ASP	A	129	50.507	23.015	56.235	1.00	79.08	6
ATOM	1025	CG	ASP	A	129	51.427	23.954	57.017	1.00	80.06	6
ATOM	1026	OD1	ASP	A	129	51.000	25.097	57.338	1.00	80.12	8

ATOM	1027	OD2	ASP	A	129	52.578	23.546	57.311	1.00	80.59	8
ATOM	1028	C	ASP	A	129	52.085	21.164	55.676	1.00	80.77	6
ATOM	1029	O	ASP	A	129	53.089	21.441	56.355	1.00	80.25	8
ATOM	1030	N	THR	A	130	51.724	19.907	55.389	1.00	80.58	7
ATOM	1031	CA	THR	A	130	52.541	18.824	55.925	1.00	81.44	6
ATOM	1032	CB	THR	A	130	52.508	18.858	57.465	1.00	83.89	6
ATOM	1033	OG1	THR	A	130	51.433	19.722	57.880	1.00	85.49	8
ATOM	1034	CG2	THR	A	130	53.882	19.331	58.047	1.00	83.12	6
ATOM	1035	C	THR	A	130	52.309	17.374	55.529	1.00	80.12	6
ATOM	1036	O	THR	A	130	51.199	16.974	55.148	1.00	78.43	8
ATOM	1037	N	GLU	A	131	53.404	16.611	55.654	1.00	79.90	7
ATOM	1038	CA	GLU	A	131	53.459	15.165	55.432	1.00	80.19	6
ATOM	1039	CB	GLU	A	131	52.364	14.489	56.272	1.00	82.93	6
ATOM	1040	CG	GLU	A	131	52.693	14.372	57.760	1.00	86.59	6
ATOM	1041	CD	GLU	A	131	51.440	14.289	58.632	1.00	88.67	6
ATOM	1042	OE1	GLU	A	131	50.524	13.470	58.311	1.00	89.43	8
ATOM	1043	OE2	GLU	A	131	51.380	15.050	59.638	1.00	88.79	8
ATOM	1044	C	GLU	A	131	53.378	14.637	54.012	1.00	79.05	6
ATOM	1045	O	GLU	A	131	54.337	14.716	53.231	1.00	77.86	8
ATOM	1046	N	SER	A	132	52.227	14.033	53.727	1.00	77.68	7
ATOM	1047	CA	SER	A	132	51.915	13.474	52.426	1.00	76.46	6
ATOM	1048	CB	SER	A	132	50.796	12.429	52.576	1.00	76.05	6
ATOM	1049	OG	SER	A	132	49.642	12.990	53.176	1.00	74.46	8
ATOM	1050	C	SER	A	132	51.462	14.653	51.533	1.00	75.70	6
ATOM	1051	O	SER	A	132	51.123	14.479	50.355	1.00	75.58	8
ATOM	1052	N	GLY	A	133	51.468	15.848	52.127	1.00	73.94	7
ATOM	1053	CA	GLY	A	133	51.094	17.056	51.421	1.00	71.52	6
ATOM	1054	C	GLY	A	133	49.754	16.971	50.735	1.00	70.11	6
ATOM	1055	O	GLY	A	133	48.927	16.115	51.060	1.00	69.95	8
ATOM	1056	N	ALA	A	134	49.540	17.864	49.774	1.00	68.35	7
ATOM	1057	CA	ALA	A	134	48.290	17.895	49.033	1.00	65.73	6
ATOM	1058	CB	ALA	A	134	47.748	19.321	48.982	1.00	65.87	6
ATOM	1059	C	ALA	A	134	48.476	17.359	47.621	1.00	63.96	6
ATOM	1060	O	ALA	A	134	49.600	17.219	47.124	1.00	61.93	8
ATOM	1061	N	THR	A	135	47.353	17.048	46.985	1.00	63.38	7
ATOM	1062	CA	THR	A	135	47.359	16.549	45.621	1.00	62.44	6
ATOM	1063	CB	THR	A	135	47.003	15.066	45.562	1.00	62.52	6
ATOM	1064	OG1	THR	A	135	47.951	14.323	46.345	1.00	62.25	8
ATOM	1065	CG2	THR	A	135	47.040	14.574	44.122	1.00	61.31	6
ATOM	1066	C	THR	A	135	46.350	17.355	44.820	1.00	61.68	6
ATOM	1067	O	THR	A	135	45.120	17.188	44.944	1.00	60.36	8
ATOM	1068	N	CYS	A	136	46.900	18.259	44.017	1.00	59.30	7
ATOM	1069	CA	CYS	A	136	46.115	19.129	43.178	1.00	56.11	6
ATOM	1070	C	CYS	A	136	46.111	18.538	41.778	1.00	55.58	6
ATOM	1071	O	CYS	A	136	47.168	18.370	41.163	1.00	53.10	8
ATOM	1072	CB	CYS	A	136	46.739	20.518	43.181	1.00	55.44	6
ATOM	1073	SG	CYS	A	136	46.010	21.663	41.978	1.00	54.51	16
ATOM	1074	N	ARG	A	137	44.917	18.191	41.298	1.00	55.48	7
ATOM	1075	CA	ARG	A	137	44.764	17.611	39.968	1.00	56.07	6
ATOM	1076	CB	ARG	A	137	43.786	16.431	39.990	1.00	58.27	6
ATOM	1077	CG	ARG	A	137	44.213	15.318	40.915	1.00	62.94	6
ATOM	1078	CD	ARG	A	137	43.017	14.517	41.384	1.00	67.01	6
ATOM	1079	NE	ARG	A	137	43.308	13.821	42.641	1.00	72.70	7
ATOM	1080	CZ	ARG	A	137	44.131	12.772	42.762	1.00	74.69	6
ATOM	1081	NH1	ARG	A	137	44.765	12.270	41.696	1.00	74.12	7
ATOM	1082	NH2	ARG	A	137	44.326	12.226	43.958	1.00	74.27	7
ATOM	1083	C	ARG	A	137	44.265	18.670	39.010	1.00	53.72	6
ATOM	1084	O	ARG	A	137	43.325	19.396	39.301	1.00	51.52	8
ATOM	1085	N	ILE	A	138	44.917	18.738	37.860	1.00	52.05	7
ATOM	1086	CA	ILE	A	138	44.582	19.696	36.825	1.00	50.25	6
ATOM	1087	CB	ILE	A	138	45.778	20.624	36.557	1.00	49.78	6

ATOM	1088	CG2	ILE	A	138	45.449	21.566	35.421	1.00	48.31	6
ATOM	1089	CG1	ILE	A	138	46.150	21.389	37.837	1.00	48.07	6
ATOM	1090	CD1	ILE	A	138	47.444	22.144	37.750	1.00	41.58	6
ATOM	1091	C	ILE	A	138	44.270	18.925	35.555	1.00	49.76	6
ATOM	1092	O	ILE	A	138	45.119	18.190	35.058	1.00	50.40	8
ATOM	1093	N	LYS	A	139	43.059	19.081	35.032	1.00	49.44	7
ATOM	1094	CA	LYS	A	139	42.672	18.374	33.809	1.00	51.81	6
ATOM	1095	CB	LYS	A	139	41.285	17.713	33.969	1.00	52.86	6
ATOM	1096	CG	LYS	A	139	41.176	16.772	35.164	1.00	56.41	6
ATOM	1097	CD	LYS	A	139	39.919	15.940	35.137	1.00	57.01	6
ATOM	1098	CE	LYS	A	139	39.978	14.888	34.047	1.00	60.31	6
ATOM	1099	NZ	LYS	A	139	38.728	14.066	33.965	1.00	59.02	7
ATOM	1100	C	LYS	A	139	42.628	19.317	32.615	1.00	51.20	6
ATOM	1101	O	LYS	A	139	41.964	20.340	32.673	1.00	51.87	8
ATOM	1102	N	ILE	A	140	43.325	18.979	31.535	1.00	49.23	7
ATOM	1103	CA	ILE	A	140	43.295	19.826	30.354	1.00	49.38	6
ATOM	1104	CB	ILE	A	140	44.578	20.710	30.278	1.00	50.36	6
ATOM	1105	CG2	ILE	A	140	44.889	21.277	31.653	1.00	51.45	6
ATOM	1106	CG1	ILE	A	140	45.794	19.900	29.868	1.00	50.82	6
ATOM	1107	CD1	ILE	A	140	47.103	20.630	30.148	1.00	51.49	6
ATOM	1108	C	ILE	A	140	43.088	19.025	29.066	1.00	47.91	6
ATOM	1109	O	ILE	A	140	43.721	18.006	28.859	1.00	46.67	8
ATOM	1110	N	GLY	A	141	42.168	19.485	28.220	1.00	48.53	7
ATOM	1111	CA	GLY	A	141	41.885	18.811	26.959	1.00	47.60	6
ATOM	1112	C	GLY	A	141	41.255	19.765	25.958	1.00	48.49	6
ATOM	1113	O	GLY	A	141	40.938	20.900	26.317	1.00	49.03	8
ATOM	1114	N	SER	A	142	41.070	19.329	24.712	1.00	46.01	7
ATOM	1115	CA	SER	A	142	40.466	20.195	23.699	1.00	43.95	6
ATOM	1116	CB	SER	A	142	40.306	19.466	22.370	1.00	44.36	6
ATOM	1117	OG	SER	A	142	39.494	20.214	21.477	1.00	39.73	8
ATOM	1118	C	SER	A	142	39.107	20.686	24.144	1.00	45.09	6
ATOM	1119	O	SER	A	142	38.319	19.934	24.714	1.00	47.13	8
ATOM	1120	N	TRP	A	143	38.822	21.947	23.862	1.00	43.97	7
ATOM	1121	CA	TRP	A	143	37.564	22.537	24.256	1.00	41.28	6
ATOM	1122	CB	TRP	A	143	37.754	24.033	24.473	1.00	42.28	6
ATOM	1123	CG	TRP	A	143	36.577	24.697	25.126	1.00	42.52	6
ATOM	1124	CD2	TRP	A	143	36.215	24.610	26.505	1.00	39.43	6
ATOM	1125	CE2	TRP	A	143	35.025	25.359	26.676	1.00	39.15	6
ATOM	1126	CE3	TRP	A	143	36.778	23.969	27.613	1.00	37.16	6
ATOM	1127	CD1	TRP	A	143	35.618	25.480	24.526	1.00	41.93	6
ATOM	1128	NE1	TRP	A	143	34.681	25.880	25.456	1.00	40.50	7
ATOM	1129	CZ2	TRP	A	143	34.393	25.480	27.911	1.00	39.06	6
ATOM	1130	CZ3	TRP	A	143	36.150	24.090	28.837	1.00	39.37	6
ATOM	1131	CH2	TRP	A	143	34.968	24.840	28.978	1.00	39.40	6
ATOM	1132	C	TRP	A	143	36.450	22.307	23.258	1.00	41.37	6
ATOM	1133	O	TRP	A	143	35.287	22.239	23.632	1.00	42.45	8
ATOM	1134	N	THR	A	144	36.790	22.179	21.983	1.00	41.97	7
ATOM	1135	CA	THR	A	144	35.760	21.992	20.979	1.00	41.13	6
ATOM	1136	CB	THR	A	144	35.703	23.191	20.051	1.00	39.00	6
ATOM	1137	OG1	THR	A	144	36.994	23.416	19.490	1.00	39.19	8
ATOM	1138	CG2	THR	A	144	35.288	24.420	20.818	1.00	37.78	6
ATOM	1139	C	THR	A	144	35.879	20.738	20.148	1.00	42.54	6
ATOM	1140	O	THR	A	144	34.941	20.385	19.443	1.00	45.82	8
ATOM	1141	N	HIS	A	145	37.012	20.054	20.233	1.00	43.18	7
ATOM	1142	CA	HIS	A	145	37.187	18.837	19.459	1.00	46.20	6
ATOM	1143	CB	HIS	A	145	38.517	18.875	18.707	1.00	46.05	6
ATOM	1144	CG	HIS	A	145	38.588	19.933	17.646	1.00	46.56	6
ATOM	1145	CD2	HIS	A	145	37.994	20.022	16.432	1.00	45.44	6
ATOM	1146	ND1	HIS	A	145	39.366	21.061	17.772	1.00	44.61	7
ATOM	1147	CE1	HIS	A	145	39.250	21.797	16.682	1.00	43.87	6
ATOM	1148	NE2	HIS	A	145	38.423	21.189	15.853	1.00	41.35	7

ATOM	1149	C	HIS	A	145	37.105	17.570	20.303	1.00	47.36	6
ATOM	1150	O	HIS	A	145	37.811	17.422	21.298	1.00	47.71	8
ATOM	1151	N	HIS	A	146	36.230	16.656	19.898	1.00	48.75	7
ATOM	1152	CA	HIS	A	146	36.067	15.400	20.609	1.00	50.47	6
ATOM	1153	CB	HIS	A	146	34.658	14.846	20.365	1.00	49.28	6
ATOM	1154	CG	HIS	A	146	34.314	14.694	18.919	1.00	50.42	6
ATOM	1155	CD2	HIS	A	146	34.954	14.057	17.910	1.00	50.68	6
ATOM	1156	ND1	HIS	A	146	33.183	15.248	18.362	1.00	51.90	7
ATOM	1157	CE1	HIS	A	146	33.138	14.962	17.073	1.00	49.57	6
ATOM	1158	NE2	HIS	A	146	34.202	14.239	16.774	1.00	51.03	7
ATOM	1159	C	HIS	A	146	37.137	14.396	20.167	1.00	49.74	6
ATOM	1160	O	HIS	A	146	37.927	14.673	19.268	1.00	49.87	8
ATOM	1161	N	SER	A	147	37.145	13.234	20.809	1.00	50.23	7
ATOM	1162	CA	SER	A	147	38.101	12.158	20.543	1.00	50.98	6
ATOM	1163	CB	SER	A	147	37.722	10.934	21.372	1.00	50.73	6
ATOM	1164	OG	SER	A	147	36.346	10.642	21.240	1.00	51.84	8
ATOM	1165	C	SER	A	147	38.314	11.730	19.096	1.00	51.53	6
ATOM	1166	O	SER	A	147	39.374	11.228	18.754	1.00	50.53	8
ATOM	1167	N	ARG	A	148	37.319	11.925	18.245	1.00	53.75	7
ATOM	1168	CA	ARG	A	148	37.444	11.528	16.850	1.00	56.68	6
ATOM	1169	CB	ARG	A	148	36.052	11.408	16.221	1.00	60.77	6
ATOM	1170	CG	ARG	A	148	35.100	10.487	16.985	1.00	70.28	6
ATOM	1171	CD	ARG	A	148	33.673	10.516	16.423	1.00	76.18	6
ATOM	1172	NE	ARG	A	148	32.702	9.919	17.351	1.00	83.11	7
ATOM	1173	CZ	ARG	A	148	32.685	8.632	17.719	1.00	85.65	6
ATOM	1174	NH1	ARG	A	148	33.595	7.781	17.243	1.00	86.70	7
ATOM	1175	NH2	ARG	A	148	31.746	8.187	18.549	1.00	85.60	7
ATOM	1176	C	ARG	A	148	38.295	12.502	16.025	1.00	56.73	6
ATOM	1177	O	ARG	A	148	38.774	12.157	14.938	1.00	56.48	8
ATOM	1178	N	GLU	A	149	38.477	13.714	16.553	1.00	55.77	7
ATOM	1179	CA	GLU	A	149	39.233	14.767	15.884	1.00	51.96	6
ATOM	1180	CB	GLU	A	149	38.384	16.037	15.821	1.00	52.02	6
ATOM	1181	CG	GLU	A	149	36.918	15.748	15.527	1.00	51.38	6
ATOM	1182	CD	GLU	A	149	36.065	16.989	15.423	1.00	49.98	6
ATOM	1183	OE1	GLU	A	149	36.220	17.879	16.273	1.00	50.58	8
ATOM	1184	OE2	GLU	A	149	35.226	17.070	14.506	1.00	46.84	8
ATOM	1185	C	GLU	A	149	40.531	15.030	16.627	1.00	50.15	6
ATOM	1186	O	GLU	A	149	41.584	15.167	16.013	1.00	49.33	8
ATOM	1187	N	ILE	A	150	40.454	15.100	17.950	1.00	47.25	7
ATOM	1188	CA	ILE	A	150	41.643	15.309	18.748	1.00	48.44	6
ATOM	1189	CB	ILE	A	150	41.712	16.740	19.374	1.00	48.83	6
ATOM	1190	CG2	ILE	A	150	42.759	16.793	20.481	1.00	44.42	6
ATOM	1191	CG1	ILE	A	150	42.104	17.769	18.316	1.00	49.22	6
ATOM	1192	CD1	ILE	A	150	42.185	19.175	18.839	1.00	45.68	6
ATOM	1193	C	ILE	A	150	41.707	14.310	19.881	1.00	50.37	6
ATOM	1194	O	ILE	A	150	40.712	14.031	20.536	1.00	50.37	8
ATOM	1195	N	SER	A	151	42.902	13.781	20.104	1.00	52.48	7
ATOM	1196	CA	SER	A	151	43.156	12.841	21.178	1.00	54.49	6
ATOM	1197	CB	SER	A	151	43.437	11.452	20.611	1.00	54.22	6
ATOM	1198	OG	SER	A	151	44.619	11.457	19.844	1.00	54.28	8
ATOM	1199	C	SER	A	151	44.385	13.381	21.899	1.00	55.57	6
ATOM	1200	O	SER	A	151	45.347	13.798	21.257	1.00	56.29	8
ATOM	1201	N	VAL	A	152	44.337	13.400	23.227	1.00	57.03	7
ATOM	1202	CA	VAL	A	152	45.447	13.897	24.033	1.00	59.85	6
ATOM	1203	CB	VAL	A	152	44.979	14.922	25.100	1.00	59.80	6
ATOM	1204	CG1	VAL	A	152	44.170	16.021	24.447	1.00	60.14	6
ATOM	1205	CG2	VAL	A	152	44.163	14.225	26.175	1.00	61.09	6
ATOM	1206	C	VAL	A	152	46.084	12.722	24.747	1.00	61.00	6
ATOM	1207	O	VAL	A	152	45.393	11.785	25.132	1.00	59.83	8
ATOM	1208	N	ASP	A	153	47.398	12.780	24.932	1.00	63.57	7
ATOM	1209	CA	ASP	A	153	48.114	11.690	25.582	1.00	66.72	6

ATOM	1210	CB	ASP	A	153	48.620	10.724	24.505	1.00 66.16	6
ATOM	1211	CG	ASP	A	153	47.505	10.245	23.573	1.00 67.72	6
ATOM	1212	OD1	ASP	A	153	46.769	9.317	23.972	1.00 68.96	8
ATOM	1213	OD2	ASP	A	153	47.354	10.801	22.451	1.00 67.60	8
ATOM	1214	C	ASP	A	153	49.293	12.198	26.422	1.00 68.93	6
ATOM	1215	O	ASP	A	153	49.951	13.175	26.058	1.00 69.39	8
ATOM	1216	N	PRO	A	154	49.553	11.564	27.577	1.00 70.74	7
ATOM	1217	CD	PRO	A	154	48.601	10.759	28.357	1.00 71.40	6
ATOM	1218	CA	PRO	A	154	50.675	11.995	28.421	1.00 73.42	6
ATOM	1219	CB	PRO	A	154	50.421	11.266	29.735	1.00 72.22	6
ATOM	1220	CG	PRO	A	154	48.930	11.182	29.776	1.00 72.97	6
ATOM	1221	C	PRO	A	154	51.999	11.580	27.773	1.00 75.99	6
ATOM	1222	O	PRO	A	154	51.997	10.951	26.716	1.00 75.49	8
ATOM	1223	N	THR	A	155	53.121	11.916	28.406	1.00 79.97	7
ATOM	1224	CA	THR	A	155	54.433	11.580	27.851	1.00 84.54	6
ATOM	1225	CB	THR	A	155	55.002	12.797	27.084	1.00 84.38	6
ATOM	1226	OG1	THR	A	155	55.314	13.844	28.015	1.00 85.24	8
ATOM	1227	CG2	THR	A	155	53.979	13.326	26.085	1.00 83.86	6
ATOM	1228	C	THR	A	155	55.504	11.101	28.868	1.00 88.31	6
ATOM	1229	O	THR	A	155	55.179	10.480	29.905	1.00 89.23	8
ATOM	1230	N	THR	A	156	56.774	11.402	28.539	1.00 91.22	7
ATOM	1231	CA	THR	A	156	57.970	11.057	29.337	1.00 93.64	6
ATOM	1232	CB	THR	A	156	59.146	12.041	29.041	1.00 93.80	6
ATOM	1233	OG1	THR	A	156	59.430	12.048	27.631	1.00 93.55	8
ATOM	1234	CG2	THR	A	156	60.414	11.624	29.839	1.00 93.12	6
ATOM	1235	C	THR	A	156	57.778	11.031	30.862	1.00 95.49	6
ATOM	1236	O	THR	A	156	57.812	12.080	31.532	1.00 95.50	8
ATOM	1237	N	GLU	A	157	57.614	9.827	31.406	1.00 97.12	7
ATOM	1238	CA	GLU	A	157	57.411	9.649	32.841	1.00 98.24	6
ATOM	1239	CB	GLU	A	157	56.619	8.370	33.095	1.00100.23	6
ATOM	1240	CG	GLU	A	157	55.476	8.150	32.109	1.00103.23	6
ATOM	1241	CD	GLU	A	157	54.728	6.842	32.372	1.00104.38	6
ATOM	1242	OE1	GLU	A	157	55.391	5.769	32.462	1.00103.49	8
ATOM	1243	OE2	GLU	A	157	53.475	6.896	32.482	1.00105.11	8
ATOM	1244	C	GLU	A	157	58.731	9.570	33.591	1.00 98.22	6
ATOM	1245	O	GLU	A	157	58.742	9.488	34.825	1.00 98.77	8
ATOM	1246	N	ASN	A	158	59.840	9.582	32.854	1.00 97.95	7
ATOM	1247	CA	ASN	A	158	61.154	9.505	33.494	1.00 98.34	6
ATOM	1248	CB	ASN	A	158	62.244	9.212	32.455	1.00100.52	6
ATOM	1249	CG	ASN	A	158	61.953	7.969	31.634	1.00102.32	6
ATOM	1250	OD1	ASN	A	158	61.787	6.872	32.184	1.00104.16	8
ATOM	1251	ND2	ASN	A	158	61.898	8.131	30.305	1.00102.61	7
ATOM	1252	C	ASN	A	158	61.471	10.832	34.196	1.00 97.02	6
ATOM	1253	O	ASN	A	158	61.170	11.019	35.392	1.00 96.34	8
ATOM	1254	N	SER	A	159	62.093	11.729	33.423	1.00 94.95	7
ATOM	1255	CA	SER	A	159	62.492	13.069	33.857	1.00 91.51	6
ATOM	1256	CB	SER	A	159	61.878	14.091	32.890	1.00 91.99	6
ATOM	1257	OG	SER	A	159	60.550	13.708	32.529	1.00 90.83	8
ATOM	1258	C	SER	A	159	62.116	13.412	35.301	1.00 88.77	6
ATOM	1259	O	SER	A	159	60.939	13.380	35.666	1.00 88.38	8
ATOM	1260	N	ASP	A	160	63.120	13.728	36.120	1.00 85.60	7
ATOM	1261	CA	ASP	A	160	62.867	14.093	37.517	1.00 81.69	6
ATOM	1262	CB	ASP	A	160	64.107	14.716	38.164	1.00 81.79	6
ATOM	1263	CG	ASP	A	160	63.827	15.217	39.578	1.00 82.16	6
ATOM	1264	OD1	ASP	A	160	64.609	16.057	40.075	1.00 82.93	8
ATOM	1265	OD2	ASP	A	160	62.824	14.766	40.194	1.00 81.33	8
ATOM	1266	C	ASP	A	160	61.748	15.125	37.556	1.00 78.87	6
ATOM	1267	O	ASP	A	160	61.906	16.215	36.997	1.00 77.29	8
ATOM	1268	N	ASP	A	161	60.643	14.783	38.223	1.00 75.12	7
ATOM	1269	CA	ASP	A	161	59.493	15.677	38.324	1.00 71.64	6
ATOM	1270	CB	ASP	A	161	58.433	15.111	39.273	1.00 71.12	6

ATOM	1271	CG	ASP	A	161	57.719	13.895	38.698	1.00	71.43	6
ATOM	1272	OD1	ASP	A	161	57.509	13.854	37.463	1.00	70.50	8
ATOM	1273	OD2	ASP	A	161	57.353	12.983	39.480	1.00	71.76	8
ATOM	1274	C	ASP	A	161	59.814	17.097	38.756	1.00	69.97	6
ATOM	1275	O	ASP	A	161	59.009	18.001	38.545	1.00	69.41	8
ATOM	1276	N	SER	A	162	60.974	17.321	39.358	1.00	68.43	7
ATOM	1277	CA	SER	A	162	61.282	18.682	39.774	1.00	68.46	6
ATOM	1278	CB	SER	A	162	61.190	18.809	41.308	1.00	68.76	6
ATOM	1279	OG	SER	A	162	62.209	18.069	41.962	1.00	68.11	8
ATOM	1280	C	SER	A	162	62.636	19.163	39.289	1.00	67.78	6
ATOM	1281	O	SER	A	162	63.264	20.014	39.917	1.00	67.84	8
ATOM	1282	N	GLU	A	163	63.087	18.640	38.156	1.00	67.60	7
ATOM	1283	CA	GLU	A	163	64.382	19.052	37.649	1.00	68.35	6
ATOM	1284	CB	GLU	A	163	64.884	18.051	36.609	1.00	70.48	6
ATOM	1285	CG	GLU	A	163	64.380	18.242	35.193	1.00	73.24	6
ATOM	1286	CD	GLU	A	163	65.111	17.328	34.204	1.00	75.50	6
ATOM	1287	OE1	GLU	A	163	64.835	16.097	34.211	1.00	76.99	8
ATOM	1288	OE2	GLU	A	163	65.970	17.842	33.438	1.00	73.24	8
ATOM	1289	C	GLU	A	163	64.342	20.475	37.083	1.00	68.50	6
ATOM	1290	O	GLU	A	163	65.385	21.062	36.774	1.00	69.25	8
ATOM	1291	N	TYR	A	164	63.140	21.031	36.958	1.00	67.44	7
ATOM	1292	CA	TYR	A	164	62.968	22.396	36.466	1.00	65.48	6
ATOM	1293	CB	TYR	A	164	62.085	22.422	35.221	1.00	66.46	6
ATOM	1294	CG	TYR	A	164	62.709	21.754	34.029	1.00	67.56	6
ATOM	1295	CD1	TYR	A	164	62.082	20.664	33.415	1.00	68.14	6
ATOM	1296	CE1	TYR	A	164	62.664	20.011	32.328	1.00	67.68	6
ATOM	1297	CD2	TYR	A	164	63.942	22.185	33.527	1.00	66.99	6
ATOM	1298	CE2	TYR	A	164	64.539	21.538	32.435	1.00	69.28	6
ATOM	1299	CZ	TYR	A	164	63.892	20.449	31.837	1.00	68.44	6
ATOM	1300	OH	TYR	A	164	64.456	19.823	30.737	1.00	69.00	8
ATOM	1301	C	TYR	A	164	62.313	23.259	37.534	1.00	64.21	6
ATOM	1302	O	TYR	A	164	62.181	24.474	37.368	1.00	62.71	8
ATOM	1303	N	PHE	A	165	61.899	22.626	38.627	1.00	62.72	7
ATOM	1304	CA	PHE	A	165	61.241	23.343	39.705	1.00	60.48	6
ATOM	1305	CB	PHE	A	165	60.738	22.364	40.758	1.00	57.99	6
ATOM	1306	CG	PHE	A	165	59.676	22.936	41.641	1.00	57.14	6
ATOM	1307	CD1	PHE	A	165	58.424	23.252	41.115	1.00	55.84	6
ATOM	1308	CD2	PHE	A	165	59.933	23.194	42.985	1.00	55.03	6
ATOM	1309	CE1	PHE	A	165	57.439	23.818	41.902	1.00	54.80	6
ATOM	1310	CE2	PHE	A	165	58.961	23.762	43.787	1.00	57.75	6
ATOM	1311	CZ	PHE	A	165	57.699	24.079	43.242	1.00	57.78	6
ATOM	1312	C	PHE	A	165	62.159	24.369	40.354	1.00	60.44	6
ATOM	1313	O	PHE	A	165	63.348	24.121	40.547	1.00	60.73	8
ATOM	1314	N	SER	A	166	61.611	25.534	40.676	1.00	60.95	7
ATOM	1315	CA	SER	A	166	62.418	26.567	41.312	1.00	61.11	6
ATOM	1316	CB	SER	A	166	61.638	27.874	41.457	1.00	59.76	6
ATOM	1317	OG	SER	A	166	62.476	28.875	42.015	1.00	59.79	8
ATOM	1318	C	SER	A	166	62.809	26.068	42.694	1.00	61.38	6
ATOM	1319	O	SER	A	166	62.009	25.442	43.393	1.00	61.62	8
ATOM	1320	N	GLN	A	167	64.038	26.359	43.089	1.00	61.82	7
ATOM	1321	CA	GLN	A	167	64.525	25.931	44.393	1.00	62.17	6
ATOM	1322	CB	GLN	A	167	66.052	25.797	44.351	1.00	63.58	6
ATOM	1323	CG	GLN	A	167	66.745	27.065	43.861	1.00	66.42	6
ATOM	1324	CD	GLN	A	167	68.204	26.851	43.514	1.00	69.06	6
ATOM	1325	OE1	GLN	A	167	69.008	26.488	44.376	1.00	70.77	8
ATOM	1326	NE2	GLN	A	167	68.556	27.081	42.241	1.00	69.23	7
ATOM	1327	C	GLN	A	167	64.119	26.927	45.476	1.00	61.22	6
ATOM	1328	O	GLN	A	167	64.112	26.585	46.659	1.00	61.10	8
ATOM	1329	N	TYR	A	168	63.762	28.147	45.075	1.00	58.44	7
ATOM	1330	CA	TYR	A	168	63.392	29.162	46.046	1.00	56.45	6
ATOM	1331	CB	TYR	A	168	63.881	30.522	45.564	1.00	55.36	6

ATOM	1332	CG	TYR	A	168	65.335	30.469	45.158	1.00 57.58	6
ATOM	1333	CD1	TYR	A	168	65.699	30.352	43.818	1.00 57.60	6
ATOM	1334	CE1	TYR	A	168	67.031	30.233	43.439	1.00 57.86	6
ATOM	1335	CD2	TYR	A	168	66.349	30.467	46.115	1.00 57.43	6
ATOM	1336	CE2	TYR	A	168	67.683	30.347	45.749	1.00 58.19	6
ATOM	1337	CZ	TYR	A	168	68.017	30.228	44.410	1.00 59.25	6
ATOM	1338	OH	TYR	A	168	69.337	30.086	44.042	1.00 60.91	8
ATOM	1339	C	TYR	A	168	61.912	29.199	46.383	1.00 56.00	6
ATOM	1340	O	TYR	A	168	61.457	30.053	47.142	1.00 56.39	8
ATOM	1341	N	SER	A	169	61.162	28.257	45.832	1.00 55.67	7
ATOM	1342	CA	SER	A	169	59.732	28.179	46.096	1.00 56.31	6
ATOM	1343	CB	SER	A	169	59.082	27.123	45.197	1.00 57.76	6
ATOM	1344	OG	SER	A	169	57.699	26.971	45.501	1.00 55.64	8
ATOM	1345	C	SER	A	169	59.478	27.804	47.544	1.00 57.69	6
ATOM	1346	O	SER	A	169	60.246	27.066	48.152	1.00 58.82	8
ATOM	1347	N	ARG	A	170	58.385	28.302	48.096	1.00 58.68	7
ATOM	1348	CA	ARG	A	170	58.043	27.993	49.472	1.00 58.62	6
ATOM	1349	CB	ARG	A	170	56.907	28.901	49.956	1.00 60.14	6
ATOM	1350	CG	ARG	A	170	57.371	30.123	50.727	1.00 60.43	6
ATOM	1351	CD	ARG	A	170	56.401	31.291	50.589	1.00 64.30	6
ATOM	1352	NE	ARG	A	170	55.020	30.998	50.989	1.00 66.31	7
ATOM	1353	CZ	ARG	A	170	53.967	31.107	50.174	1.00 66.81	6
ATOM	1354	NH1	ARG	A	170	54.129	31.489	48.915	1.00 63.97	7
ATOM	1355	NH2	ARG	A	170	52.750	30.850	50.619	1.00 67.23	7
ATOM	1356	C	ARG	A	170	57.604	26.544	49.554	1.00 58.75	6
ATOM	1357	O	ARG	A	170	57.516	25.975	50.642	1.00 60.59	8
ATOM	1358	N	PHE	A	171	57.339	25.933	48.405	1.00 57.02	7
ATOM	1359	CA	PHE	A	171	56.882	24.552	48.404	1.00 56.54	6
ATOM	1360	CB	PHE	A	171	55.499	24.479	47.765	1.00 55.41	6
ATOM	1361	CG	PHE	A	171	54.552	25.522	48.281	1.00 55.91	6
ATOM	1362	CD1	PHE	A	171	54.685	26.856	47.893	1.00 57.70	6
ATOM	1363	CD2	PHE	A	171	53.560	25.190	49.203	1.00 56.28	6
ATOM	1364	CE1	PHE	A	171	53.845	27.847	48.419	1.00 58.19	6
ATOM	1365	CE2	PHE	A	171	52.718	26.170	49.732	1.00 55.91	6
ATOM	1366	CZ	PHE	A	171	52.864	27.505	49.337	1.00 57.16	6
ATOM	1367	C	PHE	A	171	57.844	23.612	47.695	1.00 56.77	6
ATOM	1368	O	PHE	A	171	58.841	24.045	47.113	1.00 56.03	8
ATOM	1369	N	GLU	A	172	57.552	22.319	47.765	1.00 56.23	7
ATOM	1370	CA	GLU	A	172	58.389	21.325	47.120	1.00 58.00	6
ATOM	1371	CB	GLU	A	172	59.371	20.707	48.119	1.00 60.23	6
ATOM	1372	CG	GLU	A	172	58.734	19.970	49.303	1.00 64.00	6
ATOM	1373	CD	GLU	A	172	59.769	19.445	50.313	1.00 66.01	6
ATOM	1374	OE1	GLU	A	172	60.869	19.042	49.868	1.00 69.59	8
ATOM	1375	OE2	GLU	A	172	59.487	19.421	51.541	1.00 65.33	8
ATOM	1376	C	GLU	A	172	57.497	20.259	46.518	1.00 59.67	6
ATOM	1377	O	GLU	A	172	56.356	20.064	46.955	1.00 60.12	8
ATOM	1378	N	ILE	A	173	58.006	19.579	45.496	1.00 60.16	7
ATOM	1379	CA	ILE	A	173	57.224	18.545	44.827	1.00 60.67	6
ATOM	1380	CB	ILE	A	173	57.413	18.587	43.291	1.00 61.87	6
ATOM	1381	CG2	ILE	A	173	56.659	17.422	42.644	1.00 62.56	6
ATOM	1382	CG1	ILE	A	173	56.920	19.919	42.727	1.00 61.03	6
ATOM	1383	CD1	ILE	A	173	57.165	20.062	41.244	1.00 59.49	6
ATOM	1384	C	ILE	A	173	57.579	17.150	45.296	1.00 59.83	6
ATOM	1385	O	ILE	A	173	58.751	16.770	45.360	1.00 57.21	8
ATOM	1386	N	LEU	A	174	56.554	16.381	45.616	1.00 61.63	7
ATOM	1387	CA	LEU	A	174	56.786	15.022	46.056	1.00 64.20	6
ATOM	1388	CB	LEU	A	174	55.687	14.592	47.024	1.00 63.47	6
ATOM	1389	CG	LEU	A	174	55.461	15.601	48.149	1.00 65.34	6
ATOM	1390	CD1	LEU	A	174	54.285	15.144	49.024	1.00 66.19	6
ATOM	1391	CD2	LEU	A	174	56.747	15.770	48.962	1.00 64.00	6
ATOM	1392	C	LEU	A	174	56.783	14.147	44.806	1.00 65.92	6

ATOM	1393	O	LEU	A	174	57.757	13.440	44.522	1.00	65.29	8
ATOM	1394	N	ASP	A	175	55.702	14.233	44.036	1.00	67.33	7
ATOM	1395	CA	ASP	A	175	55.583	13.436	42.827	1.00	68.45	6
ATOM	1396	CB	ASP	A	175	55.227	11.993	43.223	1.00	68.56	6
ATOM	1397	CG	ASP	A	175	55.161	11.038	42.032	1.00	68.23	6
ATOM	1398	OD1	ASP	A	175	56.141	10.964	41.244	1.00	67.58	8
ATOM	1399	OD2	ASP	A	175	54.121	10.347	41.905	1.00	67.56	8
ATOM	1400	C	ASP	A	175	54.542	14.023	41.872	1.00	69.02	6
ATOM	1401	O	ASP	A	175	53.617	14.735	42.286	1.00	69.85	8
ATOM	1402	N	VAL	A	176	54.714	13.727	40.587	1.00	68.72	7
ATOM	1403	CA	VAL	A	176	53.809	14.198	39.552	1.00	67.76	6
ATOM	1404	CB	VAL	A	176	54.461	15.324	38.694	1.00	67.60	6
ATOM	1405	CG1	VAL	A	176	53.533	15.721	37.542	1.00	66.09	6
ATOM	1406	CG2	VAL	A	176	54.771	16.532	39.564	1.00	65.31	6
ATOM	1407	C	VAL	A	176	53.495	13.025	38.645	1.00	67.31	6
ATOM	1408	O	VAL	A	176	54.399	12.308	38.230	1.00	66.10	8
ATOM	1409	N	THR	A	177	52.213	12.833	38.348	1.00	68.30	7
ATOM	1410	CA	THR	A	177	51.781	11.763	37.463	1.00	69.37	6
ATOM	1411	CB	THR	A	177	51.241	10.565	38.259	1.00	69.49	6
ATOM	1412	OG1	THR	A	177	50.218	11.007	39.160	1.00	69.60	8
ATOM	1413	CG2	THR	A	177	52.366	9.905	39.045	1.00	69.19	6
ATOM	1414	C	THR	A	177	50.696	12.276	36.528	1.00	70.72	6
ATOM	1415	O	THR	A	177	49.879	13.119	36.917	1.00	72.04	8
ATOM	1416	N	GLN	A	178	50.692	11.771	35.297	1.00	71.85	7
ATOM	1417	CA	GLN	A	178	49.706	12.191	34.302	1.00	73.03	6
ATOM	1418	CB	GLN	A	178	50.392	12.916	33.144	1.00	75.20	6
ATOM	1419	CG	GLN	A	178	51.681	13.640	33.533	1.00	78.41	6
ATOM	1420	CD	GLN	A	178	52.059	14.733	32.539	1.00	79.92	6
ATOM	1421	OE1	GLN	A	178	52.078	14.509	31.315	1.00	81.52	8
ATOM	1422	NE2	GLN	A	178	52.370	15.924	33.061	1.00	78.36	7
ATOM	1423	C	GLN	A	178	49.014	10.964	33.764	1.00	72.67	6
ATOM	1424	O	GLN	A	178	49.679	10.043	33.293	1.00	73.74	8
ATOM	1425	N	LYS	A	179	47.686	10.947	33.827	1.00	72.17	7
ATOM	1426	CA	LYS	A	179	46.916	9.807	33.337	1.00	71.53	6
ATOM	1427	CB	LYS	A	179	46.327	9.038	34.519	1.00	74.09	6
ATOM	1428	CG	LYS	A	179	47.352	8.781	35.644	1.00	79.46	6
ATOM	1429	CD	LYS	A	179	46.703	8.189	36.905	1.00	81.06	6
ATOM	1430	CE	LYS	A	179	47.635	8.300	38.119	1.00	80.77	6
ATOM	1431	NZ	LYS	A	179	47.968	9.715	38.443	1.00	80.83	7
ATOM	1432	C	LYS	A	179	45.795	10.316	32.470	1.00	70.00	6
ATOM	1433	O	LYS	A	179	44.878	10.939	32.980	1.00	73.37	8
ATOM	1434	N	LYS	A	180	45.845	10.060	31.170	1.00	67.55	7
ATOM	1435	CA	LYS	A	180	44.780	10.538	30.294	1.00	67.72	6
ATOM	1436	CB	LYS	A	180	45.171	10.327	28.829	1.00	66.54	6
ATOM	1437	CG	LYS	A	180	45.120	8.909	28.344	1.00	63.87	6
ATOM	1438	CD	LYS	A	180	43.751	8.573	27.796	1.00	64.72	6
ATOM	1439	CE	LYS	A	180	43.404	9.412	26.552	1.00	65.43	6
ATOM	1440	NZ	LYS	A	180	44.217	9.057	25.339	1.00	65.01	7
ATOM	1441	C	LYS	A	180	43.445	9.854	30.586	1.00	67.22	6
ATOM	1442	O	LYS	A	180	43.373	9.021	31.471	1.00	68.12	8
ATOM	1443	N	ASN	A	181	42.388	10.231	29.871	1.00	67.59	7
ATOM	1444	CA	ASN	A	181	41.083	9.600	30.053	1.00	68.03	6
ATOM	1445	CB	ASN	A	181	40.710	9.514	31.545	1.00	69.44	6
ATOM	1446	CG	ASN	A	181	40.940	10.803	32.291	1.00	68.81	6
ATOM	1447	OD1	ASN	A	181	40.552	11.872	31.834	1.00	71.29	8
ATOM	1448	ND2	ASN	A	181	41.556	10.706	33.463	1.00	67.88	7
ATOM	1449	C	ASN	A	181	39.917	10.194	29.272	1.00	67.66	6
ATOM	1450	O	ASN	A	181	39.576	11.350	29.437	1.00	68.16	8
ATOM	1451	N	SER	A	182	39.302	9.377	28.420	1.00	68.81	7
ATOM	1452	CA	SER	A	182	38.160	9.802	27.615	1.00	68.00	6
ATOM	1453	CB	SER	A	182	37.861	8.745	26.553	1.00	67.42	6

ATOM	1454	OG	SER	A	182	36.905	9.223	25.626	1.00	70.87	8
ATOM	1455	C	SER	A	182	36.953	9.974	28.541	1.00	67.36	6
ATOM	1456	O	SER	A	182	36.915	9.385	29.617	1.00	67.61	8
ATOM	1457	N	VAL	A	183	35.973	10.771	28.126	1.00	65.82	7
ATOM	1458	CA	VAL	A	183	34.790	11.017	28.950	1.00	64.66	6
ATOM	1459	CB	VAL	A	183	35.151	11.912	30.163	1.00	63.68	6
ATOM	1460	CG1	VAL	A	183	36.153	12.956	29.748	1.00	65.08	6
ATOM	1461	CG2	VAL	A	183	33.901	12.581	30.718	1.00	61.80	6
ATOM	1462	C	VAL	A	183	33.632	11.666	28.204	1.00	64.12	6
ATOM	1463	O	VAL	A	183	33.828	12.597	27.440	1.00	64.83	8
ATOM	1464	N	THR	A	184	32.422	11.170	28.432	1.00	65.00	7
ATOM	1465	CA	THR	A	184	31.240	11.737	27.793	1.00	67.07	6
ATOM	1466	CB	THR	A	184	30.303	10.641	27.258	1.00	64.63	6
ATOM	1467	OG1	THR	A	184	30.977	9.911	26.224	1.00	61.46	8
ATOM	1468	CG2	THR	A	184	29.030	11.260	26.685	1.00	67.30	6
ATOM	1469	C	THR	A	184	30.490	12.596	28.808	1.00	69.96	6
ATOM	1470	O	THR	A	184	30.413	12.238	29.993	1.00	71.87	8
ATOM	1471	N	TYR	A	185	29.961	13.735	28.362	1.00	71.00	7
ATOM	1472	CA	TYR	A	185	29.230	14.618	29.261	1.00	72.17	6
ATOM	1473	CB	TYR	A	185	29.849	16.015	29.274	1.00	72.39	6
ATOM	1474	CG	TYR	A	185	31.335	16.005	29.525	1.00	72.53	6
ATOM	1475	CD1	TYR	A	185	32.226	15.598	28.531	1.00	71.50	6
ATOM	1476	CE1	TYR	A	185	33.601	15.535	28.775	1.00	70.43	6
ATOM	1477	CD2	TYR	A	185	31.854	16.358	30.776	1.00	73.42	6
ATOM	1478	CE2	TYR	A	185	33.236	16.300	31.031	1.00	71.16	6
ATOM	1479	CZ	TYR	A	185	34.097	15.885	30.022	1.00	70.35	6
ATOM	1480	OH	TYR	A	185	35.448	15.811	30.254	1.00	68.69	8
ATOM	1481	C	TYR	A	185	27.804	14.705	28.780	1.00	73.84	6
ATOM	1482	O	TYR	A	185	27.551	14.756	27.576	1.00	73.39	8
ATOM	1483	N	SER	A	186	26.873	14.714	29.727	1.00	76.31	7
ATOM	1484	CA	SER	A	186	25.455	14.794	29.403	1.00	78.23	6
ATOM	1485	CB	SER	A	186	24.645	14.953	30.693	1.00	78.92	6
ATOM	1486	OG	SER	A	186	25.215	15.952	31.527	1.00	77.75	8
ATOM	1487	C	SER	A	186	25.197	15.967	28.453	1.00	78.29	6
ATOM	1488	O	SER	A	186	24.348	15.879	27.553	1.00	79.09	8
ATOM	1489	N	CYS	A	187	25.949	17.047	28.653	1.00	77.81	7
ATOM	1490	CA	CYS	A	187	25.830	18.254	27.839	1.00	78.71	6
ATOM	1491	C	CYS	A	187	26.144	17.978	26.407	1.00	78.06	6
ATOM	1492	O	CYS	A	187	25.514	18.482	25.488	1.00	78.32	8
ATOM	1493	CB	CYS	A	187	26.858	19.320	28.252	1.00	79.52	6
ATOM	1494	SG	CYS	A	187	28.656	18.934	27.946	1.00	82.56	16
ATOM	1495	N	CYS	A	188	27.147	17.144	26.244	1.00	78.96	7
ATOM	1496	CA	CYS	A	188	27.706	16.918	24.947	1.00	78.72	6
ATOM	1497	C	CYS	A	188	27.817	15.468	24.454	1.00	78.19	6
ATOM	1498	O	CYS	A	188	28.454	14.618	25.096	1.00	78.27	8
ATOM	1499	CB	CYS	A	188	29.070	17.610	25.006	1.00	79.96	6
ATOM	1500	SG	CYS	A	188	29.118	19.206	25.950	1.00	80.88	16
ATOM	1501	N	PRO	A	189	27.211	15.186	23.281	1.00	77.44	7
ATOM	1502	CD	PRO	A	189	26.571	16.283	22.526	1.00	77.01	6
ATOM	1503	CA	PRO	A	189	27.125	13.918	22.532	1.00	76.01	6
ATOM	1504	CB	PRO	A	189	26.756	14.378	21.129	1.00	76.94	6
ATOM	1505	CG	PRO	A	189	25.858	15.558	21.408	1.00	77.54	6
ATOM	1506	C	PRO	A	189	28.355	12.991	22.512	1.00	75.22	6
ATOM	1507	O	PRO	A	189	28.300	11.883	23.056	1.00	76.90	8
ATOM	1508	N	GLU	A	190	29.447	13.423	21.874	1.00	72.83	7
ATOM	1509	CA	GLU	A	190	30.662	12.603	21.768	1.00	69.68	6
ATOM	1510	CB	GLU	A	190	31.535	13.102	20.629	1.00	72.91	6
ATOM	1511	CG	GLU	A	190	30.777	13.743	19.486	1.00	75.89	6
ATOM	1512	CD	GLU	A	190	30.236	12.730	18.505	1.00	77.90	6
ATOM	1513	OE1	GLU	A	190	30.974	11.765	18.170	1.00	78.51	8
ATOM	1514	OE2	GLU	A	190	29.080	12.909	18.058	1.00	79.55	8

ATOM	1515	C	GLU	A	190	31.492	12.631	23.039	1.00	66.30	6
ATOM	1516	O	GLU	A	190	31.113	13.278	24.009	1.00	65.23	8
ATOM	1517	N	ALA	A	191	32.633	11.941	23.020	1.00	63.17	7
ATOM	1518	CA	ALA	A	191	33.524	11.891	24.182	1.00	61.94	6
ATOM	1519	CB	ALA	A	191	34.102	10.493	24.341	1.00	60.63	6
ATOM	1520	C	ALA	A	191	34.666	12.904	24.055	1.00	61.30	6
ATOM	1521	O	ALA	A	191	35.148	13.165	22.950	1.00	62.21	8
ATOM	1522	N	TYR	A	192	35.105	13.468	25.179	1.00	58.30	7
ATOM	1523	CA	TYR	A	192	36.188	14.438	25.159	1.00	56.19	6
ATOM	1524	CB	TYR	A	192	35.695	15.807	25.633	1.00	55.84	6
ATOM	1525	CG	TYR	A	192	34.779	16.487	24.649	1.00	56.15	6
ATOM	1526	CD1	TYR	A	192	33.409	16.226	24.642	1.00	56.04	6
ATOM	1527	CE1	TYR	A	192	32.571	16.794	23.683	1.00	57.88	6
ATOM	1528	CD2	TYR	A	192	35.291	17.341	23.675	1.00	56.39	6
ATOM	1529	CE2	TYR	A	192	34.467	17.915	22.715	1.00	57.19	6
ATOM	1530	CZ	TYR	A	192	33.108	17.637	22.722	1.00	58.29	6
ATOM	1531	OH	TYR	A	192	32.295	18.200	21.769	1.00	58.06	8
ATOM	1532	C	TYR	A	192	37.389	14.013	25.984	1.00	56.62	6
ATOM	1533	O	TYR	A	192	37.375	14.090	27.217	1.00	57.67	8
ATOM	1534	N	GLU	A	193	38.436	13.571	25.291	1.00	57.15	7
ATOM	1535	CA	GLU	A	193	39.676	13.124	25.935	1.00	58.07	6
ATOM	1536	CB	GLU	A	193	40.651	12.523	24.901	1.00	56.63	6
ATOM	1537	CG	GLU	A	193	40.143	11.269	24.209	1.00	55.92	6
ATOM	1538	CD	GLU	A	193	41.171	10.636	23.307	1.00	56.05	6
ATOM	1539	OE1	GLU	A	193	42.339	10.509	23.743	1.00	56.33	8
ATOM	1540	OE2	GLU	A	193	40.808	10.250	22.171	1.00	57.19	8
ATOM	1541	C	GLU	A	193	40.363	14.278	26.655	1.00	58.09	6
ATOM	1542	O	GLU	A	193	40.221	15.440	26.261	1.00	59.15	8
ATOM	1543	N	ASP	A	194	41.098	13.948	27.712	1.00	57.73	7
ATOM	1544	CA	ASP	A	194	41.816	14.941	28.486	1.00	56.31	6
ATOM	1545	CB	ASP	A	194	40.856	15.738	29.386	1.00	57.85	6
ATOM	1546	CG	ASP	A	194	40.339	14.930	30.578	1.00	59.72	6
ATOM	1547	OD1	ASP	A	194	39.120	14.610	30.592	1.00	55.87	8
ATOM	1548	OD2	ASP	A	194	41.154	14.628	31.494	1.00	58.60	8
ATOM	1549	C	ASP	A	194	42.881	14.276	29.333	1.00	55.87	6
ATOM	1550	O	ASP	A	194	42.746	13.121	29.714	1.00	56.72	8
ATOM	1551	N	VAL	A	195	43.948	15.014	29.611	1.00	55.00	7
ATOM	1552	CA	VAL	A	195	45.039	14.520	30.431	1.00	55.58	6
ATOM	1553	CB	VAL	A	195	46.397	14.961	29.876	1.00	54.15	6
ATOM	1554	CG1	VAL	A	195	47.508	14.610	30.860	1.00	52.00	6
ATOM	1555	CG2	VAL	A	195	46.643	14.292	28.544	1.00	53.83	6
ATOM	1556	C	VAL	A	195	44.900	15.082	31.832	1.00	57.46	6
ATOM	1557	O	VAL	A	195	44.809	16.294	32.011	1.00	57.93	8
ATOM	1558	N	GLU	A	196	44.886	14.206	32.828	1.00	58.46	7
ATOM	1559	CA	GLU	A	196	44.767	14.654	34.204	1.00	58.24	6
ATOM	1560	CB	GLU	A	196	43.805	13.758	34.966	1.00	59.77	6
ATOM	1561	CG	GLU	A	196	43.556	14.199	36.385	1.00	63.27	6
ATOM	1562	CD	GLU	A	196	42.624	13.256	37.114	1.00	64.52	6
ATOM	1563	OE1	GLU	A	196	41.485	13.063	36.646	1.00	63.73	8
ATOM	1564	OE2	GLU	A	196	43.035	12.705	38.155	1.00	68.58	8
ATOM	1565	C	GLU	A	196	46.142	14.590	34.828	1.00	57.57	6
ATOM	1566	O	GLU	A	196	46.775	13.538	34.841	1.00	59.03	8
ATOM	1567	N	VAL	A	197	46.618	15.723	35.322	1.00	55.78	7
ATOM	1568	CA	VAL	A	197	47.929	15.766	35.943	1.00	55.65	6
ATOM	1569	CB	VAL	A	197	48.781	16.937	35.386	1.00	55.24	6
ATOM	1570	CG1	VAL	A	197	50.142	16.962	36.050	1.00	51.21	6
ATOM	1571	CG2	VAL	A	197	48.929	16.800	33.877	1.00	53.65	6
ATOM	1572	C	VAL	A	197	47.716	15.955	37.431	1.00	57.58	6
ATOM	1573	O	VAL	A	197	46.963	16.843	37.850	1.00	57.66	8
ATOM	1574	N	SER	A	198	48.355	15.102	38.231	1.00	58.29	7
ATOM	1575	CA	SER	A	198	48.229	15.194	39.677	1.00	57.91	6

ATOM	1576	CB	SER	A	198	47.951	13.822	40.275	1.00	56.54	6
ATOM	1577	OG	SER	A	198	46.654	13.401	39.908	1.00	61.46	8
ATOM	1578	C	SER	A	198	49.501	15.765	40.257	1.00	58.27	6
ATOM	1579	O	SER	A	198	50.585	15.202	40.089	1.00	58.63	8
ATOM	1580	N	LEU	A	199	49.366	16.901	40.929	1.00	58.53	7
ATOM	1581	CA	LEU	A	199	50.521	17.538	41.531	1.00	60.77	6
ATOM	1582	CB	LEU	A	199	50.519	19.046	41.274	1.00	60.73	6
ATOM	1583	CG	LEU	A	199	51.591	19.833	42.032	1.00	59.19	6
ATOM	1584	CD1	LEU	A	199	52.982	19.400	41.599	1.00	57.61	6
ATOM	1585	CD2	LEU	A	199	51.390	21.311	41.776	1.00	60.66	6
ATOM	1586	C	LEU	A	199	50.524	17.293	43.022	1.00	61.78	6
ATOM	1587	O	LEU	A	199	49.739	17.895	43.765	1.00	62.31	8
ATOM	1588	N	ASN	A	200	51.397	16.389	43.457	1.00	61.40	7
ATOM	1589	CA	ASN	A	200	51.519	16.092	44.866	1.00	58.00	6
ATOM	1590	CB	ASN	A	200	51.763	14.607	45.088	1.00	60.46	6
ATOM	1591	CG	ASN	A	200	51.926	14.267	46.553	1.00	61.99	6
ATOM	1592	OD1	ASN	A	200	51.158	14.735	47.391	1.00	63.14	8
ATOM	1593	ND2	ASN	A	200	52.928	13.447	46.871	1.00	63.54	7
ATOM	1594	C	ASN	A	200	52.708	16.906	45.345	1.00	56.52	6
ATOM	1595	O	ASN	A	200	53.859	16.664	44.957	1.00	55.31	8
ATOM	1596	N	PHE	A	201	52.406	17.901	46.166	1.00	55.49	7
ATOM	1597	CA	PHE	A	201	53.416	18.790	46.707	1.00	54.84	6
ATOM	1598	CB	PHE	A	201	53.450	20.082	45.908	1.00	50.77	6
ATOM	1599	CG	PHE	A	201	52.237	20.940	46.112	1.00	47.21	6
ATOM	1600	CD1	PHE	A	201	52.337	22.161	46.765	1.00	46.20	6
ATOM	1601	CD2	PHE	A	201	50.985	20.513	45.678	1.00	46.31	6
ATOM	1602	CE1	PHE	A	201	51.205	22.942	46.984	1.00	45.24	6
ATOM	1603	CE2	PHE	A	201	49.849	21.291	45.896	1.00	43.16	6
ATOM	1604	CZ	PHE	A	201	49.962	22.504	46.549	1.00	42.59	6
ATOM	1605	C	PHE	A	201	53.035	19.112	48.142	1.00	56.47	6
ATOM	1606	O	PHE	A	201	51.956	18.748	48.610	1.00	54.75	8
ATOM	1607	N	ARG	A	202	53.927	19.811	48.829	1.00	58.72	7
ATOM	1608	CA	ARG	A	202	53.693	20.207	50.207	1.00	61.75	6
ATOM	1609	CB	ARG	A	202	54.052	19.063	51.136	1.00	63.76	6
ATOM	1610	CG	ARG	A	202	55.544	18.822	51.130	1.00	65.86	6
ATOM	1611	CD	ARG	A	202	55.938	17.640	51.962	1.00	68.52	6
ATOM	1612	NE	ARG	A	202	57.383	17.466	51.916	1.00	69.87	7
ATOM	1613	CZ	ARG	A	202	58.013	16.409	52.405	1.00	70.56	6
ATOM	1614	NH1	ARG	A	202	57.308	15.433	52.977	1.00	71.39	7
ATOM	1615	NH2	ARG	A	202	59.340	16.332	52.315	1.00	70.56	7
ATOM	1616	C	ARG	A	202	54.579	21.406	50.556	1.00	62.74	6
ATOM	1617	O	ARG	A	202	55.588	21.675	49.890	1.00	62.41	8
ATOM	1618	N	LYS	A	203	54.200	22.121	51.606	1.00	63.53	7
ATOM	1619	CA	LYS	A	203	54.983	23.256	52.044	1.00	64.89	6
ATOM	1620	CB	LYS	A	203	54.271	23.993	53.169	1.00	65.59	6
ATOM	1621	CG	LYS	A	203	55.067	25.149	53.740	1.00	66.14	6
ATOM	1622	CD	LYS	A	203	54.348	25.777	54.911	1.00	65.85	6
ATOM	1623	CE	LYS	A	203	55.145	26.939	55.473	1.00	67.46	6
ATOM	1624	NZ	LYS	A	203	55.259	28.073	54.500	1.00	68.09	7
ATOM	1625	C	LYS	A	203	56.264	22.665	52.563	1.00	65.93	6
ATOM	1626	O	LYS	A	203	56.250	21.585	53.157	1.00	66.11	8
ATOM	1627	N	LYS	A	204	57.372	23.351	52.313	1.00	69.05	7
ATOM	1628	CA	LYS	A	204	58.659	22.863	52.767	1.00	71.58	6
ATOM	1629	CB	LYS	A	204	59.758	23.834	52.358	1.00	69.66	6
ATOM	1630	CG	LYS	A	204	59.862	23.906	50.839	1.00	69.91	6
ATOM	1631	CD	LYS	A	204	61.113	24.609	50.336	1.00	71.48	6
ATOM	1632	CE	LYS	A	204	61.195	24.491	48.809	1.00	73.18	6
ATOM	1633	NZ	LYS	A	204	62.324	25.234	48.189	1.00	72.99	7
ATOM	1634	C	LYS	A	204	58.544	22.745	54.264	1.00	74.56	6
ATOM	1635	O	LYS	A	204	57.769	23.493	54.873	1.00	77.21	8
ATOM	1636	N	GLY	A	205	59.262	21.782	54.850	1.00	75.75	7

ATOM	1637	CA	GLY	A	205	59.215	21.592	56.296	1.00 75.55	6
ATOM	1638	C	GLY	A	205	60.125	22.564	57.029	1.00 76.09	6
ATOM	1639	OT1	GLY	A	205	60.824	23.350	56.348	1.00 77.07	8
ATOM	1640	OT2	GLY	A	205	60.151	22.545	58.278	1.00 75.36	8
ATOM	1641	CB	PHE	B	1	33.107	19.922	1.832	1.00 57.02	6
ATOM	1642	CG	PHE	B	1	32.174	20.672	0.888	1.00 58.55	6
ATOM	1643	CD1	PHE	B	1	32.670	21.495	-0.120	1.00 59.39	6
ATOM	1644	CD2	PHE	B	1	30.784	20.612	1.079	1.00 58.84	6
ATOM	1645	CE1	PHE	B	1	31.795	22.248	-0.919	1.00 59.92	6
ATOM	1646	CE2	PHE	B	1	29.905	21.357	0.292	1.00 56.97	6
ATOM	1647	CZ	PHE	B	1	30.410	22.176	-0.707	1.00 58.52	6
ATOM	1648	C	PHE	B	1	35.200	18.747	2.262	1.00 56.22	6
ATOM	1649	O	PHE	B	1	34.732	18.314	3.311	1.00 58.27	8
ATOM	1650	N	PHE	B	1	33.748	17.916	0.462	1.00 54.28	7
ATOM	1651	CA	PHE	B	1	34.250	19.143	1.152	1.00 55.90	6
ATOM	1652	N	ASP	B	2	36.512	18.877	2.083	1.00 55.99	7
ATOM	1653	CA	ASP	B	2	37.383	18.526	3.204	1.00 56.44	6
ATOM	1654	CB	ASP	B	2	38.876	18.485	2.792	1.00 59.88	6
ATOM	1655	CG	ASP	B	2	39.364	19.782	2.139	1.00 65.04	6
ATOM	1656	OD1	ASP	B	2	40.076	19.729	1.091	1.00 67.12	8
ATOM	1657	OD2	ASP	B	2	39.042	20.860	2.684	1.00 68.18	8
ATOM	1658	C	ASP	B	2	37.096	19.582	4.280	1.00 55.70	6
ATOM	1659	O	ASP	B	2	36.331	20.507	4.047	1.00 54.61	8
ATOM	1660	N	ARG	B	3	37.682	19.443	5.458	1.00 55.52	7
ATOM	1661	CA	ARG	B	3	37.441	20.380	6.556	1.00 53.72	6
ATOM	1662	CB	ARG	B	3	38.114	19.838	7.806	1.00 56.23	6
ATOM	1663	CG	ARG	B	3	37.541	20.323	9.094	1.00 55.76	6
ATOM	1664	CD	ARG	B	3	37.772	19.269	10.139	1.00 55.83	6
ATOM	1665	NE	ARG	B	3	36.531	18.930	10.818	1.00 56.35	7
ATOM	1666	CZ	ARG	B	3	36.233	17.708	11.220	1.00 56.91	6
ATOM	1667	NH1	ARG	B	3	37.095	16.729	10.994	1.00 56.22	7
ATOM	1668	NH2	ARG	B	3	35.090	17.468	11.849	1.00 57.84	7
ATOM	1669	C	ARG	B	3	37.909	21.822	6.295	1.00 53.67	6
ATOM	1670	O	ARG	B	3	37.395	22.772	6.888	1.00 53.80	8
ATOM	1671	N	ALA	B	4	38.896	21.969	5.420	1.00 52.29	7
ATOM	1672	CA	ALA	B	4	39.443	23.255	5.025	1.00 50.06	6
ATOM	1673	CB	ALA	B	4	40.743	23.036	4.275	1.00 48.42	6
ATOM	1674	C	ALA	B	4	38.442	23.978	4.131	1.00 49.06	6
ATOM	1675	O	ALA	B	4	38.225	25.179	4.270	1.00 47.12	8
ATOM	1676	N	ASP	B	5	37.837	23.233	3.211	1.00 49.07	7
ATOM	1677	CA	ASP	B	5	36.869	23.801	2.288	1.00 51.75	6
ATOM	1678	CB	ASP	B	5	36.345	22.748	1.299	1.00 55.02	6
ATOM	1679	CG	ASP	B	5	37.454	22.084	0.491	1.00 60.18	6
ATOM	1680	OD1	ASP	B	5	38.347	22.794	-0.039	1.00 63.04	8
ATOM	1681	OD2	ASP	B	5	37.430	20.839	0.374	1.00 61.10	8
ATOM	1682	C	ASP	B	5	35.699	24.381	3.051	1.00 51.17	6
ATOM	1683	O	ASP	B	5	35.179	25.428	2.670	1.00 51.32	8
ATOM	1684	N	ILE	B	6	35.292	23.713	4.130	1.00 49.73	7
ATOM	1685	CA	ILE	B	6	34.164	24.178	4.926	1.00 50.09	6
ATOM	1686	CB	ILE	B	6	33.723	23.128	5.950	1.00 51.11	6
ATOM	1687	CG2	ILE	B	6	32.472	23.610	6.678	1.00 48.60	6
ATOM	1688	CG1	ILE	B	6	33.434	21.809	5.232	1.00 53.13	6
ATOM	1689	CD1	ILE	B	6	32.881	20.712	6.121	1.00 55.06	6
ATOM	1690	C	ILE	B	6	34.448	25.480	5.653	1.00 49.98	6
ATOM	1691	O	ILE	B	6	33.700	26.450	5.518	1.00 51.60	8
ATOM	1692	N	LEU	B	7	35.524	25.504	6.426	1.00 49.48	7
ATOM	1693	CA	LEU	B	7	35.908	26.705	7.160	1.00 48.15	6
ATOM	1694	CB	LEU	B	7	37.157	26.424	7.995	1.00 45.60	6
ATOM	1695	CG	LEU	B	7	36.916	25.427	9.126	1.00 45.98	6
ATOM	1696	CD1	LEU	B	7	38.221	24.935	9.696	1.00 46.59	6
ATOM	1697	CD2	LEU	B	7	36.081	26.086	10.191	1.00 44.50	6

ATOM	1698	C	LEU	B	7	36.167	27.850	6.195	1.00	47.43	6
ATOM	1699	O	LEU	B	7	35.797	28.986	6.447	1.00	46.94	8
ATOM	1700	N	TYR	B	8	36.799	27.529	5.080	1.00	49.45	7
ATOM	1701	CA	TYR	B	8	37.105	28.507	4.051	1.00	52.16	6
ATOM	1702	CB	TYR	B	8	37.800	27.821	2.877	1.00	54.75	6
ATOM	1703	CG	TYR	B	8	38.090	28.758	1.737	1.00	56.10	6
ATOM	1704	CD1	TYR	B	8	39.088	29.720	1.839	1.00	56.48	6
ATOM	1705	CE1	TYR	B	8	39.344	30.605	0.794	1.00	57.35	6
ATOM	1706	CD2	TYR	B	8	37.348	28.701	0.564	1.00	57.26	6
ATOM	1707	CE2	TYR	B	8	37.592	29.581	-0.484	1.00	57.99	6
ATOM	1708	CZ	TYR	B	8	38.590	30.528	-0.364	1.00	57.33	6
ATOM	1709	OH	TYR	B	8	38.819	31.385	-1.408	1.00	58.94	8
ATOM	1710	C	TYR	B	8	35.858	29.234	3.537	1.00	52.55	6
ATOM	1711	O	TYR	B	8	35.867	30.460	3.387	1.00	52.22	8
ATOM	1712	N	ASN	B	9	34.796	28.482	3.249	1.00	52.51	7
ATOM	1713	CA	ASN	B	9	33.566	29.086	2.752	1.00	54.09	6
ATOM	1714	CB	ASN	B	9	32.539	28.021	2.376	1.00	56.72	6
ATOM	1715	CG	ASN	B	9	32.963	27.203	1.163	1.00	60.46	6
ATOM	1716	OD1	ASN	B	9	33.966	27.509	0.512	1.00	61.72	8
ATOM	1717	ND2	ASN	B	9	32.198	26.159	0.852	1.00	61.67	7
ATOM	1718	C	ASN	B	9	32.980	30.007	3.794	1.00	54.24	6
ATOM	1719	O	ASN	B	9	32.680	31.160	3.506	1.00	54.66	8
ATOM	1720	N	ILE	B	10	32.829	29.503	5.013	1.00	54.21	7
ATOM	1721	CA	ILE	B	10	32.282	30.310	6.104	1.00	53.77	6
ATOM	1722	CB	ILE	B	10	32.303	29.543	7.429	1.00	52.00	6
ATOM	1723	CG2	ILE	B	10	31.860	30.451	8.552	1.00	50.79	6
ATOM	1724	CG1	ILE	B	10	31.389	28.323	7.339	1.00	50.43	6
ATOM	1725	CD1	ILE	B	10	31.531	27.371	8.498	1.00	47.56	6
ATOM	1726	C	ILE	B	10	33.085	31.592	6.284	1.00	55.12	6
ATOM	1727	O	ILE	B	10	32.531	32.663	6.458	1.00	56.17	8
ATOM	1728	N	ARG	B	11	34.400	31.464	6.243	1.00	56.91	7
ATOM	1729	CA	ARG	B	11	35.297	32.595	6.386	1.00	58.48	6
ATOM	1730	CB	ARG	B	11	36.739	32.110	6.243	1.00	63.85	6
ATOM	1731	CG	ARG	B	11	37.799	33.170	6.434	1.00	68.86	6
ATOM	1732	CD	ARG	B	11	37.917	33.493	7.917	1.00	77.74	6
ATOM	1733	NE	ARG	B	11	39.211	34.078	8.264	1.00	85.52	7
ATOM	1734	CZ	ARG	B	11	40.384	33.635	7.807	1.00	88.55	6
ATOM	1735	NH1	ARG	B	11	40.424	32.589	6.970	1.00	90.95	7
ATOM	1736	NH2	ARG	B	11	41.518	34.239	8.178	1.00	87.63	7
ATOM	1737	C	ARG	B	11	35.030	33.639	5.306	1.00	58.49	6
ATOM	1738	O	ARG	B	11	34.905	34.825	5.584	1.00	57.34	8
ATOM	1739	N	GLN	B	12	34.933	33.175	4.066	1.00	58.50	7
ATOM	1740	CA	GLN	B	12	34.748	34.055	2.927	1.00	57.77	6
ATOM	1741	CB	GLN	B	12	35.147	33.329	1.653	1.00	58.35	6
ATOM	1742	CG	GLN	B	12	36.124	34.100	0.814	1.00	62.22	6
ATOM	1743	CD	GLN	B	12	37.514	33.973	1.351	1.00	64.08	6
ATOM	1744	OE1	GLN	B	12	38.011	32.862	1.501	1.00	68.35	8
ATOM	1745	NE2	GLN	B	12	38.156	35.098	1.653	1.00	63.78	7
ATOM	1746	C	GLN	B	12	33.366	34.633	2.720	1.00	57.86	6
ATOM	1747	O	GLN	B	12	33.219	35.657	2.059	1.00	59.62	8
ATOM	1748	N	THR	B	13	32.345	33.994	3.266	1.00	57.21	7
ATOM	1749	CA	THR	B	13	30.987	34.479	3.054	1.00	56.88	6
ATOM	1750	CB	THR	B	13	30.101	33.373	2.468	1.00	54.90	6
ATOM	1751	OG1	THR	B	13	30.100	32.247	3.350	1.00	55.07	8
ATOM	1752	CG2	THR	B	13	30.612	32.946	1.104	1.00	56.83	6
ATOM	1753	C	THR	B	13	30.295	35.009	4.298	1.00	58.52	6
ATOM	1754	O	THR	B	13	29.275	35.698	4.206	1.00	57.64	8
ATOM	1755	N	SER	B	14	30.848	34.691	5.462	1.00	60.24	7
ATOM	1756	CA	SER	B	14	30.247	35.117	6.715	1.00	60.31	6
ATOM	1757	CB	SER	B	14	30.884	34.369	7.878	1.00	60.50	6
ATOM	1758	OG	SER	B	14	30.086	34.485	9.034	1.00	63.18	8

ATOM	1759	C	SER	B	14	30.343	36.619	6.949	1.00	59.80	6
ATOM	1760	O	SER	B	14	31.247	37.293	6.443	1.00	60.23	8
ATOM	1761	N	ARG	B	15	29.382	37.134	7.710	1.00	58.15	7
ATOM	1762	CA	ARG	B	15	29.322	38.549	8.040	1.00	55.80	6
ATOM	1763	CB	ARG	B	15	28.271	39.239	7.183	1.00	56.87	6
ATOM	1764	CG	ARG	B	15	28.540	39.145	5.684	1.00	60.72	6
ATOM	1765	CD	ARG	B	15	27.721	40.179	4.945	1.00	63.19	6
ATOM	1766	NE	ARG	B	15	28.008	41.515	5.475	1.00	67.21	7
ATOM	1767	CZ	ARG	B	15	27.307	42.616	5.196	1.00	67.82	6
ATOM	1768	NH1	ARG	B	15	26.259	42.549	4.384	1.00	69.12	7
ATOM	1769	NH2	ARG	B	15	27.660	43.789	5.722	1.00	66.84	7
ATOM	1770	C	ARG	B	15	28.962	38.655	9.511	1.00	54.09	6
ATOM	1771	O	ARG	B	15	27.795	38.651	9.880	1.00	55.59	8
ATOM	1772	N	PRO	B	16	29.979	38.747	10.377	1.00	51.42	7
ATOM	1773	CD	PRO	B	16	31.405	38.751	10.015	1.00	48.17	6
ATOM	1774	CA	PRO	B	16	29.817	38.846	11.828	1.00	48.94	6
ATOM	1775	CB	PRO	B	16	31.256	38.950	12.328	1.00	48.44	6
ATOM	1776	CG	PRO	B	16	32.038	38.262	11.284	1.00	48.62	6
ATOM	1777	C	PRO	B	16	28.974	40.014	12.300	1.00	48.35	6
ATOM	1778	O	PRO	B	16	28.475	40.006	13.420	1.00	49.87	8
ATOM	1779	N	ASP	B	17	28.825	41.026	11.456	1.00	49.55	7
ATOM	1780	CA	ASP	B	17	28.048	42.201	11.830	1.00	51.87	6
ATOM	1781	CB	ASP	B	17	28.638	43.469	11.204	1.00	55.73	6
ATOM	1782	CG	ASP	B	17	29.956	43.896	11.856	1.00	59.93	6
ATOM	1783	OD1	ASP	B	17	30.158	43.598	13.062	1.00	60.57	8
ATOM	1784	OD2	ASP	B	17	30.781	44.548	11.163	1.00	61.01	8
ATOM	1785	C	ASP	B	17	26.581	42.120	11.458	1.00	51.65	6
ATOM	1786	O	ASP	B	17	25.837	43.066	11.684	1.00	51.12	8
ATOM	1787	N	VAL	B	18	26.156	40.990	10.906	1.00	53.24	7
ATOM	1788	CA	VAL	B	18	24.772	40.848	10.495	1.00	53.38	6
ATOM	1789	CB	VAL	B	18	24.679	40.682	8.978	1.00	52.53	6
ATOM	1790	CG1	VAL	B	18	23.238	40.628	8.551	1.00	53.33	6
ATOM	1791	CG2	VAL	B	18	25.385	41.833	8.299	1.00	52.08	6
ATOM	1792	C	VAL	B	18	24.026	39.701	11.157	1.00	54.80	6
ATOM	1793	O	VAL	B	18	24.359	38.527	10.980	1.00	57.05	8
ATOM	1794	N	ILE	B	19	22.999	40.062	11.913	1.00	55.38	7
ATOM	1795	CA	ILE	B	19	22.150	39.105	12.615	1.00	54.84	6
ATOM	1796	CB	ILE	B	19	21.128	39.899	13.493	1.00	53.97	6
ATOM	1797	CG2	ILE	B	19	20.177	40.699	12.612	1.00	52.99	6
ATOM	1798	CG1	ILE	B	19	20.354	38.963	14.414	1.00	54.58	6
ATOM	1799	CD1	ILE	B	19	19.598	39.696	15.490	1.00	51.38	6
ATOM	1800	C	ILE	B	19	21.450	38.192	11.586	1.00	55.77	6
ATOM	1801	O	ILE	B	19	20.879	38.678	10.605	1.00	56.23	8
ATOM	1802	N	PRO	B	20	21.508	36.857	11.787	1.00	57.54	7
ATOM	1803	CD	PRO	B	20	22.223	36.204	12.888	1.00	57.31	6
ATOM	1804	CA	PRO	B	20	20.900	35.841	10.900	1.00	59.26	6
ATOM	1805	CB	PRO	B	20	21.478	34.521	11.417	1.00	57.46	6
ATOM	1806	CG	PRO	B	20	22.657	34.935	12.235	1.00	58.77	6
ATOM	1807	C	PRO	B	20	19.366	35.836	10.940	1.00	62.02	6
ATOM	1808	O	PRO	B	20	18.732	34.806	11.185	1.00	61.74	8
ATOM	1809	N	THR	B	21	18.781	36.997	10.679	1.00	65.81	7
ATOM	1810	CA	THR	B	21	17.337	37.160	10.705	1.00	69.72	6
ATOM	1811	CB	THR	B	21	16.974	38.658	10.971	1.00	67.96	6
ATOM	1812	OG1	THR	B	21	16.710	38.837	12.367	1.00	69.51	8
ATOM	1813	CG2	THR	B	21	15.765	39.087	10.178	1.00	68.09	6
ATOM	1814	C	THR	B	21	16.606	36.658	9.455	1.00	73.11	6
ATOM	1815	O	THR	B	21	17.000	36.942	8.315	1.00	71.83	8
ATOM	1816	N	GLN	B	22	15.532	35.907	9.694	1.00	77.49	7
ATOM	1817	CA	GLN	B	22	14.684	35.370	8.629	1.00	80.52	6
ATOM	1818	CB	GLN	B	22	14.492	33.871	8.842	1.00	81.72	6
ATOM	1819	CG	GLN	B	22	15.793	33.097	8.917	1.00	83.16	6

ATOM	1820	CD	GLN	B	22	15.654	31.832	9.753	1.00	85.69	6
ATOM	1821	OE1	GLN	B	22	15.421	31.901	10.976	1.00	86.08	8
ATOM	1822	NE2	GLN	B	22	15.787	30.665	9.103	1.00	85.85	7
ATOM	1823	C	GLN	B	22	13.326	36.091	8.717	1.00	81.72	6
ATOM	1824	O	GLN	B	22	12.526	35.837	9.632	1.00	80.46	8
ATOM	1825	N	ARG	B	23	13.075	36.990	7.765	1.00	84.00	7
ATOM	1826	CA	ARG	B	23	11.829	37.769	7.744	1.00	86.23	6
ATOM	1827	CB	ARG	B	23	10.599	36.840	7.695	1.00	87.50	6
ATOM	1828	CG	ARG	B	23	10.348	36.215	6.314	1.00	89.89	6
ATOM	1829	CD	ARG	B	23	10.796	34.734	6.215	1.00	90.83	6
ATOM	1830	NE	ARG	B	23	10.694	34.242	4.833	1.00	93.76	7
ATOM	1831	CZ	ARG	B	23	9.590	34.302	4.068	1.00	95.64	6
ATOM	1832	NH1	ARG	B	23	8.452	34.832	4.534	1.00	96.17	7
ATOM	1833	NH2	ARG	B	23	9.627	33.855	2.811	1.00	95.03	7
ATOM	1834	C	ARG	B	23	11.754	38.657	8.987	1.00	86.03	6
ATOM	1835	O	ARG	B	23	12.776	39.137	9.476	1.00	85.87	8
ATOM	1836	N	ASP	B	24	10.548	38.879	9.497	1.00	86.08	7
ATOM	1837	CA	ASP	B	24	10.393	39.703	10.693	1.00	85.72	6
ATOM	1838	CB	ASP	B	24	8.975	40.301	10.799	1.00	89.17	6
ATOM	1839	CG	ASP	B	24	8.226	40.339	9.453	1.00	90.77	6
ATOM	1840	OD1	ASP	B	24	8.743	40.965	8.486	1.00	92.05	8
ATOM	1841	OD2	ASP	B	24	7.113	39.746	9.376	1.00	89.95	8
ATOM	1842	C	ASP	B	24	10.622	38.798	11.891	1.00	83.93	6
ATOM	1843	O	ASP	B	24	10.445	39.218	13.045	1.00	83.66	8
ATOM	1844	N	ARG	B	25	10.994	37.549	11.613	1.00	81.18	7
ATOM	1845	CA	ARG	B	25	11.237	36.584	12.677	1.00	78.99	6
ATOM	1846	CB	ARG	B	25	11.318	35.159	12.128	1.00	82.30	6
ATOM	1847	CG	ARG	B	25	10.001	34.541	11.696	1.00	87.15	6
ATOM	1848	CD	ARG	B	25	10.171	33.024	11.485	1.00	91.09	6
ATOM	1849	NE	ARG	B	25	8.908	32.371	11.140	1.00	95.87	7
ATOM	1850	CZ	ARG	B	25	8.747	31.053	11.005	1.00	98.43	6
ATOM	1851	NH1	ARG	B	25	9.785	30.235	11.186	1.00	97.96	7
ATOM	1852	NH2	ARG	B	25	7.538	30.549	10.709	1.00	99.56	7
ATOM	1853	C	ARG	B	25	12.527	36.876	13.426	1.00	75.18	6
ATOM	1854	O	ARG	B	25	13.573	37.105	12.813	1.00	75.11	8
ATOM	1855	N	PRO	B	26	12.463	36.879	14.767	1.00	71.32	7
ATOM	1856	CD	PRO	B	26	11.233	36.885	15.569	1.00	69.54	6
ATOM	1857	CA	PRO	B	26	13.629	37.134	15.617	1.00	68.20	6
ATOM	1858	CB	PRO	B	26	13.020	37.298	17.007	1.00	68.04	6
ATOM	1859	CG	PRO	B	26	11.627	37.763	16.720	1.00	68.94	6
ATOM	1860	C	PRO	B	26	14.543	35.917	15.572	1.00	65.66	6
ATOM	1861	O	PRO	B	26	14.114	34.832	15.183	1.00	65.23	8
ATOM	1862	N	VAL	B	27	15.801	36.093	15.956	1.00	62.13	7
ATOM	1863	CA	VAL	B	27	16.716	34.969	15.990	1.00	58.35	6
ATOM	1864	CB	VAL	B	27	18.185	35.416	15.851	1.00	57.74	6
ATOM	1865	CG1	VAL	B	27	19.127	34.308	16.328	1.00	54.93	6
ATOM	1866	CG2	VAL	B	27	18.479	35.737	14.393	1.00	54.94	6
ATOM	1867	C	VAL	B	27	16.491	34.348	17.349	1.00	56.29	6
ATOM	1868	O	VAL	B	27	16.517	35.043	18.360	1.00	56.31	8
ATOM	1869	N	ALA	B	28	16.243	33.045	17.379	1.00	54.44	7
ATOM	1870	CA	ALA	B	28	16.008	32.384	18.645	1.00	52.98	6
ATOM	1871	CB	ALA	B	28	15.095	31.209	18.461	1.00	52.15	6
ATOM	1872	C	ALA	B	28	17.318	31.938	19.262	1.00	52.73	6
ATOM	1873	O	ALA	B	28	17.959	31.004	18.782	1.00	51.86	8
ATOM	1874	N	VAL	B	29	17.696	32.632	20.334	1.00	51.10	7
ATOM	1875	CA	VAL	B	29	18.911	32.353	21.080	1.00	49.08	6
ATOM	1876	CB	VAL	B	29	19.741	33.642	21.324	1.00	49.72	6
ATOM	1877	CG1	VAL	B	29	20.986	33.323	22.140	1.00	46.43	6
ATOM	1878	CG2	VAL	B	29	20.117	34.272	19.996	1.00	49.12	6
ATOM	1879	C	VAL	B	29	18.553	31.762	22.428	1.00	48.65	6
ATOM	1880	O	VAL	B	29	17.731	32.301	23.161	1.00	48.71	8

ATOM	1881	N	SER	B	30	19.169	30.638	22.746	1.00	50.09	7
ATOM	1882	CA	SER	B	30	18.925	29.997	24.018	1.00	53.68	6
ATOM	1883	CB	SER	B	30	18.587	28.521	23.817	1.00	53.36	6
ATOM	1884	OG	SER	B	30	19.653	27.845	23.180	1.00	57.88	8
ATOM	1885	C	SER	B	30	20.201	30.150	24.823	1.00	56.00	6
ATOM	1886	O	SER	B	30	21.297	29.933	24.306	1.00	57.56	8
ATOM	1887	N	VAL	B	31	20.049	30.542	26.084	1.00	57.69	7
ATOM	1888	CA	VAL	B	31	21.175	30.752	26.980	1.00	57.19	6
ATOM	1889	CB	VAL	B	31	21.227	32.198	27.460	1.00	57.32	6
ATOM	1890	CG1	VAL	B	31	22.536	32.449	28.185	1.00	58.47	6
ATOM	1891	CG2	VAL	B	31	21.044	33.147	26.288	1.00	56.64	6
ATOM	1892	C	VAL	B	31	21.016	29.878	28.204	1.00	57.98	6
ATOM	1893	O	VAL	B	31	19.938	29.815	28.787	1.00	59.53	8
ATOM	1894	N	SER	B	32	22.101	29.232	28.611	1.00	58.26	7
ATOM	1895	CA	SER	B	32	22.069	28.356	29.765	1.00	58.30	6
ATOM	1896	CB	SER	B	32	21.806	26.914	29.298	1.00	60.26	6
ATOM	1897	OG	SER	B	32	21.881	25.975	30.361	1.00	61.39	8
ATOM	1898	C	SER	B	32	23.374	28.414	30.530	1.00	58.22	6
ATOM	1899	O	SER	B	32	24.402	27.983	30.024	1.00	62.28	8
ATOM	1900	N	LEU	B	33	23.340	28.937	31.753	1.00	56.90	7
ATOM	1901	CA	LEU	B	33	24.548	29.002	32.572	1.00	56.09	6
ATOM	1902	CB	LEU	B	33	24.489	30.183	33.541	1.00	54.84	6
ATOM	1903	CG	LEU	B	33	24.257	31.555	32.914	1.00	55.33	6
ATOM	1904	CD1	LEU	B	33	24.483	32.647	33.962	1.00	53.97	6
ATOM	1905	CD2	LEU	B	33	25.201	31.731	31.737	1.00	56.27	6
ATOM	1906	C	LEU	B	33	24.725	27.728	33.379	1.00	55.50	6
ATOM	1907	O	LEU	B	33	23.770	27.220	33.950	1.00	56.54	8
ATOM	1908	N	LYS	B	34	25.948	27.215	33.413	1.00	55.65	7
ATOM	1909	CA	LYS	B	34	26.270	26.018	34.183	1.00	56.27	6
ATOM	1910	CB	LYS	B	34	26.815	24.905	33.279	1.00	60.64	6
ATOM	1911	CG	LYS	B	34	25.908	24.528	32.102	1.00	66.07	6
ATOM	1912	CD	LYS	B	34	24.552	23.965	32.566	1.00	72.18	6
ATOM	1913	CE	LYS	B	34	23.611	23.670	31.373	1.00	74.46	6
ATOM	1914	NZ	LYS	B	34	22.303	23.068	31.799	1.00	74.04	7
ATOM	1915	C	LYS	B	34	27.365	26.493	35.108	1.00	54.54	6
ATOM	1916	O	LYS	B	34	28.463	26.811	34.655	1.00	55.93	8
ATOM	1917	N	PHE	B	35	27.079	26.564	36.401	1.00	52.21	7
ATOM	1918	CA	PHE	B	35	28.086	27.045	37.336	1.00	49.54	6
ATOM	1919	CB	PHE	B	35	27.422	27.491	38.633	1.00	46.23	6
ATOM	1920	CG	PHE	B	35	26.545	28.682	38.450	1.00	47.55	6
ATOM	1921	CD1	PHE	B	35	25.230	28.536	38.035	1.00	48.89	6
ATOM	1922	CD2	PHE	B	35	27.056	29.968	38.603	1.00	48.56	6
ATOM	1923	CE1	PHE	B	35	24.434	29.653	37.771	1.00	47.34	6
ATOM	1924	CE2	PHE	B	35	26.269	31.087	38.343	1.00	45.87	6
ATOM	1925	CZ	PHE	B	35	24.958	30.927	37.926	1.00	47.81	6
ATOM	1926	C	PHE	B	35	29.224	26.072	37.595	1.00	49.37	6
ATOM	1927	O	PHE	B	35	29.020	24.880	37.833	1.00	48.82	8
ATOM	1928	N	ILE	B	36	30.434	26.609	37.530	1.00	47.17	7
ATOM	1929	CA	ILE	B	36	31.634	25.820	37.706	1.00	45.02	6
ATOM	1930	CB	ILE	B	36	32.641	26.106	36.574	1.00	42.09	6
ATOM	1931	CG2	ILE	B	36	33.858	25.230	36.717	1.00	38.48	6
ATOM	1932	CG1	ILE	B	36	31.966	25.897	35.224	1.00	41.05	6
ATOM	1933	CD1	ILE	B	36	31.393	24.520	35.028	1.00	41.45	6
ATOM	1934	C	ILE	B	36	32.284	26.141	39.029	1.00	45.51	6
ATOM	1935	O	ILE	B	36	32.977	25.304	39.603	1.00	45.83	8
ATOM	1936	N	ASN	B	37	32.068	27.351	39.522	1.00	45.06	7
ATOM	1937	CA	ASN	B	37	32.678	27.719	40.792	1.00	45.81	6
ATOM	1938	CB	ASN	B	37	34.200	27.712	40.652	1.00	43.65	6
ATOM	1939	CG	ASN	B	37	34.900	27.384	41.950	1.00	47.86	6
ATOM	1940	OD1	ASN	B	37	34.518	27.864	43.025	1.00	49.43	8
ATOM	1941	ND2	ASN	B	37	35.942	26.572	41.862	1.00	46.99	7

ATOM	1942	C	ASN	B	37	32.222	29.077	41.322	1.00 45.58	6
ATOM	1943	O	ASN	B	37	31.767	29.931	40.566	1.00 44.62	8
ATOM	1944	N	ILE	B	38	32.335	29.248	42.635	1.00 45.83	7
ATOM	1945	CA	ILE	B	38	31.973	30.489	43.301	1.00 47.98	6
ATOM	1946	CB	ILE	B	38	30.781	30.287	44.214	1.00 46.41	6
ATOM	1947	CG2	ILE	B	38	30.510	31.550	44.976	1.00 46.45	6
ATOM	1948	CG1	ILE	B	38	29.567	29.905	43.356	1.00 47.23	6
ATOM	1949	CD1	ILE	B	38	28.365	29.406	44.105	1.00 48.96	6
ATOM	1950	C	ILE	B	38	33.221	30.805	44.086	1.00 50.65	6
ATOM	1951	O	ILE	B	38	33.546	30.109	45.040	1.00 52.37	8
ATOM	1952	N	LEU	B	39	33.926	31.855	43.668	1.00 52.96	7
ATOM	1953	CA	LEU	B	39	35.207	32.214	44.264	1.00 53.68	6
ATOM	1954	CB	LEU	B	39	36.137	32.698	43.157	1.00 53.70	6
ATOM	1955	CG	LEU	B	39	36.204	31.706	42.000	1.00 53.99	6
ATOM	1956	CD1	LEU	B	39	37.099	32.257	40.904	1.00 53.07	6
ATOM	1957	CD2	LEU	B	39	36.718	30.364	42.510	1.00 51.88	6
ATOM	1958	C	LEU	B	39	35.272	33.188	45.418	1.00 54.85	6
ATOM	1959	O	LEU	B	39	36.061	32.994	46.342	1.00 55.07	8
ATOM	1960	N	GLU	B	40	34.489	34.255	45.359	1.00 55.18	7
ATOM	1961	CA	GLU	B	40	34.509	35.220	46.446	1.00 58.32	6
ATOM	1962	CB	GLU	B	40	35.423	36.400	46.144	1.00 59.68	6
ATOM	1963	CG	GLU	B	40	36.879	36.041	46.018	1.00 65.11	6
ATOM	1964	CD	GLU	B	40	37.749	37.271	45.846	1.00 69.72	6
ATOM	1965	OE1	GLU	B	40	37.534	38.034	44.867	1.00 72.04	8
ATOM	1966	OE2	GLU	B	40	38.648	37.477	46.693	1.00 70.63	8
ATOM	1967	C	GLU	B	40	33.128	35.738	46.685	1.00 59.54	6
ATOM	1968	O	GLU	B	40	32.393	36.057	45.747	1.00 59.65	8
ATOM	1969	N	VAL	B	41	32.772	35.816	47.956	1.00 60.26	7
ATOM	1970	CA	VAL	B	41	31.468	36.304	48.323	1.00 58.68	6
ATOM	1971	CB	VAL	B	41	30.599	35.159	48.862	1.00 59.00	6
ATOM	1972	CG1	VAL	B	41	29.318	35.711	49.450	1.00 61.18	6
ATOM	1973	CG2	VAL	B	41	30.279	34.186	47.740	1.00 59.58	6
ATOM	1974	C	VAL	B	41	31.666	37.368	49.379	1.00 58.15	6
ATOM	1975	O	VAL	B	41	32.594	37.290	50.187	1.00 56.97	8
ATOM	1976	N	ASN	B	42	30.811	38.383	49.337	1.00 58.17	7
ATOM	1977	CA	ASN	B	42	30.863	39.466	50.302	1.00 58.74	6
ATOM	1978	CB	ASN	B	42	31.609	40.673	49.730	1.00 58.84	6
ATOM	1979	CG	ASN	B	42	31.962	41.702	50.795	1.00 58.68	6
ATOM	1980	OD1	ASN	B	42	31.122	42.100	51.593	1.00 58.91	8
ATOM	1981	ND2	ASN	B	42	33.215	42.138	50.806	1.00 58.72	7
ATOM	1982	C	ASN	B	42	29.412	39.823	50.577	1.00 60.60	6
ATOM	1983	O	ASN	B	42	28.738	40.457	49.747	1.00 60.01	8
ATOM	1984	N	GLU	B	43	28.926	39.401	51.742	1.00 61.86	7
ATOM	1985	CA	GLU	B	43	27.543	39.669	52.111	1.00 62.81	6
ATOM	1986	CB	GLU	B	43	27.117	38.760	53.267	1.00 64.87	6
ATOM	1987	CG	GLU	B	43	25.640	38.871	53.591	1.00 67.01	6
ATOM	1988	CD	GLU	B	43	25.152	37.779	54.525	1.00 69.52	6
ATOM	1989	OE1	GLU	B	43	23.973	37.842	54.945	1.00 68.10	8
ATOM	1990	OE2	GLU	B	43	25.944	36.854	54.831	1.00 70.46	8
ATOM	1991	C	GLU	B	43	27.332	41.132	52.476	1.00 60.60	6
ATOM	1992	O	GLU	B	43	26.223	41.649	52.387	1.00 59.23	8
ATOM	1993	N	ILE	B	44	28.408	41.792	52.882	1.00 60.18	7
ATOM	1994	CA	ILE	B	44	28.356	43.199	53.254	1.00 61.54	6
ATOM	1995	CB	ILE	B	44	29.674	43.669	53.910	1.00 62.98	6
ATOM	1996	CG2	ILE	B	44	29.601	45.172	54.183	1.00 61.14	6
ATOM	1997	CG1	ILE	B	44	29.950	42.877	55.194	1.00 63.64	6
ATOM	1998	CD1	ILE	B	44	29.004	43.205	56.335	1.00 65.05	6
ATOM	1999	C	ILE	B	44	28.141	44.069	52.016	1.00 62.14	6
ATOM	2000	O	ILE	B	44	27.318	44.992	52.024	1.00 62.54	8
ATOM	2001	N	THR	B	45	28.894	43.773	50.959	1.00 60.63	7
ATOM	2002	CA	THR	B	45	28.806	44.527	49.721	1.00 59.11	6

ATOM	2003	CB	THR	B	45	30.190	44.696	49.090	1.00	58.49	6
ATOM	2004	OG1	THR	B	45	30.749	43.403	48.815	1.00	60.11	8
ATOM	2005	CG2	THR	B	45	31.106	45.444	50.036	1.00	56.17	6
ATOM	2006	C	THR	B	45	27.879	43.894	48.688	1.00	58.30	6
ATOM	2007	O	THR	B	45	27.555	44.521	47.675	1.00	58.45	8
ATOM	2008	N	ASN	B	46	27.450	42.660	48.933	1.00	56.14	7
ATOM	2009	CA	ASN	B	46	26.560	42.001	47.986	1.00	55.54	6
ATOM	2010	CB	ASN	B	46	25.242	42.770	47.894	1.00	54.26	6
ATOM	2011	CG	ASN	B	46	24.161	42.171	48.767	1.00	56.06	6
ATOM	2012	OD1	ASN	B	46	23.195	42.835	49.103	1.00	55.63	8
ATOM	2013	ND2	ASN	B	46	24.314	40.898	49.123	1.00	56.99	7
ATOM	2014	C	ASN	B	46	27.190	41.867	46.591	1.00	54.59	6
ATOM	2015	O	ASN	B	46	26.589	42.228	45.574	1.00	52.67	8
ATOM	2016	N	GLU	B	47	28.408	41.337	46.565	1.00	53.06	7
ATOM	2017	CA	GLU	B	47	29.141	41.131	45.330	1.00	51.52	6
ATOM	2018	CB	GLU	B	47	30.320	42.090	45.267	1.00	49.41	6
ATOM	2019	CG	GLU	B	47	29.902	43.534	45.211	1.00	51.44	6
ATOM	2020	CD	GLU	B	47	31.084	44.472	45.232	1.00	53.91	6
ATOM	2021	OE1	GLU	B	47	32.183	44.015	44.862	1.00	51.27	8
ATOM	2022	OE2	GLU	B	47	30.911	45.662	45.604	1.00	58.92	8
ATOM	2023	C	GLU	B	47	29.627	39.697	45.262	1.00	50.23	6
ATOM	2024	O	GLU	B	47	30.100	39.150	46.245	1.00	50.97	8
ATOM	2025	N	VAL	B	48	29.509	39.090	44.091	1.00	50.68	7
ATOM	2026	CA	VAL	B	48	29.928	37.706	43.909	1.00	50.46	6
ATOM	2027	CB	VAL	B	48	28.712	36.793	43.633	1.00	49.57	6
ATOM	2028	CG1	VAL	B	48	29.162	35.370	43.440	1.00	53.01	6
ATOM	2029	CG2	VAL	B	48	27.749	36.861	44.781	1.00	50.46	6
ATOM	2030	C	VAL	B	48	30.910	37.554	42.757	1.00	49.70	6
ATOM	2031	O	VAL	B	48	30.785	38.204	41.727	1.00	50.33	8
ATOM	2032	N	ASP	B	49	31.891	36.688	42.950	1.00	48.84	7
ATOM	2033	CA	ASP	B	49	32.888	36.414	41.935	1.00	49.56	6
ATOM	2034	CB	ASP	B	49	34.283	36.610	42.514	1.00	51.66	6
ATOM	2035	CG	ASP	B	49	35.320	36.772	41.456	1.00	50.41	6
ATOM	2036	OD1	ASP	B	49	35.214	36.073	40.443	1.00	52.66	8
ATOM	2037	OD2	ASP	B	49	36.240	37.586	41.639	1.00	51.65	8
ATOM	2038	C	ASP	B	49	32.648	34.949	41.590	1.00	49.62	6
ATOM	2039	O	ASP	B	49	32.973	34.052	42.364	1.00	49.38	8
ATOM	2040	N	VAL	B	50	32.078	34.720	40.416	1.00	49.68	7
ATOM	2041	CA	VAL	B	50	31.721	33.381	39.982	1.00	48.91	6
ATOM	2042	CB	VAL	B	50	30.168	33.242	40.000	1.00	50.39	6
ATOM	2043	CG1	VAL	B	50	29.565	33.968	38.807	1.00	47.68	6
ATOM	2044	CG2	VAL	B	50	29.767	31.781	40.006	1.00	52.12	6
ATOM	2045	C	VAL	B	50	32.241	32.978	38.598	1.00	47.99	6
ATOM	2046	O	VAL	B	50	32.533	33.824	37.758	1.00	48.54	8
ATOM	2047	N	VAL	B	51	32.349	31.669	38.383	1.00	45.73	7
ATOM	2048	CA	VAL	B	51	32.802	31.091	37.116	1.00	44.16	6
ATOM	2049	CB	VAL	B	51	34.037	30.178	37.313	1.00	43.78	6
ATOM	2050	CG1	VAL	B	51	34.324	29.416	36.031	1.00	40.41	6
ATOM	2051	CG2	VAL	B	51	35.245	31.005	37.728	1.00	40.89	6
ATOM	2052	C	VAL	B	51	31.673	30.227	36.569	1.00	45.01	6
ATOM	2053	O	VAL	B	51	31.075	29.458	37.318	1.00	48.28	8
ATOM	2054	N	PHE	B	52	31.382	30.328	35.275	1.00	42.51	7
ATOM	2055	CA	PHE	B	52	30.307	29.535	34.708	1.00	41.24	6
ATOM	2056	CB	PHE	B	52	28.981	30.224	34.993	1.00	41.72	6
ATOM	2057	CG	PHE	B	52	28.876	31.595	34.394	1.00	42.31	6
ATOM	2058	CD1	PHE	B	52	28.448	31.767	33.088	1.00	42.63	6
ATOM	2059	CD2	PHE	B	52	29.248	32.711	35.123	1.00	43.12	6
ATOM	2060	CE1	PHE	B	52	28.394	33.025	32.521	1.00	43.87	6
ATOM	2061	CE2	PHE	B	52	29.197	33.976	34.562	1.00	43.32	6
ATOM	2062	CZ	PHE	B	52	28.770	34.132	33.261	1.00	43.87	6
ATOM	2063	C	PHE	B	52	30.463	29.345	33.217	1.00	43.44	6

ATOM	2064	O	PHE	B	52	31.264	30.008	32.585	1.00	46.26	8
ATOM	2065	N	TRP	B	53	29.692	28.428	32.655	1.00	44.90	7
ATOM	2066	CA	TRP	B	53	29.725	28.188	31.223	1.00	47.46	6
ATOM	2067	CB	TRP	B	53	29.655	26.698	30.907	1.00	47.31	6
ATOM	2068	CG	TRP	B	53	30.869	25.949	31.278	1.00	49.36	6
ATOM	2069	CD2	TRP	B	53	31.029	24.535	31.246	1.00	50.82	6
ATOM	2070	CE2	TRP	B	53	32.342	24.253	31.686	1.00	49.80	6
ATOM	2071	CE3	TRP	B	53	30.189	23.473	30.887	1.00	51.30	6
ATOM	2072	CD1	TRP	B	53	32.057	26.463	31.719	1.00	50.05	6
ATOM	2073	NE1	TRP	B	53	32.947	25.448	31.968	1.00	50.43	7
ATOM	2074	CZ2	TRP	B	53	32.835	22.955	31.779	1.00	50.23	6
ATOM	2075	CZ3	TRP	B	53	30.676	22.182	30.977	1.00	49.78	6
ATOM	2076	CH2	TRP	B	53	31.990	21.932	31.421	1.00	50.88	6
ATOM	2077	C	TRP	B	53	28.516	28.860	30.619	1.00	48.93	6
ATOM	2078	O	TRP	B	53	27.388	28.490	30.912	1.00	48.69	8
ATOM	2079	N	GLN	B	54	28.746	29.846	29.770	1.00	50.46	7
ATOM	2080	CA	GLN	B	54	27.643	30.543	29.155	1.00	51.66	6
ATOM	2081	CB	GLN	B	54	28.036	31.984	28.844	1.00	51.35	6
ATOM	2082	CG	GLN	B	54	26.871	32.851	28.407	1.00	53.49	6
ATOM	2083	CD	GLN	B	54	27.117	34.326	28.693	1.00	57.50	6
ATOM	2084	OE1	GLN	B	54	27.399	34.711	29.837	1.00	57.95	8
ATOM	2085	NE2	GLN	B	54	27.016	35.161	27.659	1.00	58.04	7
ATOM	2086	C	GLN	B	54	27.273	29.790	27.898	1.00	52.38	6
ATOM	2087	O	GLN	B	54	27.564	30.209	26.786	1.00	54.42	8
ATOM	2088	N	GLN	B	55	26.638	28.650	28.101	1.00	52.78	7
ATOM	2089	CA	GLN	B	55	26.203	27.793	27.017	1.00	53.84	6
ATOM	2090	CB	GLN	B	55	25.672	26.501	27.623	1.00	58.14	6
ATOM	2091	CG	GLN	B	55	24.985	25.549	26.663	1.00	66.74	6
ATOM	2092	CD	GLN	B	55	24.756	24.190	27.315	1.00	70.87	6
ATOM	2093	OE1	GLN	B	55	24.456	24.108	28.528	1.00	73.46	8
ATOM	2094	NE2	GLN	B	55	24.897	23.117	26.527	1.00	69.32	7
ATOM	2095	C	GLN	B	55	25.145	28.495	26.168	1.00	51.37	6
ATOM	2096	O	GLN	B	55	23.993	28.631	26.563	1.00	52.24	8
ATOM	2097	N	THR	B	56	25.558	28.935	24.989	1.00	48.92	7
ATOM	2098	CA	THR	B	56	24.690	29.660	24.083	1.00	47.03	6
ATOM	2099	CB	THR	B	56	25.307	31.018	23.741	1.00	47.18	6
ATOM	2100	OG1	THR	B	56	25.758	31.647	24.946	1.00	46.91	8
ATOM	2101	CG2	THR	B	56	24.291	31.909	23.056	1.00	45.50	6
ATOM	2102	C	THR	B	56	24.466	28.896	22.787	1.00	46.66	6
ATOM	2103	O	THR	B	56	25.351	28.202	22.306	1.00	46.60	8
ATOM	2104	N	THR	B	57	23.273	29.034	22.220	1.00	45.86	7
ATOM	2105	CA	THR	B	57	22.942	28.350	20.984	1.00	44.53	6
ATOM	2106	CB	THR	B	57	22.320	26.958	21.247	1.00	44.84	6
ATOM	2107	OG1	THR	B	57	23.271	26.115	21.910	1.00	41.11	8
ATOM	2108	CG2	THR	B	57	21.942	26.306	19.936	1.00	46.63	6
ATOM	2109	C	THR	B	57	21.967	29.152	20.162	1.00	43.27	6
ATOM	2110	O	THR	B	57	21.106	29.825	20.700	1.00	44.01	8
ATOM	2111	N	TRP	B	58	22.122	29.086	18.849	1.00	41.40	7
ATOM	2112	CA	TRP	B	58	21.235	29.792	17.945	1.00	42.18	6
ATOM	2113	CB	TRP	B	58	21.500	31.302	17.968	1.00	40.63	6
ATOM	2114	CG	TRP	B	58	22.800	31.729	17.377	1.00	40.64	6
ATOM	2115	CD2	TRP	B	58	24.048	31.827	18.054	1.00	37.47	6
ATOM	2116	CE2	TRP	B	58	24.998	32.252	17.113	1.00	37.44	6
ATOM	2117	CE3	TRP	B	58	24.456	31.594	19.371	1.00	37.69	6
ATOM	2118	CD1	TRP	B	58	23.036	32.088	16.087	1.00	39.23	6
ATOM	2119	NE1	TRP	B	58	24.354	32.404	15.917	1.00	36.19	7
ATOM	2120	CZ2	TRP	B	58	26.336	32.452	17.444	1.00	40.36	6
ATOM	2121	CZ3	TRP	B	58	25.778	31.789	19.701	1.00	38.85	6
ATOM	2122	CH2	TRP	B	58	26.708	32.215	18.742	1.00	40.16	6
ATOM	2123	C	TRP	B	58	21.430	29.217	16.561	1.00	43.00	6
ATOM	2124	O	TRP	B	58	22.226	28.320	16.383	1.00	44.24	8

ATOM	2125	N	SER	B	59	20.711	29.729	15.579	1.00	47.57	7
ATOM	2126	CA	SER	B	59	20.814	29.181	14.246	1.00	50.36	6
ATOM	2127	CB	SER	B	59	19.517	28.410	13.937	1.00	52.43	6
ATOM	2128	OG	SER	B	59	19.677	27.455	12.901	1.00	58.14	8
ATOM	2129	C	SER	B	59	21.073	30.250	13.191	1.00	51.80	6
ATOM	2130	O	SER	B	59	20.440	31.307	13.184	1.00	48.66	8
ATOM	2131	N	ASP	B	60	22.018	29.954	12.303	1.00	53.93	7
ATOM	2132	CA	ASP	B	60	22.393	30.844	11.206	1.00	56.01	6
ATOM	2133	CB	ASP	B	60	23.766	31.462	11.474	1.00	57.13	6
ATOM	2134	CG	ASP	B	60	24.163	32.503	10.437	1.00	58.21	6
ATOM	2135	OD1	ASP	B	60	23.714	32.413	9.275	1.00	56.08	8
ATOM	2136	OD2	ASP	B	60	24.952	33.407	10.786	1.00	59.82	8
ATOM	2137	C	ASP	B	60	22.453	29.976	9.953	1.00	57.25	6
ATOM	2138	O	ASP	B	60	23.458	29.315	9.683	1.00	57.02	8
ATOM	2139	N	ARG	B	61	21.370	29.979	9.192	1.00	59.51	7
ATOM	2140	CA	ARG	B	61	21.281	29.171	7.981	1.00	62.14	6
ATOM	2141	CB	ARG	B	61	19.852	29.202	7.418	1.00	65.88	6
ATOM	2142	CG	ARG	B	61	18.842	28.288	8.125	1.00	71.80	6
ATOM	2143	CD	ARG	B	61	17.562	28.189	7.282	1.00	79.30	6
ATOM	2144	NE	ARG	B	61	16.561	27.245	7.806	1.00	85.93	7
ATOM	2145	CZ	ARG	B	61	15.393	26.967	7.210	1.00	88.02	6
ATOM	2146	NH1	ARG	B	61	15.059	27.553	6.059	1.00	89.55	7
ATOM	2147	NH2	ARG	B	61	14.550	26.101	7.762	1.00	88.72	7
ATOM	2148	C	ARG	B	61	22.256	29.537	6.868	1.00	61.20	6
ATOM	2149	O	ARG	B	61	22.488	28.725	5.972	1.00	61.95	8
ATOM	2150	N	THR	B	62	22.819	30.742	6.898	1.00	59.72	7
ATOM	2151	CA	THR	B	62	23.755	31.133	5.846	1.00	59.39	6
ATOM	2152	CB	THR	B	62	24.072	32.653	5.878	1.00	61.53	6
ATOM	2153	OG1	THR	B	62	24.790	32.981	7.077	1.00	62.67	8
ATOM	2154	CG2	THR	B	62	22.783	33.461	5.826	1.00	61.46	6
ATOM	2155	C	THR	B	62	25.055	30.355	5.992	1.00	58.40	6
ATOM	2156	O	THR	B	62	25.923	30.410	5.129	1.00	58.95	8
ATOM	2157	N	LEU	B	63	25.176	29.626	7.095	1.00	57.74	7
ATOM	2158	CA	LEU	B	63	26.365	28.831	7.381	1.00	55.00	6
ATOM	2159	CB	LEU	B	63	26.677	28.871	8.880	1.00	53.55	6
ATOM	2160	CG	LEU	B	63	26.908	30.230	9.531	1.00	52.72	6
ATOM	2161	CD1	LEU	B	63	27.061	30.070	11.038	1.00	53.77	6
ATOM	2162	CD2	LEU	B	63	28.141	30.866	8.929	1.00	52.77	6
ATOM	2163	C	LEU	B	63	26.163	27.377	6.971	1.00	54.84	6
ATOM	2164	O	LEU	B	63	27.125	26.624	6.858	1.00	55.28	8
ATOM	2165	N	ALA	B	64	24.911	26.986	6.767	1.00	53.09	7
ATOM	2166	CA	ALA	B	64	24.579	25.621	6.403	1.00	54.25	6
ATOM	2167	CB	ALA	B	64	23.078	25.474	6.274	1.00	54.84	6
ATOM	2168	C	ALA	B	64	25.235	25.173	5.116	1.00	54.35	6
ATOM	2169	O	ALA	B	64	25.441	25.973	4.208	1.00	56.81	8
ATOM	2170	N	TRP	B	65	25.543	23.884	5.040	1.00	50.85	7
ATOM	2171	CA	TRP	B	65	26.148	23.305	3.851	1.00	50.36	6
ATOM	2172	CB	TRP	B	65	27.674	23.449	3.895	1.00	47.85	6
ATOM	2173	CG	TRP	B	65	28.356	22.496	4.836	1.00	44.59	6
ATOM	2174	CD2	TRP	B	65	28.626	22.704	6.229	1.00	42.42	6
ATOM	2175	CE2	TRP	B	65	29.244	21.535	6.711	1.00	41.31	6
ATOM	2176	CE3	TRP	B	65	28.406	23.766	7.115	1.00	39.86	6
ATOM	2177	CD1	TRP	B	65	28.809	21.247	4.544	1.00	43.65	6
ATOM	2178	NE1	TRP	B	65	29.344	20.664	5.662	1.00	42.95	7
ATOM	2179	CZ2	TRP	B	65	29.645	21.393	8.041	1.00	41.27	6
ATOM	2180	CZ3	TRP	B	65	28.807	23.624	8.439	1.00	39.24	6
ATOM	2181	CH2	TRP	B	65	29.419	22.445	8.886	1.00	40.26	6
ATOM	2182	C	TRP	B	65	25.751	21.835	3.839	1.00	51.92	6
ATOM	2183	O	TRP	B	65	25.269	21.312	4.846	1.00	51.65	8
ATOM	2184	N	ASN	B	66	25.933	21.173	2.703	1.00	54.28	7
ATOM	2185	CA	ASN	B	66	25.579	19.760	2.599	1.00	56.88	6

ATOM	2186	CB	ASN	B	66	25.361	19.349	1.139	1.00	59.16	6
ATOM	2187	CG	ASN	B	66	25.067	17.869	1.006	1.00	62.92	6
ATOM	2188	OD1	ASN	B	66	25.084	17.308	-0.090	1.00	64.20	8
ATOM	2189	ND2	ASN	B	66	24.792	17.223	2.138	1.00	63.82	7
ATOM	2190	C	ASN	B	66	26.684	18.903	3.197	1.00	56.22	6
ATOM	2191	O	ASN	B	66	27.826	18.942	2.747	1.00	54.74	8
ATOM	2192	N	SER	B	67	26.336	18.112	4.200	1.00	57.45	7
ATOM	2193	CA	SER	B	67	27.323	17.276	4.866	1.00	60.21	6
ATOM	2194	CB	SER	B	67	27.251	17.503	6.376	1.00	60.70	6
ATOM	2195	OG	SER	B	67	25.956	17.197	6.844	1.00	59.26	8
ATOM	2196	C	SER	B	67	27.139	15.796	4.554	1.00	60.90	6
ATOM	2197	O	SER	B	67	27.705	14.926	5.221	1.00	59.74	8
ATOM	2198	N	SER	B	68	26.350	15.519	3.528	1.00	62.89	7
ATOM	2199	CA	SER	B	68	26.094	14.148	3.129	1.00	64.44	6
ATOM	2200	CB	SER	B	68	25.141	14.127	1.933	1.00	64.07	6
ATOM	2201	OG	SER	B	68	25.569	15.023	0.923	1.00	65.05	8
ATOM	2202	C	SER	B	68	27.399	13.437	2.790	1.00	65.22	6
ATOM	2203	O	SER	B	68	27.491	12.215	2.898	1.00	65.18	8
ATOM	2204	N	HIS	B	69	28.414	14.203	2.401	1.00	66.21	7
ATOM	2205	CA	HIS	B	69	29.702	13.617	2.054	1.00	66.70	6
ATOM	2206	CB	HIS	B	69	29.832	13.502	0.539	1.00	69.64	6
ATOM	2207	CG	HIS	B	69	29.047	12.363	-0.025	1.00	74.89	6
ATOM	2208	CD2	HIS	B	69	29.433	11.123	-0.417	1.00	76.05	6
ATOM	2209	ND1	HIS	B	69	27.673	12.393	-0.143	1.00	76.35	7
ATOM	2210	CE1	HIS	B	69	27.245	11.221	-0.583	1.00	76.49	6
ATOM	2211	NE2	HIS	B	69	28.293	10.433	-0.757	1.00	76.65	7
ATOM	2212	C	HIS	B	69	30.895	14.352	2.633	1.00	65.56	6
ATOM	2213	O	HIS	B	69	31.919	14.538	1.971	1.00	63.93	8
ATOM	2214	N	SER	B	70	30.746	14.737	3.897	1.00	65.07	7
ATOM	2215	CA	SER	B	70	31.772	15.463	4.632	1.00	63.00	6
ATOM	2216	CB	SER	B	70	31.954	16.854	4.004	1.00	61.97	6
ATOM	2217	OG	SER	B	70	30.716	17.393	3.551	1.00	59.22	8
ATOM	2218	C	SER	B	70	31.353	15.576	6.105	1.00	62.92	6
ATOM	2219	O	SER	B	70	30.288	15.077	6.507	1.00	62.73	8
ATOM	2220	N	PRO	B	71	32.204	16.199	6.937	1.00	62.42	7
ATOM	2221	CD	PRO	B	71	33.624	16.490	6.672	1.00	61.13	6
ATOM	2222	CA	PRO	B	71	31.901	16.371	8.361	1.00	61.29	6
ATOM	2223	CB	PRO	B	71	33.124	17.103	8.879	1.00	61.30	6
ATOM	2224	CG	PRO	B	71	34.214	16.490	8.063	1.00	60.40	6
ATOM	2225	C	PRO	B	71	30.619	17.159	8.575	1.00	61.12	6
ATOM	2226	O	PRO	B	71	30.222	17.964	7.733	1.00	60.52	8
ATOM	2227	N	ASP	B	72	29.973	16.916	9.708	1.00	62.69	7
ATOM	2228	CA	ASP	B	72	28.714	17.587	10.046	1.00	62.55	6
ATOM	2229	CB	ASP	B	72	27.839	16.649	10.883	1.00	64.34	6
ATOM	2230	CG	ASP	B	72	27.143	15.613	10.040	1.00	67.53	6
ATOM	2231	OD1	ASP	B	72	25.937	15.794	9.767	1.00	67.60	8
ATOM	2232	OD2	ASP	B	72	27.808	14.627	9.631	1.00	70.97	8
ATOM	2233	C	ASP	B	72	28.962	18.858	10.827	1.00	60.43	6
ATOM	2234	O	ASP	B	72	28.137	19.780	10.815	1.00	58.20	8
ATOM	2235	N	GLN	B	73	30.123	18.883	11.483	1.00	58.87	7
ATOM	2236	CA	GLN	B	73	30.549	19.981	12.339	1.00	58.03	6
ATOM	2237	CB	GLN	B	73	30.400	19.583	13.788	1.00	60.56	6
ATOM	2238	CG	GLN	B	73	29.025	19.532	14.346	1.00	62.56	6
ATOM	2239	CD	GLN	B	73	29.096	19.033	15.763	1.00	64.10	6
ATOM	2240	OE1	GLN	B	73	29.599	17.945	16.003	1.00	67.42	8
ATOM	2241	NE2	GLN	B	73	28.628	19.830	16.711	1.00	65.84	7
ATOM	2242	C	GLN	B	73	31.998	20.392	12.165	1.00	55.43	6
ATOM	2243	O	GLN	B	73	32.845	19.591	11.754	1.00	56.41	8
ATOM	2244	N	VAL	B	74	32.275	21.642	12.522	1.00	50.91	7
ATOM	2245	CA	VAL	B	74	33.621	22.197	12.464	1.00	48.23	6
ATOM	2246	CB	VAL	B	74	33.925	22.849	11.107	1.00	46.99	6

ATOM	2247	CG1	VAL	B	74	34.009	21.782	10.026	1.00	48.63	6
ATOM	2248	CG2	VAL	B	74	32.864	23.871	10.777	1.00	45.41	6
ATOM	2249	C	VAL	B	74	33.734	23.259	13.532	1.00	46.89	6
ATOM	2250	O	VAL	B	74	32.731	23.812	13.964	1.00	46.87	8
ATOM	2251	N	SER	B	75	34.951	23.524	13.980	1.00	44.18	7
ATOM	2252	CA	SER	B	75	35.177	24.551	14.982	1.00	41.30	6
ATOM	2253	CB	SER	B	75	36.314	24.145	15.920	1.00	39.05	6
ATOM	2254	OG	SER	B	75	35.850	23.290	16.932	1.00	30.94	8
ATOM	2255	C	SER	B	75	35.513	25.856	14.264	1.00	40.02	6
ATOM	2256	O	SER	B	75	36.478	25.936	13.516	1.00	39.74	8
ATOM	2257	N	VAL	B	76	34.701	26.875	14.497	1.00	39.53	7
ATOM	2258	CA	VAL	B	76	34.885	28.167	13.861	1.00	40.26	6
ATOM	2259	CB	VAL	B	76	33.607	28.580	13.124	1.00	42.73	6
ATOM	2260	CG1	VAL	B	76	33.788	29.928	12.483	1.00	43.36	6
ATOM	2261	CG2	VAL	B	76	33.244	27.539	12.090	1.00	40.50	6
ATOM	2262	C	VAL	B	76	35.218	29.256	14.861	1.00	40.57	6
ATOM	2263	O	VAL	B	76	34.626	29.322	15.926	1.00	41.80	8
ATOM	2264	N	PRO	B	77	36.188	30.120	14.541	1.00	40.43	7
ATOM	2265	CD	PRO	B	77	37.176	30.053	13.460	1.00	39.25	6
ATOM	2266	CA	PRO	B	77	36.527	31.189	15.479	1.00	39.73	6
ATOM	2267	CB	PRO	B	77	37.717	31.853	14.816	1.00	40.77	6
ATOM	2268	CG	PRO	B	77	38.342	30.728	14.078	1.00	40.80	6
ATOM	2269	C	PRO	B	77	35.346	32.141	15.622	1.00	38.02	6
ATOM	2270	O	PRO	B	77	34.663	32.438	14.658	1.00	39.36	8
ATOM	2271	N	ILE	B	78	35.105	32.600	16.835	1.00	37.63	7
ATOM	2272	CA	ILE	B	78	34.018	33.515	17.129	1.00	39.61	6
ATOM	2273	CB	ILE	B	78	34.107	33.946	18.602	1.00	41.86	6
ATOM	2274	CG2	ILE	B	78	33.311	35.183	18.861	1.00	40.86	6
ATOM	2275	CG1	ILE	B	78	33.622	32.799	19.469	1.00	45.04	6
ATOM	2276	CD1	ILE	B	78	32.313	32.232	18.983	1.00	46.64	6
ATOM	2277	C	ILE	B	78	34.000	34.741	16.231	1.00	41.00	6
ATOM	2278	O	ILE	B	78	32.947	35.225	15.846	1.00	41.00	8
ATOM	2279	N	SER	B	79	35.185	35.227	15.898	1.00	43.87	7
ATOM	2280	CA	SER	B	79	35.368	36.399	15.047	1.00	44.52	6
ATOM	2281	CB	SER	B	79	36.842	36.792	15.061	1.00	46.91	6
ATOM	2282	OG	SER	B	79	37.657	35.687	14.696	1.00	49.85	8
ATOM	2283	C	SER	B	79	34.914	36.244	13.593	1.00	43.47	6
ATOM	2284	O	SER	B	79	34.805	37.228	12.876	1.00	43.49	8
ATOM	2285	N	SER	B	80	34.656	35.016	13.160	1.00	43.24	7
ATOM	2286	CA	SER	B	80	34.227	34.769	11.793	1.00	44.14	6
ATOM	2287	CB	SER	B	80	34.955	33.552	11.221	1.00	44.85	6
ATOM	2288	OG	SER	B	80	36.354	33.781	11.115	1.00	52.06	8
ATOM	2289	C	SER	B	80	32.731	34.545	11.690	1.00	44.49	6
ATOM	2290	O	SER	B	80	32.213	34.308	10.609	1.00	44.54	8
ATOM	2291	N	LEU	B	81	32.039	34.625	12.820	1.00	45.89	7
ATOM	2292	CA	LEU	B	81	30.589	34.418	12.858	1.00	45.78	6
ATOM	2293	CB	LEU	B	81	30.250	33.187	13.700	1.00	42.48	6
ATOM	2294	CG	LEU	B	81	30.945	31.867	13.420	1.00	42.60	6
ATOM	2295	CD1	LEU	B	81	30.769	30.949	14.584	1.00	41.27	6
ATOM	2296	CD2	LEU	B	81	30.379	31.266	12.165	1.00	45.70	6
ATOM	2297	C	LEU	B	81	29.909	35.611	13.513	1.00	45.11	6
ATOM	2298	O	LEU	B	81	30.562	36.439	14.154	1.00	46.02	8
ATOM	2299	N	TRP	B	82	28.596	35.696	13.344	1.00	42.92	7
ATOM	2300	CA	TRP	B	82	27.829	36.737	13.984	1.00	40.24	6
ATOM	2301	CB	TRP	B	82	26.493	36.962	13.290	1.00	42.22	6
ATOM	2302	CG	TRP	B	82	25.535	37.766	14.126	1.00	43.85	6
ATOM	2303	CD2	TRP	B	82	24.580	37.257	15.072	1.00	44.14	6
ATOM	2304	CE2	TRP	B	82	23.972	38.369	15.687	1.00	42.05	6
ATOM	2305	CE3	TRP	B	82	24.185	35.964	15.461	1.00	42.43	6
ATOM	2306	CD1	TRP	B	82	25.459	39.118	14.204	1.00	42.92	6
ATOM	2307	NE1	TRP	B	82	24.527	39.490	15.138	1.00	41.43	7

ATOM	2308	CZ2	TRP	B	82	22.991	38.238	16.671	1.00	42.94	6
ATOM	2309	CZ3	TRP	B	82	23.211	35.832	16.442	1.00	41.79	6
ATOM	2310	CH2	TRP	B	82	22.625	36.965	17.036	1.00	42.57	6
ATOM	2311	C	TRP	B	82	27.579	36.100	15.323	1.00	39.43	6
ATOM	2312	O	TRP	B	82	27.379	34.904	15.410	1.00	41.05	8
ATOM	2313	N	VAL	B	83	27.594	36.892	16.373	1.00	41.18	7
ATOM	2314	CA	VAL	B	83	27.363	36.359	17.699	1.00	40.57	6
ATOM	2315	CB	VAL	B	83	28.714	36.210	18.444	1.00	41.00	6
ATOM	2316	CG1	VAL	B	83	28.494	35.956	19.903	1.00	45.57	6
ATOM	2317	CG2	VAL	B	83	29.491	35.066	17.856	1.00	40.97	6
ATOM	2318	C	VAL	B	83	26.399	37.275	18.460	1.00	40.40	6
ATOM	2319	O	VAL	B	83	26.424	38.487	18.301	1.00	42.78	8
ATOM	2320	N	PRO	B	84	25.510	36.693	19.271	1.00	40.62	7
ATOM	2321	CD	PRO	B	84	25.296	35.250	19.465	1.00	43.06	6
ATOM	2322	CA	PRO	B	84	24.540	37.460	20.052	1.00	39.62	6
ATOM	2323	CB	PRO	B	84	23.839	36.384	20.880	1.00	39.00	6
ATOM	2324	CG	PRO	B	84	23.899	35.212	20.013	1.00	43.18	6
ATOM	2325	C	PRO	B	84	25.246	38.474	20.937	1.00	37.37	6
ATOM	2326	O	PRO	B	84	26.215	38.140	21.603	1.00	34.20	8
ATOM	2327	N	ASP	B	85	24.753	39.706	20.950	1.00	36.29	7
ATOM	2328	CA	ASP	B	85	25.341	40.736	21.777	1.00	37.57	6
ATOM	2329	CB	ASP	B	85	25.112	42.107	21.152	1.00	38.52	6
ATOM	2330	CG	ASP	B	85	23.661	42.418	20.952	1.00	40.81	6
ATOM	2331	OD1	ASP	B	85	22.925	41.501	20.578	1.00	41.81	8
ATOM	2332	OD2	ASP	B	85	23.254	43.579	21.148	1.00	41.12	8
ATOM	2333	C	ASP	B	85	24.776	40.687	23.193	1.00	39.08	6
ATOM	2334	O	ASP	B	85	24.261	41.668	23.714	1.00	36.01	8
ATOM	2335	N	LEU	B	86	24.902	39.522	23.811	1.00	38.19	7
ATOM	2336	CA	LEU	B	86	24.421	39.306	25.161	1.00	39.63	6
ATOM	2337	CB	LEU	B	86	24.459	37.819	25.502	1.00	37.18	6
ATOM	2338	CG	LEU	B	86	23.585	36.939	24.621	1.00	38.33	6
ATOM	2339	CD1	LEU	B	86	23.700	35.493	25.065	1.00	33.72	6
ATOM	2340	CD2	LEU	B	86	22.159	37.433	24.693	1.00	35.49	6
ATOM	2341	C	LEU	B	86	25.223	40.061	26.201	1.00	40.05	6
ATOM	2342	O	LEU	B	86	26.432	40.251	26.065	1.00	42.26	8
ATOM	2343	N	ALA	B	87	24.541	40.467	27.260	1.00	40.28	7
ATOM	2344	CA	ALA	B	87	25.180	41.193	28.339	1.00	40.51	6
ATOM	2345	CB	ALA	B	87	25.048	42.698	28.091	1.00	40.62	6
ATOM	2346	C	ALA	B	87	24.521	40.826	29.660	1.00	40.28	6
ATOM	2347	O	ALA	B	87	23.306	40.702	29.729	1.00	40.56	8
ATOM	2348	N	ALA	B	88	25.316	40.634	30.703	1.00	39.13	7
ATOM	2349	CA	ALA	B	88	24.756	40.340	32.014	1.00	38.99	6
ATOM	2350	CB	ALA	B	88	25.749	39.577	32.850	1.00	37.09	6
ATOM	2351	C	ALA	B	88	24.433	41.686	32.665	1.00	40.68	6
ATOM	2352	O	ALA	B	88	25.319	42.392	33.134	1.00	38.34	8
ATOM	2353	N	TYR	B	89	23.153	42.033	32.667	1.00	42.45	7
ATOM	2354	CA	TYR	B	89	22.654	43.285	33.232	1.00	44.08	6
ATOM	2355	CB	TYR	B	89	21.133	43.209	33.363	1.00	46.62	6
ATOM	2356	CG	TYR	B	89	20.395	43.055	32.056	1.00	51.23	6
ATOM	2357	CD1	TYR	B	89	19.022	42.816	32.036	1.00	54.25	6
ATOM	2358	CE1	TYR	B	89	18.322	42.711	30.826	1.00	55.90	6
ATOM	2359	CD2	TYR	B	89	21.054	43.179	30.835	1.00	52.13	6
ATOM	2360	CE2	TYR	B	89	20.366	43.078	29.626	1.00	54.28	6
ATOM	2361	CZ	TYR	B	89	19.001	42.847	29.629	1.00	55.97	6
ATOM	2362	OH	TYR	B	89	18.313	42.787	28.440	1.00	59.26	8
ATOM	2363	C	TYR	B	89	23.243	43.725	34.579	1.00	43.48	6
ATOM	2364	O	TYR	B	89	23.409	44.917	34.820	1.00	42.18	8
ATOM	2365	N	ASN	B	90	23.540	42.784	35.466	1.00	42.08	7
ATOM	2366	CA	ASN	B	90	24.102	43.155	36.755	1.00	40.43	6
ATOM	2367	CB	ASN	B	90	23.262	42.581	37.904	1.00	39.29	6
ATOM	2368	CG	ASN	B	90	23.084	41.082	37.824	1.00	40.77	6

ATOM	2369	OD1	ASN	B	90	22.778	40.536	36.774	1.00	40.90	8
ATOM	2370	ND2	ASN	B	90	23.257	40.412	38.948	1.00	42.41	7
ATOM	2371	C	ASN	B	90	25.554	42.768	36.921	1.00	41.50	6
ATOM	2372	O	ASN	B	90	26.031	42.618	38.042	1.00	42.85	8
ATOM	2373	N	ALA	B	91	26.250	42.605	35.798	1.00	43.60	7
ATOM	2374	CA	ALA	B	91	27.669	42.266	35.811	1.00	43.31	6
ATOM	2375	CB	ALA	B	91	28.156	41.933	34.415	1.00	42.36	6
ATOM	2376	C	ALA	B	91	28.359	43.513	36.336	1.00	44.47	6
ATOM	2377	O	ALA	B	91	28.048	44.637	35.934	1.00	43.75	8
ATOM	2378	N	ILE	B	92	29.295	43.299	37.244	1.00	44.99	7
ATOM	2379	CA	ILE	B	92	30.009	44.379	37.895	1.00	45.69	6
ATOM	2380	CB	ILE	B	92	30.052	44.061	39.418	1.00	46.91	6
ATOM	2381	CG2	ILE	B	92	31.419	43.514	39.831	1.00	49.50	6
ATOM	2382	CG1	ILE	B	92	29.726	45.288	40.232	1.00	48.64	6
ATOM	2383	CD1	ILE	B	92	29.920	45.030	41.718	1.00	53.73	6
ATOM	2384	C	ILE	B	92	31.428	44.532	37.302	1.00	45.86	6
ATOM	2385	O	ILE	B	92	32.156	45.487	37.611	1.00	45.24	8
ATOM	2386	N	SER	B	93	31.804	43.581	36.453	1.00	41.25	7
ATOM	2387	CA	SER	B	93	33.104	43.578	35.813	1.00	38.58	6
ATOM	2388	CB	SER	B	93	34.056	42.662	36.568	1.00	35.19	6
ATOM	2389	OG	SER	B	93	33.682	41.315	36.388	1.00	35.43	8
ATOM	2390	C	SER	B	93	32.852	43.015	34.431	1.00	40.88	6
ATOM	2391	O	SER	B	93	31.776	42.493	34.174	1.00	39.63	8
ATOM	2392	N	LYS	B	94	33.815	43.131	33.524	1.00	43.16	7
ATOM	2393	CA	LYS	B	94	33.598	42.557	32.212	1.00	43.98	6
ATOM	2394	CB	LYS	B	94	34.355	43.325	31.127	1.00	46.29	6
ATOM	2395	CG	LYS	B	94	35.769	43.727	31.434	1.00	50.31	6
ATOM	2396	CD	LYS	B	94	36.225	44.764	30.401	1.00	52.39	6
ATOM	2397	CE	LYS	B	94	35.853	44.341	28.978	1.00	52.02	6
ATOM	2398	NZ	LYS	B	94	36.333	45.308	27.965	1.00	54.82	7
ATOM	2399	C	LYS	B	94	33.963	41.075	32.230	1.00	43.71	6
ATOM	2400	O	LYS	B	94	34.673	40.602	33.114	1.00	44.78	8
ATOM	2401	N	PRO	B	95	33.443	40.310	31.267	1.00	44.16	7
ATOM	2402	CD	PRO	B	95	32.562	40.750	30.171	1.00	42.37	6
ATOM	2403	CA	PRO	B	95	33.704	38.873	31.184	1.00	39.82	6
ATOM	2404	CB	PRO	B	95	32.836	38.422	30.016	1.00	40.83	6
ATOM	2405	CG	PRO	B	95	31.813	39.505	29.881	1.00	42.58	6
ATOM	2406	C	PRO	B	95	35.141	38.524	30.941	1.00	39.41	6
ATOM	2407	O	PRO	B	95	35.772	39.048	30.032	1.00	40.47	8
ATOM	2408	N	GLU	B	96	35.663	37.637	31.765	1.00	39.61	7
ATOM	2409	CA	GLU	B	96	37.020	37.175	31.582	1.00	39.82	6
ATOM	2410	CB	GLU	B	96	37.765	37.046	32.915	1.00	41.36	6
ATOM	2411	CG	GLU	B	96	39.238	36.644	32.763	1.00	50.17	6
ATOM	2412	CD	GLU	B	96	39.989	36.540	34.094	1.00	55.05	6
ATOM	2413	OE1	GLU	B	96	39.506	37.129	35.084	1.00	57.32	8
ATOM	2414	OE2	GLU	B	96	41.067	35.888	34.153	1.00	56.17	8
ATOM	2415	C	GLU	B	96	36.802	35.804	30.966	1.00	39.55	6
ATOM	2416	O	GLU	B	96	36.537	34.840	31.676	1.00	38.71	8
ATOM	2417	N	VAL	B	97	36.864	35.736	29.638	1.00	36.87	7
ATOM	2418	CA	VAL	B	97	36.690	34.475	28.938	1.00	35.52	6
ATOM	2419	CB	VAL	B	97	36.457	34.702	27.448	1.00	35.28	6
ATOM	2420	CG1	VAL	B	97	36.249	33.378	26.752	1.00	33.50	6
ATOM	2421	CG2	VAL	B	97	35.249	35.586	27.255	1.00	31.71	6
ATOM	2422	C	VAL	B	97	37.935	33.640	29.157	1.00	35.07	6
ATOM	2423	O	VAL	B	97	39.025	34.005	28.741	1.00	37.13	8
ATOM	2424	N	LEU	B	98	37.759	32.511	29.823	1.00	35.85	7
ATOM	2425	CA	LEU	B	98	38.866	31.631	30.167	1.00	36.60	6
ATOM	2426	CB	LEU	B	98	38.554	30.913	31.482	1.00	37.34	6
ATOM	2427	CG	LEU	B	98	38.127	31.727	32.701	1.00	39.09	6
ATOM	2428	CD1	LEU	B	98	37.534	30.812	33.739	1.00	37.97	6
ATOM	2429	CD2	LEU	B	98	39.306	32.469	33.259	1.00	41.28	6

ATOM	2430	C	LEU	B	98	39.198	30.581	29.128	1.00	36.56	6
ATOM	2431	O	LEU	B	98	40.195	29.889	29.251	1.00	37.06	8
ATOM	2432	N	THR	B	99	38.371	30.467	28.103	1.00	36.66	7
ATOM	2433	CA	THR	B	99	38.578	29.438	27.100	1.00	37.03	6
ATOM	2434	CB	THR	B	99	37.405	28.414	27.142	1.00	40.73	6
ATOM	2435	OG1	THR	B	99	36.152	29.097	26.972	1.00	42.70	8
ATOM	2436	CG2	THR	B	99	37.400	27.676	28.466	1.00	37.60	6
ATOM	2437	C	THR	B	99	38.725	29.932	25.680	1.00	34.89	6
ATOM	2438	O	THR	B	99	38.401	31.073	25.378	1.00	35.25	8
ATOM	2439	N	PRO	B	100	39.231	29.066	24.786	1.00	35.40	7
ATOM	2440	CD	PRO	B	100	39.818	27.745	25.056	1.00	33.38	6
ATOM	2441	CA	PRO	B	100	39.413	29.420	23.380	1.00	35.17	6
ATOM	2442	CB	PRO	B	100	39.783	28.095	22.745	1.00	33.58	6
ATOM	2443	CG	PRO	B	100	40.603	27.476	23.789	1.00	34.20	6
ATOM	2444	C	PRO	B	100	38.107	29.961	22.852	1.00	37.17	6
ATOM	2445	O	PRO	B	100	37.052	29.396	23.103	1.00	38.59	8
ATOM	2446	N	GLN	B	101	38.168	31.066	22.130	1.00	39.08	7
ATOM	2447	CA	GLN	B	101	36.949	31.636	21.621	1.00	40.23	6
ATOM	2448	CB	GLN	B	101	37.071	33.155	21.576	1.00	39.84	6
ATOM	2449	CG	GLN	B	101	36.866	33.742	22.960	1.00	45.68	6
ATOM	2450	CD	GLN	B	101	37.334	35.158	23.075	1.00	47.02	6
ATOM	2451	OE1	GLN	B	101	36.871	36.035	22.350	1.00	50.05	8
ATOM	2452	NE2	GLN	B	101	38.260	35.398	23.997	1.00	45.46	7
ATOM	2453	C	GLN	B	101	36.536	31.057	20.295	1.00	39.08	6
ATOM	2454	O	GLN	B	101	36.496	31.747	19.282	1.00	37.88	8
ATOM	2455	N	LEU	B	102	36.212	29.768	20.342	1.00	40.24	7
ATOM	2456	CA	LEU	B	102	35.770	28.997	19.183	1.00	39.64	6
ATOM	2457	CB	LEU	B	102	36.652	27.759	18.982	1.00	37.23	6
ATOM	2458	CG	LEU	B	102	38.155	27.988	18.842	1.00	37.24	6
ATOM	2459	CD1	LEU	B	102	38.852	26.666	18.659	1.00	33.59	6
ATOM	2460	CD2	LEU	B	102	38.429	28.893	17.665	1.00	36.66	6
ATOM	2461	C	LEU	B	102	34.349	28.528	19.394	1.00	39.73	6
ATOM	2462	O	LEU	B	102	33.948	28.210	20.502	1.00	38.45	8
ATOM	2463	N	ALA	B	103	33.586	28.492	18.317	1.00	41.12	7
ATOM	2464	CA	ALA	B	103	32.218	28.017	18.375	1.00	40.48	6
ATOM	2465	CB	ALA	B	103	31.271	29.034	17.760	1.00	39.15	6
ATOM	2466	C	ALA	B	103	32.163	26.711	17.599	1.00	40.28	6
ATOM	2467	O	ALA	B	103	33.109	26.337	16.917	1.00	38.52	8
ATOM	2468	N	ARG	B	104	31.045	26.014	17.715	1.00	42.85	7
ATOM	2469	CA	ARG	B	104	30.876	24.755	17.019	1.00	44.21	6
ATOM	2470	CB	ARG	B	104	30.557	23.659	18.027	1.00	43.23	6
ATOM	2471	CG	ARG	B	104	30.760	22.273	17.496	1.00	45.99	6
ATOM	2472	CD	ARG	B	104	32.214	21.957	17.217	1.00	44.48	6
ATOM	2473	NE	ARG	B	104	32.306	20.612	16.652	1.00	45.67	7
ATOM	2474	CZ	ARG	B	104	33.434	19.985	16.341	1.00	42.29	6
ATOM	2475	NH1	ARG	B	104	34.593	20.576	16.534	1.00	40.18	7
ATOM	2476	NH2	ARG	B	104	33.397	18.755	15.847	1.00	43.70	7
ATOM	2477	C	ARG	B	104	29.736	24.954	16.040	1.00	44.71	6
ATOM	2478	O	ARG	B	104	28.655	25.377	16.425	1.00	43.84	8
ATOM	2479	N	VAL	B	105	29.990	24.686	14.767	1.00	45.98	7
ATOM	2480	CA	VAL	B	105	28.955	24.862	13.761	1.00	46.86	6
ATOM	2481	CB	VAL	B	105	29.404	25.834	12.663	1.00	43.67	6
ATOM	2482	CG1	VAL	B	105	28.257	26.111	11.715	1.00	42.93	6
ATOM	2483	CG2	VAL	B	105	29.885	27.116	13.281	1.00	41.79	6
ATOM	2484	C	VAL	B	105	28.546	23.546	13.112	1.00	50.58	6
ATOM	2485	O	VAL	B	105	29.393	22.808	12.589	1.00	51.09	8
ATOM	2486	N	VAL	B	106	27.243	23.266	13.158	1.00	51.24	7
ATOM	2487	CA	VAL	B	106	26.677	22.056	12.577	1.00	52.00	6
ATOM	2488	CB	VAL	B	106	25.464	21.592	13.387	1.00	52.31	6
ATOM	2489	CG1	VAL	B	106	25.038	20.207	12.931	1.00	52.15	6
ATOM	2490	CG2	VAL	B	106	25.798	21.607	14.865	1.00	50.55	6

ATOM	2491	C	VAL	B	106	26.243	22.369	11.147	1.00	52.00	6
ATOM	2492	O	VAL	B	106	25.782	23.474	10.870	1.00	52.80	8
ATOM	2493	N	SER	B	107	26.388	21.401	10.248	1.00	51.28	7
ATOM	2494	CA	SER	B	107	26.038	21.592	8.845	1.00	52.41	6
ATOM	2495	CB	SER	B	107	26.175	20.272	8.097	1.00	54.05	6
ATOM	2496	OG	SER	B	107	25.609	19.216	8.855	1.00	58.60	8
ATOM	2497	C	SER	B	107	24.676	22.198	8.544	1.00	52.33	6
ATOM	2498	O	SER	B	107	24.469	22.728	7.460	1.00	52.31	8
ATOM	2499	N	ASP	B	108	23.753	22.132	9.494	1.00	54.48	7
ATOM	2500	CA	ASP	B	108	22.417	22.687	9.285	1.00	57.36	6
ATOM	2501	CB	ASP	B	108	21.376	21.830	10.007	1.00	59.13	6
ATOM	2502	CG	ASP	B	108	21.474	21.933	11.512	1.00	61.77	6
ATOM	2503	OD1	ASP	B	108	22.604	21.993	12.034	1.00	63.26	8
ATOM	2504	OD2	ASP	B	108	20.419	21.941	12.180	1.00	63.13	8
ATOM	2505	C	ASP	B	108	22.266	24.152	9.715	1.00	58.76	6
ATOM	2506	O	ASP	B	108	21.163	24.696	9.711	1.00	60.28	8
ATOM	2507	N	GLY	B	109	23.376	24.784	10.087	1.00	59.97	7
ATOM	2508	CA	GLY	B	109	23.346	26.175	10.489	1.00	58.62	6
ATOM	2509	C	GLY	B	109	23.213	26.394	11.983	1.00	59.08	6
ATOM	2510	O	GLY	B	109	23.123	27.534	12.437	1.00	58.71	8
ATOM	2511	N	GLU	B	110	23.187	25.317	12.758	1.00	58.29	7
ATOM	2512	CA	GLU	B	110	23.062	25.451	14.202	1.00	57.49	6
ATOM	2513	CB	GLU	B	110	22.619	24.125	14.827	1.00	60.94	6
ATOM	2514	CG	GLU	B	110	21.947	24.234	16.208	1.00	64.96	6
ATOM	2515	CD	GLU	B	110	20.623	25.007	16.159	1.00	69.09	6
ATOM	2516	OE1	GLU	B	110	20.054	25.121	15.044	1.00	70.48	8
ATOM	2517	OE2	GLU	B	110	20.146	25.493	17.223	1.00	67.90	8
ATOM	2518	C	GLU	B	110	24.432	25.838	14.723	1.00	56.48	6
ATOM	2519	O	GLU	B	110	25.447	25.291	14.282	1.00	58.51	8
ATOM	2520	N	VAL	B	111	24.461	26.780	15.656	1.00	52.94	7
ATOM	2521	CA	VAL	B	111	25.706	27.254	16.237	1.00	49.98	6
ATOM	2522	CB	VAL	B	111	25.933	28.743	15.914	1.00	50.06	6
ATOM	2523	CG1	VAL	B	111	27.259	29.199	16.502	1.00	48.91	6
ATOM	2524	CG2	VAL	B	111	25.894	28.973	14.406	1.00	49.75	6
ATOM	2525	C	VAL	B	111	25.702	27.095	17.749	1.00	49.14	6
ATOM	2526	O	VAL	B	111	24.730	27.431	18.413	1.00	47.85	8
ATOM	2527	N	LEU	B	112	26.795	26.581	18.292	1.00	49.78	7
ATOM	2528	CA	LEU	B	112	26.907	26.404	19.733	1.00	50.84	6
ATOM	2529	CB	LEU	B	112	26.903	24.914	20.107	1.00	54.21	6
ATOM	2530	CG	LEU	B	112	26.075	23.868	19.337	1.00	56.22	6
ATOM	2531	CD1	LEU	B	112	24.673	24.393	19.025	1.00	58.51	6
ATOM	2532	CD2	LEU	B	112	26.802	23.504	18.065	1.00	54.95	6
ATOM	2533	C	LEU	B	112	28.202	27.038	20.242	1.00	50.58	6
ATOM	2534	O	LEU	B	112	29.300	26.651	19.829	1.00	51.33	8
ATOM	2535	N	TYR	B	113	28.073	28.013	21.134	1.00	47.63	7
ATOM	2536	CA	TYR	B	113	29.227	28.681	21.709	1.00	46.01	6
ATOM	2537	CB	TYR	B	113	29.266	30.154	21.279	1.00	45.50	6
ATOM	2538	CG	TYR	B	113	30.415	30.970	21.868	1.00	45.48	6
ATOM	2539	CD1	TYR	B	113	31.715	30.468	21.902	1.00	43.49	6
ATOM	2540	CE1	TYR	B	113	32.766	31.225	22.412	1.00	42.81	6
ATOM	2541	CD2	TYR	B	113	30.200	32.262	22.367	1.00	44.88	6
ATOM	2542	CE2	TYR	B	113	31.246	33.022	22.876	1.00	42.75	6
ATOM	2543	CZ	TYR	B	113	32.528	32.499	22.897	1.00	45.11	6
ATOM	2544	OH	TYR	B	113	33.579	33.248	23.397	1.00	46.12	8
ATOM	2545	C	TYR	B	113	29.081	28.561	23.208	1.00	45.62	6
ATOM	2546	O	TYR	B	113	28.130	29.064	23.783	1.00	48.17	8
ATOM	2547	N	MET	B	114	30.025	27.887	23.842	1.00	45.82	7
ATOM	2548	CA	MET	B	114	29.966	27.691	25.280	1.00	47.40	6
ATOM	2549	CB	MET	B	114	29.652	26.237	25.578	1.00	51.46	6
ATOM	2550	CG	MET	B	114	29.408	25.958	27.030	1.00	56.47	6
ATOM	2551	SD	MET	B	114	29.463	24.204	27.290	1.00	61.08	16

ATOM	2552	CE	MET	B	114	27.833	23.732	26.736	1.00 59.81	6
ATOM	2553	C	MET	B	114	31.281	28.060	25.944	1.00 47.40	6
ATOM	2554	O	MET	B	114	32.093	27.187	26.268	1.00 46.46	8
ATOM	2555	N	PRO	B	115	31.511	29.364	26.158	1.00 46.76	7
ATOM	2556	CD	PRO	B	115	30.680	30.502	25.712	1.00 45.52	6
ATOM	2557	CA	PRO	B	115	32.744	29.832	26.786	1.00 44.75	6
ATOM	2558	CB	PRO	B	115	32.834	31.259	26.285	1.00 47.19	6
ATOM	2559	CG	PRO	B	115	31.382	31.687	26.316	1.00 45.23	6
ATOM	2560	C	PRO	B	115	32.653	29.776	28.303	1.00 45.76	6
ATOM	2561	O	PRO	B	115	31.567	29.933	28.865	1.00 46.79	8
ATOM	2562	N	SER	B	116	33.783	29.545	28.965	1.00 44.58	7
ATOM	2563	CA	SER	B	116	33.797	29.527	30.416	1.00 42.97	6
ATOM	2564	CB	SER	B	116	34.867	28.605	30.935	1.00 42.63	6
ATOM	2565	OG	SER	B	116	34.810	28.586	32.342	1.00 46.80	8
ATOM	2566	C	SER	B	116	34.124	30.939	30.832	1.00 43.61	6
ATOM	2567	O	SER	B	116	35.144	31.473	30.431	1.00 45.91	8
ATOM	2568	N	ILE	B	117	33.270	31.547	31.643	1.00 42.76	7
ATOM	2569	CA	ILE	B	117	33.483	32.923	32.052	1.00 40.88	6
ATOM	2570	CB	ILE	B	117	32.340	33.816	31.515	1.00 39.30	6
ATOM	2571	CG2	ILE	B	117	32.512	35.249	31.995	1.00 40.17	6
ATOM	2572	CG1	ILE	B	117	32.317	33.760	29.992	1.00 37.44	6
ATOM	2573	CD1	ILE	B	117	31.069	34.332	29.394	1.00 36.96	6
ATOM	2574	C	ILE	B	117	33.592	33.158	33.545	1.00 42.01	6
ATOM	2575	O	ILE	B	117	32.840	32.585	34.329	1.00 44.14	8
ATOM	2576	N	ARG	B	118	34.554	33.986	33.939	1.00 42.44	7
ATOM	2577	CA	ARG	B	118	34.683	34.363	35.339	1.00 42.12	6
ATOM	2578	CB	ARG	B	118	36.120	34.283	35.835	1.00 39.55	6
ATOM	2579	CG	ARG	B	118	36.241	34.873	37.226	1.00 40.13	6
ATOM	2580	CD	ARG	B	118	37.520	34.517	37.933	1.00 40.72	6
ATOM	2581	NE	ARG	B	118	37.546	35.120	39.259	1.00 43.73	7
ATOM	2582	CZ	ARG	B	118	38.424	34.821	40.204	1.00 43.99	6
ATOM	2583	NH1	ARG	B	118	39.356	33.915	39.973	1.00 45.99	7
ATOM	2584	NH2	ARG	B	118	38.367	35.427	41.376	1.00 44.09	7
ATOM	2585	C	ARG	B	118	34.215	35.819	35.332	1.00 42.68	6
ATOM	2586	O	ARG	B	118	34.657	36.604	34.503	1.00 43.76	8
ATOM	2587	N	GLN	B	119	33.324	36.190	36.239	1.00 41.50	7
ATOM	2588	CA	GLN	B	119	32.815	37.553	36.229	1.00 40.73	6
ATOM	2589	CB	GLN	B	119	31.817	37.664	35.080	1.00 37.47	6
ATOM	2590	CG	GLN	B	119	31.199	39.002	34.850	1.00 37.63	6
ATOM	2591	CD	GLN	B	119	30.414	39.031	33.553	1.00 38.05	6
ATOM	2592	OE1	GLN	B	119	29.835	38.028	33.137	1.00 40.82	8
ATOM	2593	NE2	GLN	B	119	30.380	40.181	32.914	1.00 38.24	7
ATOM	2594	C	GLN	B	119	32.171	37.897	37.561	1.00 41.65	6
ATOM	2595	O	GLN	B	119	31.660	37.028	38.245	1.00 43.20	8
ATOM	2596	N	ARG	B	120	32.208	39.163	37.945	1.00 43.19	7
ATOM	2597	CA	ARG	B	120	31.606	39.561	39.209	1.00 46.59	6
ATOM	2598	CB	ARG	B	120	32.500	40.540	39.955	1.00 48.44	6
ATOM	2599	CG	ARG	B	120	33.874	40.005	40.232	1.00 57.79	6
ATOM	2600	CD	ARG	B	120	34.423	40.632	41.493	1.00 64.95	6
ATOM	2601	NE	ARG	B	120	33.964	39.971	42.727	1.00 67.80	7
ATOM	2602	CZ	ARG	B	120	33.571	40.624	43.818	1.00 68.76	6
ATOM	2603	NH1	ARG	B	120	33.565	41.958	43.827	1.00 66.34	7
ATOM	2604	NH2	ARG	B	120	33.219	39.944	44.913	1.00 69.34	7
ATOM	2605	C	ARG	B	120	30.241	40.184	38.999	1.00 45.42	6
ATOM	2606	O	ARG	B	120	29.991	40.825	37.979	1.00 43.82	8
ATOM	2607	N	PHE	B	121	29.361	39.983	39.972	1.00 45.27	7
ATOM	2608	CA	PHE	B	121	28.012	40.515	39.882	1.00 46.73	6
ATOM	2609	CB	PHE	B	121	26.998	39.411	39.558	1.00 44.66	6
ATOM	2610	CG	PHE	B	121	27.320	38.639	38.324	1.00 41.56	6
ATOM	2611	CD1	PHE	B	121	28.265	37.621	38.355	1.00 38.98	6
ATOM	2612	CD2	PHE	B	121	26.698	38.942	37.123	1.00 40.65	6

ATOM	2613	CE1	PHE	B	121	28.585	36.920	37.212	1.00 38.44	6
ATOM	2614	CE2	PHE	B	121	27.013	38.245	35.977	1.00 38.36	6
ATOM	2615	CZ	PHE	B	121	27.959	37.232	36.020	1.00 37.80	6
ATOM	2616	C	PHE	B	121	27.549	41.193	41.142	1.00 47.76	6
ATOM	2617	O	PHE	B	121	28.094	40.972	42.224	1.00 45.87	8
ATOM	2618	N	SER	B	122	26.521	42.021	40.966	1.00 49.39	7
ATOM	2619	CA	SER	B	122	25.881	42.735	42.054	1.00 51.30	6
ATOM	2620	CB	SER	B	122	25.677	44.200	41.680	1.00 50.63	6
ATOM	2621	OG	SER	B	122	25.026	44.887	42.726	1.00 52.75	8
ATOM	2622	C	SER	B	122	24.530	42.041	42.235	1.00 52.14	6
ATOM	2623	O	SER	B	122	23.659	42.135	41.377	1.00 51.12	8
ATOM	2624	N	CYS	B	123	24.371	41.323	43.340	1.00 53.84	7
ATOM	2625	CA	CYS	B	123	23.133	40.605	43.603	1.00 56.99	6
ATOM	2626	C	CYS	B	123	22.973	40.343	45.111	1.00 58.94	6
ATOM	2627	O	CYS	B	123	23.837	40.727	45.911	1.00 58.00	8
ATOM	2628	CB	CYS	B	123	23.135	39.282	42.830	1.00 55.83	6
ATOM	2629	SG	CYS	B	123	24.561	38.231	43.250	1.00 57.55	16
ATOM	2630	N	ASP	B	124	21.874	39.687	45.491	1.00 59.24	7
ATOM	2631	CA	ASP	B	124	21.619	39.412	46.893	1.00 59.17	6
ATOM	2632	CB	ASP	B	124	20.148	39.085	47.114	1.00 61.47	6
ATOM	2633	CG	ASP	B	124	19.670	39.487	48.505	1.00 62.03	6
ATOM	2634	OD1	ASP	B	124	20.462	39.403	49.470	1.00 60.72	8
ATOM	2635	OD2	ASP	B	124	18.493	39.886	48.628	1.00 63.80	8
ATOM	2636	C	ASP	B	124	22.470	38.274	47.434	1.00 59.25	6
ATOM	2637	O	ASP	B	124	22.309	37.122	47.036	1.00 58.84	8
ATOM	2638	N	VAL	B	125	23.365	38.612	48.356	1.00 59.36	7
ATOM	2639	CA	VAL	B	125	24.260	37.647	48.979	1.00 59.62	6
ATOM	2640	CB	VAL	B	125	25.683	38.230	49.080	1.00 57.35	6
ATOM	2641	CG1	VAL	B	125	26.599	37.280	49.798	1.00 54.50	6
ATOM	2642	CG2	VAL	B	125	26.212	38.519	47.702	1.00 58.35	6
ATOM	2643	C	VAL	B	125	23.766	37.277	50.378	1.00 62.42	6
ATOM	2644	O	VAL	B	125	24.161	36.254	50.938	1.00 64.51	8
ATOM	2645	N	SER	B	126	22.892	38.105	50.939	1.00 63.61	7
ATOM	2646	CA	SER	B	126	22.375	37.857	52.283	1.00 64.32	6
ATOM	2647	CB	SER	B	126	21.260	38.857	52.613	1.00 63.21	6
ATOM	2648	OG	SER	B	126	20.175	38.715	51.715	1.00 59.22	8
ATOM	2649	C	SER	B	126	21.858	36.429	52.444	1.00 64.47	6
ATOM	2650	O	SER	B	126	21.082	35.940	51.626	1.00 63.31	8
ATOM	2651	N	GLY	B	127	22.313	35.764	53.496	1.00 65.55	7
ATOM	2652	CA	GLY	B	127	21.872	34.409	53.748	1.00 68.84	6
ATOM	2653	C	GLY	B	127	22.847	33.351	53.282	1.00 70.32	6
ATOM	2654	O	GLY	B	127	22.634	32.161	53.500	1.00 71.17	8
ATOM	2655	N	VAL	B	128	23.923	33.776	52.638	1.00 71.67	7
ATOM	2656	CA	VAL	B	128	24.910	32.826	52.148	1.00 72.95	6
ATOM	2657	CB	VAL	B	128	26.107	33.522	51.467	1.00 71.97	6
ATOM	2658	CG1	VAL	B	128	25.686	34.081	50.149	1.00 73.72	6
ATOM	2659	CG2	VAL	B	128	26.654	34.614	52.359	1.00 69.90	6
ATOM	2660	C	VAL	B	128	25.504	31.942	53.212	1.00 73.83	6
ATOM	2661	O	VAL	B	128	25.628	30.743	53.016	1.00 73.27	8
ATOM	2662	N	ASP	B	129	25.884	32.542	54.332	1.00 75.83	7
ATOM	2663	CA	ASP	B	129	26.532	31.789	55.384	1.00 78.34	6
ATOM	2664	CB	ASP	B	129	27.008	32.715	56.504	1.00 79.36	6
ATOM	2665	CG	ASP	B	129	28.209	32.141	57.257	1.00 81.22	6
ATOM	2666	OD1	ASP	B	129	29.166	32.909	57.523	1.00 81.78	8
ATOM	2667	OD2	ASP	B	129	28.202	30.922	57.576	1.00 81.70	8
ATOM	2668	C	ASP	B	129	25.720	30.648	55.972	1.00 80.31	6
ATOM	2669	O	ASP	B	129	26.293	29.783	56.660	1.00 81.06	8
ATOM	2670	N	THR	B	130	24.412	30.603	55.706	1.00 80.80	7
ATOM	2671	CA	THR	B	130	23.640	29.501	56.259	1.00 81.78	6
ATOM	2672	CB	THR	B	130	23.681	29.563	57.799	1.00 85.11	6
ATOM	2673	OG1	THR	B	130	24.158	30.862	58.195	1.00 84.93	8

ATOM	2674	CG2	THR	B	130	24.582	28.416	58.388	1.00	85.83	6
ATOM	2675	C	THR	B	130	22.182	29.286	55.881	1.00	80.84	6
ATOM	2676	O	THR	B	130	21.460	30.224	55.506	1.00	78.93	8
ATOM	2677	N	GLU	B	131	21.784	28.014	56.028	1.00	80.92	7
ATOM	2678	CA	GLU	B	131	20.416	27.510	55.832	1.00	80.70	6
ATOM	2679	CB	GLU	B	131	19.435	28.339	56.689	1.00	83.05	6
ATOM	2680	CG	GLU	B	131	19.467	28.017	58.187	1.00	84.49	6
ATOM	2681	CD	GLU	B	131	19.024	29.189	59.051	1.00	85.34	6
ATOM	2682	OE1	GLU	B	131	17.948	29.773	58.762	1.00	86.44	8
ATOM	2683	OE2	GLU	B	131	19.757	29.521	60.019	1.00	85.14	8
ATOM	2684	C	GLU	B	131	19.864	27.420	54.426	1.00	79.07	6
ATOM	2685	O	GLU	B	131	20.207	26.520	53.643	1.00	76.96	8
ATOM	2686	N	SER	B	132	18.941	28.338	54.156	1.00	78.17	7
ATOM	2687	CA	SER	B	132	18.298	28.449	52.858	1.00	77.92	6
ATOM	2688	CB	SER	B	132	16.953	29.195	53.001	1.00	77.07	6
ATOM	2689	OG	SER	B	132	17.130	30.486	53.575	1.00	77.45	8
ATOM	2690	C	SER	B	132	19.277	29.220	51.945	1.00	76.88	6
ATOM	2691	O	SER	B	132	19.000	29.463	50.759	1.00	77.41	8
ATOM	2692	N	GLY	B	133	20.424	29.588	52.520	1.00	74.38	7
ATOM	2693	CA	GLY	B	133	21.442	30.308	51.782	1.00	72.04	6
ATOM	2694	C	GLY	B	133	20.943	31.569	51.105	1.00	71.42	6
ATOM	2695	O	GLY	B	133	19.888	32.104	51.450	1.00	71.39	8
ATOM	2696	N	ALA	B	134	21.708	32.044	50.125	1.00	69.68	7
ATOM	2697	CA	ALA	B	134	21.345	33.251	49.390	1.00	66.69	6
ATOM	2698	CB	ALA	B	134	22.534	34.194	49.315	1.00	66.34	6
ATOM	2699	C	ALA	B	134	20.874	32.908	47.993	1.00	64.53	6
ATOM	2700	O	ALA	B	134	21.095	31.802	47.504	1.00	64.56	8
ATOM	2701	N	THR	B	135	20.207	33.865	47.369	1.00	62.63	7
ATOM	2702	CA	THR	B	135	19.719	33.696	46.017	1.00	62.23	6
ATOM	2703	CB	THR	B	135	18.205	33.577	45.980	1.00	62.17	6
ATOM	2704	OG1	THR	B	135	17.812	32.456	46.775	1.00	64.85	8
ATOM	2705	CG2	THR	B	135	17.721	33.370	44.543	1.00	62.33	6
ATOM	2706	C	THR	B	135	20.159	34.900	45.194	1.00	62.39	6
ATOM	2707	O	THR	B	135	19.618	36.009	45.308	1.00	62.56	8
ATOM	2708	N	CYS	B	136	21.174	34.661	44.379	1.00	61.14	7
ATOM	2709	CA	CYS	B	136	21.754	35.668	43.526	1.00	58.61	6
ATOM	2710	C	CYS	B	136	21.159	35.497	42.134	1.00	56.85	6
ATOM	2711	O	CYS	B	136	21.308	34.452	41.503	1.00	55.78	8
ATOM	2712	CB	CYS	B	136	23.276	35.474	43.527	1.00	58.82	6
ATOM	2713	SG	CYS	B	136	24.201	36.455	42.315	1.00	60.36	16
ATOM	2714	N	ARG	B	137	20.453	36.519	41.670	1.00	55.98	7
ATOM	2715	CA	ARG	B	137	19.845	36.457	40.353	1.00	56.14	6
ATOM	2716	CB	ARG	B	137	18.421	37.009	40.383	1.00	57.73	6
ATOM	2717	CG	ARG	B	137	17.502	36.250	41.303	1.00	62.21	6
ATOM	2718	CD	ARG	B	137	16.367	37.136	41.792	1.00	68.77	6
ATOM	2719	NE	ARG	B	137	15.827	36.666	43.071	1.00	74.27	7
ATOM	2720	CZ	ARG	B	137	15.070	35.575	43.224	1.00	76.32	6
ATOM	2721	NH1	ARG	B	137	14.739	34.822	42.174	1.00	77.05	7
ATOM	2722	NH2	ARG	B	137	14.652	35.221	44.434	1.00	75.79	7
ATOM	2723	C	ARG	B	137	20.672	37.253	39.366	1.00	55.38	6
ATOM	2724	O	ARG	B	137	21.052	38.389	39.637	1.00	57.67	8
ATOM	2725	N	ILE	B	138	20.933	36.646	38.215	1.00	52.27	7
ATOM	2726	CA	ILE	B	138	21.716	37.255	37.163	1.00	48.96	6
ATOM	2727	CB	ILE	B	138	22.977	36.411	36.890	1.00	45.32	6
ATOM	2728	CG2	ILE	B	138	23.751	37.007	35.749	1.00	42.82	6
ATOM	2729	CG1	ILE	B	138	23.822	36.309	38.160	1.00	42.90	6
ATOM	2730	CD1	ILE	B	138	24.931	35.313	38.067	1.00	40.32	6
ATOM	2731	C	ILE	B	138	20.863	37.313	35.900	1.00	48.66	6
ATOM	2732	O	ILE	B	138	20.420	36.286	35.406	1.00	49.73	8
ATOM	2733	N	LYS	B	139	20.628	38.506	35.375	1.00	48.12	7
ATOM	2734	CA	LYS	B	139	19.822	38.642	34.165	1.00	51.18	6

ATOM	2735	CB	LYS	B	139	18.775	39.759	34.326	1.00 52.93	6
ATOM	2736	CG	LYS	B	139	17.908	39.625	35.553	1.00 56.09	6
ATOM	2737	CD	LYS	B	139	16.721	40.567	35.523	1.00 58.54	6
ATOM	2738	CE	LYS	B	139	15.716	40.155	34.461	1.00 59.19	6
ATOM	2739	NZ	LYS	B	139	14.539	41.062	34.435	1.00 59.74	7
ATOM	2740	C	LYS	B	139	20.686	38.966	32.957	1.00 50.79	6
ATOM	2741	O	LYS	B	139	21.461	39.919	32.998	1.00 53.10	8
ATOM	2742	N	ILE	B	140	20.561	38.192	31.883	1.00 47.96	7
ATOM	2743	CA	ILE	B	140	21.348	38.480	30.696	1.00 49.36	6
ATOM	2744	CB	ILE	B	140	22.590	37.531	30.607	1.00 49.96	6
ATOM	2745	CG2	ILE	B	140	23.254	37.411	31.973	1.00 52.22	6
ATOM	2746	CG1	ILE	B	140	22.192	36.126	30.217	1.00 50.93	6
ATOM	2747	CD1	ILE	B	140	23.312	35.115	30.483	1.00 54.24	6
ATOM	2748	C	ILE	B	140	20.520	38.444	29.410	1.00 48.36	6
ATOM	2749	O	ILE	B	140	19.727	37.545	29.211	1.00 49.73	8
ATOM	2750	N	GLY	B	141	20.685	39.448	28.557	1.00 46.46	7
ATOM	2751	CA	GLY	B	141	19.941	39.500	27.313	1.00 47.33	6
ATOM	2752	C	GLY	B	141	20.631	40.387	26.293	1.00 46.71	6
ATOM	2753	O	GLY	B	141	21.623	41.025	26.625	1.00 47.72	8
ATOM	2754	N	SER	B	142	20.131	40.425	25.058	1.00 45.43	7
ATOM	2755	CA	SER	B	142	20.739	41.267	24.026	1.00 44.63	6
ATOM	2756	CB	SER	B	142	19.990	41.165	22.706	1.00 42.45	6
ATOM	2757	OG	SER	B	142	20.431	42.168	21.814	1.00 40.68	8
ATOM	2758	C	SER	B	142	20.774	42.728	24.457	1.00 46.01	6
ATOM	2759	O	SER	B	142	19.812	43.256	25.031	1.00 46.34	8
ATOM	2760	N	TRP	B	143	21.888	43.384	24.162	1.00 46.69	7
ATOM	2761	CA	TRP	B	143	22.069	44.761	24.549	1.00 45.07	6
ATOM	2762	CB	TRP	B	143	23.553	45.044	24.758	1.00 44.45	6
ATOM	2763	CG	TRP	B	143	23.816	46.368	25.388	1.00 43.71	6
ATOM	2764	CD2	TRP	B	143	23.642	46.697	26.762	1.00 40.44	6
ATOM	2765	CE2	TRP	B	143	23.999	48.055	26.920	1.00 40.05	6
ATOM	2766	CE3	TRP	B	143	23.221	45.975	27.880	1.00 38.96	6
ATOM	2767	CD1	TRP	B	143	24.262	47.517	24.773	1.00 43.74	6
ATOM	2768	NE1	TRP	B	143	24.373	48.534	25.691	1.00 40.21	7
ATOM	2769	CZ2	TRP	B	143	23.947	48.694	28.149	1.00 38.81	6
ATOM	2770	CZ3	TRP	B	143	23.171	46.612	29.097	1.00 35.11	6
ATOM	2771	CH2	TRP	B	143	23.531	47.956	29.224	1.00 37.51	6
ATOM	2772	C	TRP	B	143	21.499	45.730	23.545	1.00 46.35	6
ATOM	2773	O	TRP	B	143	21.062	46.813	23.909	1.00 48.58	8
ATOM	2774	N	THR	B	144	21.477	45.358	22.277	1.00 45.22	7
ATOM	2775	CA	THR	B	144	20.963	46.287	21.290	1.00 45.21	6
ATOM	2776	CB	THR	B	144	22.072	46.696	20.328	1.00 44.02	6
ATOM	2777	OG1	THR	B	144	22.669	45.524	19.763	1.00 44.19	8
ATOM	2778	CG2	THR	B	144	23.129	47.487	21.069	1.00 42.50	6
ATOM	2779	C	THR	B	144	19.778	45.793	20.485	1.00 48.06	6
ATOM	2780	O	THR	B	144	19.136	46.576	19.783	1.00 50.29	8
ATOM	2781	N	HIS	B	145	19.474	44.504	20.584	1.00 47.78	7
ATOM	2782	CA	HIS	B	145	18.364	43.970	19.820	1.00 48.99	6
ATOM	2783	CB	HIS	B	145	18.800	42.716	19.055	1.00 47.81	6
ATOM	2784	CG	HIS	B	145	19.805	42.974	17.974	1.00 46.09	6
ATOM	2785	CD2	HIS	B	145	19.677	43.532	16.748	1.00 44.37	6
ATOM	2786	ND1	HIS	B	145	21.125	42.602	18.086	1.00 45.57	7
ATOM	2787	CE1	HIS	B	145	21.766	42.915	16.975	1.00 44.33	6
ATOM	2788	NE2	HIS	B	145	20.909	43.481	16.146	1.00 41.88	7
ATOM	2789	C	HIS	B	145	17.149	43.656	20.682	1.00 50.77	6
ATOM	2790	O	HIS	B	145	17.235	42.933	21.668	1.00 52.14	8
ATOM	2791	N	HIS	B	146	16.010	44.213	20.302	1.00 52.05	7
ATOM	2792	CA	HIS	B	146	14.774	43.974	21.027	1.00 54.32	6
ATOM	2793	CB	HIS	B	146	13.797	45.130	20.800	1.00 52.48	6
ATOM	2794	CG	HIS	B	146	13.526	45.413	19.360	1.00 52.25	6
ATOM	2795	CD2	HIS	B	146	13.106	44.605	18.357	1.00 53.49	6

ATOM	2796	ND1	HIS	B	146	13.726	46.653	18.795	1.00	53.68	7
ATOM	2797	CE1	HIS	B	146	13.448	46.597	17.504	1.00	55.84	6
ATOM	2798	NE2	HIS	B	146	13.070	45.364	17.212	1.00	55.30	7
ATOM	2799	C	HIS	B	146	14.149	42.647	20.576	1.00	57.05	6
ATOM	2800	O	HIS	B	146	14.640	41.984	19.644	1.00	58.04	8
ATOM	2801	N	SER	B	147	13.057	42.280	21.243	1.00	58.47	7
ATOM	2802	CA	SER	B	147	12.328	41.037	20.997	1.00	58.52	6
ATOM	2803	CB	SER	B	147	11.071	41.021	21.861	1.00	58.93	6
ATOM	2804	OG	SER	B	147	10.386	42.252	21.740	1.00	63.53	8
ATOM	2805	C	SER	B	147	11.955	40.708	19.557	1.00	57.13	6
ATOM	2806	O	SER	B	147	11.776	39.545	19.215	1.00	56.86	8
ATOM	2807	N	ARG	B	148	11.841	41.716	18.709	1.00	56.50	7
ATOM	2808	CA	ARG	B	148	11.473	41.462	17.323	1.00	58.81	6
ATOM	2809	CB	ARG	B	148	10.905	42.734	16.691	1.00	62.56	6
ATOM	2810	CG	ARG	B	148	9.781	43.380	17.493	1.00	70.38	6
ATOM	2811	CD	ARG	B	148	9.337	44.731	16.897	1.00	76.49	6
ATOM	2812	NE	ARG	B	148	8.480	45.487	17.819	1.00	82.57	7
ATOM	2813	CZ	ARG	B	148	7.263	45.104	18.222	1.00	84.74	6
ATOM	2814	NH1	ARG	B	148	6.728	43.965	17.791	1.00	85.52	7
ATOM	2815	NH2	ARG	B	148	6.573	45.864	19.064	1.00	85.55	7
ATOM	2816	C	ARG	B	148	12.655	40.963	16.490	1.00	57.83	6
ATOM	2817	O	ARG	B	148	12.474	40.423	15.395	1.00	58.23	8
ATOM	2818	N	GLU	B	149	13.864	41.147	17.011	1.00	56.99	7
ATOM	2819	CA	GLU	B	149	15.072	40.743	16.306	1.00	53.60	6
ATOM	2820	CB	GLU	B	149	16.015	41.933	16.216	1.00	52.91	6
ATOM	2821	CG	GLU	B	149	15.280	43.243	15.955	1.00	51.82	6
ATOM	2822	CD	GLU	B	149	16.208	44.437	15.841	1.00	54.76	6
ATOM	2823	OE1	GLU	B	149	17.132	44.562	16.672	1.00	55.52	8
ATOM	2824	OE2	GLU	B	149	16.010	45.261	14.929	1.00	52.75	8
ATOM	2825	C	GLU	B	149	15.729	39.584	17.036	1.00	52.38	6
ATOM	2826	O	GLU	B	149	16.150	38.606	16.421	1.00	51.81	8
ATOM	2827	N	ILE	B	150	15.811	39.693	18.355	1.00	51.32	7
ATOM	2828	CA	ILE	B	150	16.382	38.619	19.154	1.00	51.11	6
ATOM	2829	CB	ILE	B	150	17.770	38.989	19.757	1.00	48.77	6
ATOM	2830	CG2	ILE	B	150	18.155	37.995	20.843	1.00	43.40	6
ATOM	2831	CG1	ILE	B	150	18.842	38.967	18.672	1.00	47.30	6
ATOM	2832	CD1	ILE	B	150	20.219	39.315	19.168	1.00	45.12	6
ATOM	2833	C	ILE	B	150	15.453	38.254	20.297	1.00	53.02	6
ATOM	2834	O	ILE	B	150	14.842	39.116	20.932	1.00	52.00	8
ATOM	2835	N	SER	B	151	15.350	36.955	20.539	1.00	55.16	7
ATOM	2836	CA	SER	B	151	14.542	36.436	21.628	1.00	56.52	6
ATOM	2837	CB	SER	B	151	13.280	35.733	21.089	1.00	57.06	6
ATOM	2838	OG	SER	B	151	13.594	34.585	20.323	1.00	54.91	8
ATOM	2839	C	SER	B	151	15.452	35.447	22.337	1.00	56.69	6
ATOM	2840	O	SER	B	151	16.144	34.676	21.685	1.00	57.55	8
ATOM	2841	N	VAL	B	152	15.480	35.504	23.661	1.00	58.35	7
ATOM	2842	CA	VAL	B	152	16.306	34.600	24.456	1.00	60.89	6
ATOM	2843	CB	VAL	B	152	17.135	35.362	25.502	1.00	60.77	6
ATOM	2844	CG1	VAL	B	152	17.890	36.489	24.844	1.00	59.09	6
ATOM	2845	CG2	VAL	B	152	16.220	35.903	26.586	1.00	62.75	6
ATOM	2846	C	VAL	B	152	15.389	33.632	25.194	1.00	62.80	6
ATOM	2847	O	VAL	B	152	14.287	34.012	25.597	1.00	63.08	8
ATOM	2848	N	ASP	B	153	15.845	32.395	25.387	1.00	64.20	7
ATOM	2849	CA	ASP	B	153	15.028	31.390	26.061	1.00	66.36	6
ATOM	2850	CB	ASP	B	153	14.232	30.611	25.016	1.00	67.03	6
ATOM	2851	CG	ASP	B	153	13.427	31.518	24.095	1.00	68.33	6
ATOM	2852	OD1	ASP	B	153	12.327	31.949	24.504	1.00	65.39	8
ATOM	2853	OD2	ASP	B	153	13.905	31.810	22.969	1.00	70.09	8
ATOM	2854	C	ASP	B	153	15.877	30.416	26.872	1.00	68.77	6
ATOM	2855	O	ASP	B	153	16.974	30.049	26.453	1.00	69.28	8
ATOM	2856	N	PRO	B	154	15.404	30.017	28.067	1.00	70.46	7

ATOM	2857	CD	PRO	B	154	14.409	30.740	28.876	1.00	69.92	6
ATOM	2858	CA	PRO	B	154	16.157	29.070	28.898	1.00	72.29	6
ATOM	2859	CB	PRO	B	154	15.410	29.108	30.225	1.00	70.76	6
ATOM	2860	CG	PRO	B	154	14.902	30.494	30.281	1.00	69.28	6
ATOM	2861	C	PRO	B	154	16.151	27.668	28.250	1.00	75.71	6
ATOM	2862	O	PRO	B	154	15.548	27.467	27.187	1.00	75.41	8
ATOM	2863	N	THR	B	155	16.807	26.700	28.888	1.00	79.33	7
ATOM	2864	CA	THR	B	155	16.887	25.350	28.332	1.00	83.13	6
ATOM	2865	CB	THR	B	155	18.208	25.187	27.542	1.00	82.37	6
ATOM	2866	OG1	THR	B	155	19.316	25.233	28.453	1.00	83.94	8
ATOM	2867	CG2	THR	B	155	18.378	26.311	26.545	1.00	81.49	6
ATOM	2868	C	THR	B	155	16.785	24.189	29.348	1.00	86.65	6
ATOM	2869	O	THR	B	155	16.122	24.298	30.385	1.00	87.45	8
ATOM	2870	N	THR	B	156	17.452	23.078	29.013	1.00	90.57	7
ATOM	2871	CA	THR	B	156	17.504	21.839	29.813	1.00	93.48	6
ATOM	2872	CB	THR	B	156	18.799	21.025	29.491	1.00	93.70	6
ATOM	2873	OG1	THR	B	156	18.861	20.761	28.077	1.00	92.52	8
ATOM	2874	CG2	THR	B	156	18.825	19.694	30.301	1.00	93.12	6
ATOM	2875	C	THR	B	156	17.448	22.012	31.337	1.00	95.82	6
ATOM	2876	O	THR	B	156	18.471	22.286	31.990	1.00	95.51	8
ATOM	2877	N	GLU	B	157	16.257	21.809	31.897	1.00	98.15	7
ATOM	2878	CA	GLU	B	157	16.047	21.946	33.337	1.00	100.26	6
ATOM	2879	CB	GLU	B	157	14.583	22.308	33.606	1.00	102.01	6
ATOM	2880	CG	GLU	B	157	14.023	23.363	32.643	1.00	104.88	6
ATOM	2881	CD	GLU	B	157	12.539	23.649	32.902	1.00	106.35	6
ATOM	2882	OE1	GLU	B	157	11.745	22.665	32.965	1.00	106.79	8
ATOM	2883	OE2	GLU	B	157	12.178	24.850	33.030	1.00	105.97	8
ATOM	2884	C	GLU	B	157	16.397	20.662	34.102	1.00	100.31	6
ATOM	2885	O	GLU	B	157	16.352	20.631	35.348	1.00	100.47	8
ATOM	2886	N	ASN	B	158	16.726	19.601	33.364	1.00	99.66	7
ATOM	2887	CA	ASN	B	158	17.065	18.329	34.003	1.00	99.04	6
ATOM	2888	CB	ASN	B	158	17.084	17.198	32.969	1.00	100.65	6
ATOM	2889	CG	ASN	B	158	15.793	17.113	32.170	1.00	101.63	6
ATOM	2890	OD1	ASN	B	158	14.701	16.919	32.733	1.00	101.77	8
ATOM	2891	ND2	ASN	B	158	15.909	17.254	30.847	1.00	102.28	7
ATOM	2892	C	ASN	B	158	18.439	18.424	34.672	1.00	97.31	6
ATOM	2893	O	ASN	B	158	18.546	18.748	35.872	1.00	97.45	8
ATOM	2894	N	SER	B	159	19.473	18.120	33.881	1.00	94.36	7
ATOM	2895	CA	SER	B	159	20.879	18.156	34.300	1.00	90.64	6
ATOM	2896	CB	SER	B	159	21.645	19.051	33.325	1.00	91.05	6
ATOM	2897	OG	SER	B	159	20.831	20.167	32.948	1.00	91.42	8
ATOM	2898	C	SER	B	159	21.129	18.622	35.742	1.00	87.58	6
ATOM	2899	O	SER	B	159	20.770	19.741	36.114	1.00	87.04	8
ATOM	2900	N	ASP	B	160	21.744	17.767	36.553	1.00	84.29	7
ATOM	2901	CA	ASP	B	160	22.035	18.137	37.938	1.00	80.73	6
ATOM	2902	CB	ASP	B	160	23.003	17.149	38.582	1.00	79.96	6
ATOM	2903	CG	ASP	B	160	23.404	17.566	39.991	1.00	79.90	6
ATOM	2904	OD1	ASP	B	160	24.459	17.087	40.471	1.00	79.39	8
ATOM	2905	OD2	ASP	B	160	22.659	18.362	40.617	1.00	79.13	8
ATOM	2906	C	ASP	B	160	22.687	19.514	37.956	1.00	79.03	6
ATOM	2907	O	ASP	B	160	23.782	19.687	37.394	1.00	78.08	8
ATOM	2908	N	ASP	B	161	22.022	20.473	38.612	1.00	76.06	7
ATOM	2909	CA	ASP	B	161	22.506	21.851	38.706	1.00	71.50	6
ATOM	2910	CB	ASP	B	161	21.655	22.683	39.675	1.00	70.10	6
ATOM	2911	CG	ASP	B	161	20.275	22.977	39.130	1.00	69.41	6
ATOM	2912	OD1	ASP	B	161	20.140	23.189	37.905	1.00	68.26	8
ATOM	2913	OD2	ASP	B	161	19.319	23.007	39.929	1.00	71.44	8
ATOM	2914	C	ASP	B	161	23.957	21.979	39.110	1.00	69.84	6
ATOM	2915	O	ASP	B	161	24.569	23.008	38.843	1.00	71.09	8
ATOM	2916	N	SER	B	162	24.527	20.960	39.740	1.00	67.23	7
ATOM	2917	CA	SER	B	162	25.928	21.078	40.136	1.00	67.27	6

ATOM	2918	CB	SER	B	162	26.051	21.210	41.661	1.00	67.18	6
ATOM	2919	OG	SER	B	162	25.648	20.020	42.315	1.00	66.16	8
ATOM	2920	C	SER	B	162	26.787	19.922	39.653	1.00	66.71	6
ATOM	2921	O	SER	B	162	27.786	19.576	40.289	1.00	64.25	8
ATOM	2922	N	GLU	B	163	26.410	19.330	38.523	1.00	67.10	7
ATOM	2923	CA	GLU	B	163	27.192	18.220	38.005	1.00	68.36	6
ATOM	2924	CB	GLU	B	163	26.378	17.421	36.970	1.00	70.98	6
ATOM	2925	CG	GLU	B	163	26.411	17.926	35.545	1.00	72.60	6
ATOM	2926	CD	GLU	B	163	25.726	16.946	34.594	1.00	74.62	6
ATOM	2927	OE1	GLU	B	163	24.477	16.828	34.649	1.00	76.45	8
ATOM	2928	OE2	GLU	B	163	26.428	16.285	33.798	1.00	74.37	8
ATOM	2929	C	GLU	B	163	28.530	18.688	37.410	1.00	67.51	6
ATOM	2930	O	GLU	B	163	29.379	17.868	37.070	1.00	67.13	8
ATOM	2931	N	TYR	B	164	28.709	20.008	37.294	1.00	66.57	7
ATOM	2932	CA	TYR	B	164	29.943	20.583	36.771	1.00	64.39	6
ATOM	2933	CB	TYR	B	164	29.671	21.419	35.526	1.00	64.28	6
ATOM	2934	CG	TYR	B	164	29.192	20.602	34.354	1.00	66.44	6
ATOM	2935	CD1	TYR	B	164	27.948	20.860	33.766	1.00	66.70	6
ATOM	2936	CE1	TYR	B	164	27.490	20.105	32.690	1.00	66.59	6
ATOM	2937	CD2	TYR	B	164	29.973	19.556	33.832	1.00	65.02	6
ATOM	2938	CE2	TYR	B	164	29.524	18.790	32.756	1.00	65.71	6
ATOM	2939	CZ	TYR	B	164	28.277	19.075	32.184	1.00	66.77	6
ATOM	2940	OH	TYR	B	164	27.819	18.369	31.084	1.00	67.83	8
ATOM	2941	C	TYR	B	164	30.584	21.463	37.826	1.00	63.28	6
ATOM	2942	O	TYR	B	164	31.717	21.936	37.662	1.00	61.67	8
ATOM	2943	N	PHE	B	165	29.859	21.673	38.918	1.00	61.88	7
ATOM	2944	CA	PHE	B	165	30.357	22.517	39.990	1.00	60.70	6
ATOM	2945	CB	PHE	B	165	29.288	22.704	41.067	1.00	58.78	6
ATOM	2946	CG	PHE	B	165	29.523	23.905	41.941	1.00	57.08	6
ATOM	2947	CD1	PHE	B	165	29.420	25.184	41.413	1.00	56.05	6
ATOM	2948	CD2	PHE	B	165	29.888	23.757	43.272	1.00	54.09	6
ATOM	2949	CE1	PHE	B	165	29.680	26.296	42.200	1.00	55.95	6
ATOM	2950	CE2	PHE	B	165	30.149	24.858	44.063	1.00	55.48	6
ATOM	2951	CZ	PHE	B	165	30.048	26.131	43.530	1.00	56.15	6
ATOM	2952	C	PHE	B	165	31.626	21.960	40.614	1.00	59.91	6
ATOM	2953	O	PHE	B	165	31.757	20.760	40.808	1.00	60.17	8
ATOM	2954	N	SER	B	166	32.572	22.839	40.919	1.00	60.28	7
ATOM	2955	CA	SER	B	166	33.807	22.390	41.532	1.00	60.24	6
ATOM	2956	CB	SER	B	166	34.810	23.534	41.647	1.00	59.33	6
ATOM	2957	OG	SER	B	166	36.012	23.081	42.239	1.00	59.12	8
ATOM	2958	C	SER	B	166	33.468	21.877	42.916	1.00	60.82	6
ATOM	2959	O	SER	B	166	32.614	22.434	43.611	1.00	60.12	8
ATOM	2960	N	GLN	B	167	34.148	20.815	43.319	1.00	61.73	7
ATOM	2961	CA	GLN	B	167	33.907	20.228	44.623	1.00	62.29	6
ATOM	2962	CB	GLN	B	167	34.228	18.737	44.576	1.00	63.96	6
ATOM	2963	CG	GLN	B	167	35.620	18.442	44.068	1.00	66.77	6
ATOM	2964	CD	GLN	B	167	35.827	16.969	43.736	1.00	68.16	6
ATOM	2965	OE1	GLN	B	167	35.710	16.103	44.605	1.00	66.24	8
ATOM	2966	NE2	GLN	B	167	36.136	16.682	42.465	1.00	68.10	7
ATOM	2967	C	GLN	B	167	34.740	20.912	45.689	1.00	60.72	6
ATOM	2968	O	GLN	B	167	34.433	20.814	46.880	1.00	62.24	8
ATOM	2969	N	TYR	B	168	35.778	21.626	45.269	1.00	57.81	7
ATOM	2970	CA	TYR	B	168	36.637	22.291	46.235	1.00	56.47	6
ATOM	2971	CB	TYR	B	168	38.078	22.236	45.741	1.00	55.55	6
ATOM	2972	CG	TYR	B	168	38.457	20.836	45.330	1.00	55.77	6
ATOM	2973	CD1	TYR	B	168	38.420	20.447	43.988	1.00	53.38	6
ATOM	2974	CE1	TYR	B	168	38.698	19.139	43.617	1.00	53.39	6
ATOM	2975	CD2	TYR	B	168	38.785	19.872	46.286	1.00	55.32	6
ATOM	2976	CE2	TYR	B	168	39.060	18.561	45.922	1.00	54.41	6
ATOM	2977	CZ	TYR	B	168	39.013	18.207	44.591	1.00	54.89	6
ATOM	2978	OH	TYR	B	168	39.270	16.919	44.227	1.00	56.81	8

ATOM	2979	C	TYR	B	168	36.222	23.712	46.586	1.00 55.31	6
ATOM	2980	O	TYR	B	168	36.891	24.395	47.356	1.00 54.88	8
ATOM	2981	N	SER	B	169	35.097	24.140	46.033	1.00 55.16	7
ATOM	2982	CA	SER	B	169	34.570	25.469	46.299	1.00 57.04	6
ATOM	2983	CB	SER	B	169	33.363	25.755	45.412	1.00 55.22	6
ATOM	2984	OG	SER	B	169	32.775	26.991	45.769	1.00 55.21	8
ATOM	2985	C	SER	B	169	34.147	25.617	47.754	1.00 60.21	6
ATOM	2986	O	SER	B	169	33.664	24.671	48.380	1.00 62.02	8
ATOM	2987	N	ARG	B	170	34.321	26.815	48.298	1.00 61.79	7
ATOM	2988	CA	ARG	B	170	33.938	27.059	49.678	1.00 60.59	6
ATOM	2989	CB	ARG	B	170	34.467	28.417	50.150	1.00 61.26	6
ATOM	2990	CG	ARG	B	170	35.781	28.342	50.904	1.00 61.61	6
ATOM	2991	CD	ARG	B	170	36.588	29.628	50.764	1.00 66.75	6
ATOM	2992	NE	ARG	B	170	35.866	30.846	51.158	1.00 69.32	7
ATOM	2993	CZ	ARG	B	170	35.634	31.877	50.342	1.00 68.59	6
ATOM	2994	NH1	ARG	B	170	36.053	31.840	49.079	1.00 65.59	7
ATOM	2995	NH2	ARG	B	170	35.017	32.959	50.803	1.00 69.04	7
ATOM	2996	C	ARG	B	170	32.431	27.041	49.785	1.00 58.91	6
ATOM	2997	O	ARG	B	170	31.892	26.981	50.883	1.00 61.10	8
ATOM	2998	N	PHE	B	171	31.748	27.077	48.650	1.00 56.02	7
ATOM	2999	CA	PHE	B	171	30.294	27.093	48.674	1.00 56.85	6
ATOM	3000	CB	PHE	B	171	29.782	28.384	48.033	1.00 56.79	6
ATOM	3001	CG	PHE	B	171	30.498	29.608	48.529	1.00 59.30	6
ATOM	3002	CD1	PHE	B	171	31.806	29.889	48.110	1.00 59.59	6
ATOM	3003	CD2	PHE	B	171	29.900	30.447	49.462	1.00 58.28	6
ATOM	3004	CE1	PHE	B	171	32.497	30.983	48.616	1.00 58.87	6
ATOM	3005	CE2	PHE	B	171	30.586	31.546	49.978	1.00 57.19	6
ATOM	3006	CZ	PHE	B	171	31.883	31.817	49.556	1.00 58.74	6
ATOM	3007	C	PHE	B	171	29.694	25.892	47.987	1.00 57.50	6
ATOM	3008	O	PHE	B	171	30.412	25.063	47.439	1.00 57.83	8
ATOM	3009	N	GLU	B	172	28.372	25.793	48.036	1.00 58.25	7
ATOM	3010	CA	GLU	B	172	27.671	24.681	47.416	1.00 58.95	6
ATOM	3011	CB	GLU	B	172	27.418	23.555	48.436	1.00 61.94	6
ATOM	3012	CG	GLU	B	172	26.521	23.921	49.634	1.00 65.83	6
ATOM	3013	CD	GLU	B	172	26.352	22.769	50.637	1.00 67.36	6
ATOM	3014	OE1	GLU	B	172	26.275	21.593	50.192	1.00 67.12	8
ATOM	3015	OE2	GLU	B	172	26.280	23.043	51.868	1.00 67.97	8
ATOM	3016	C	GLU	B	172	26.369	25.197	46.844	1.00 59.12	6
ATOM	3017	O	GLU	B	172	25.837	26.217	47.302	1.00 58.48	8
ATOM	3018	N	ILE	B	173	25.865	24.502	45.831	1.00 59.47	7
ATOM	3019	CA	ILE	B	173	24.630	24.911	45.180	1.00 60.85	6
ATOM	3020	CB	ILE	B	173	24.715	24.729	43.653	1.00 62.04	6
ATOM	3021	CG2	ILE	B	173	23.369	25.077	42.998	1.00 60.25	6
ATOM	3022	CG1	ILE	B	173	25.832	25.603	43.087	1.00 62.02	6
ATOM	3023	CD1	ILE	B	173	26.018	25.413	41.600	1.00 63.88	6
ATOM	3024	C	ILE	B	173	23.415	24.148	45.667	1.00 61.72	6
ATOM	3025	O	ILE	B	173	23.415	22.919	45.733	1.00 61.55	8
ATOM	3026	N	LEU	B	174	22.369	24.883	45.999	1.00 62.91	7
ATOM	3027	CA	LEU	B	174	21.158	24.253	46.460	1.00 63.63	6
ATOM	3028	CB	LEU	B	174	20.438	25.166	47.443	1.00 63.66	6
ATOM	3029	CG	LEU	B	174	21.339	25.698	48.556	1.00 64.21	6
ATOM	3030	CD1	LEU	B	174	20.543	26.678	49.428	1.00 63.13	6
ATOM	3031	CD2	LEU	B	174	21.914	24.532	49.369	1.00 61.09	6
ATOM	3032	C	LEU	B	174	20.307	24.010	45.232	1.00 64.20	6
ATOM	3033	O	LEU	B	174	19.891	22.885	44.962	1.00 65.99	8
ATOM	3034	N	ASP	B	175	20.068	25.058	44.459	1.00 64.89	7
ATOM	3035	CA	ASP	B	175	19.250	24.895	43.268	1.00 66.77	6
ATOM	3036	CB	ASP	B	175	17.764	24.785	43.691	1.00 68.40	6
ATOM	3037	CG	ASP	B	175	16.806	24.566	42.508	1.00 70.08	6
ATOM	3038	OD1	ASP	B	175	17.038	23.631	41.695	1.00 71.56	8
ATOM	3039	OD2	ASP	B	175	15.809	25.322	42.404	1.00 67.36	8

ATOM	3040	C	ASP	B	175	19.480	26.067	42.298	1.00	67.13	6
ATOM	3041	O	ASP	B	175	19.910	27.160	42.703	1.00	67.04	8
ATOM	3042	N	VAL	B	176	19.214	25.818	41.018	1.00	66.07	7
ATOM	3043	CA	VAL	B	176	19.364	26.819	39.981	1.00	65.28	6
ATOM	3044	CB	VAL	B	176	20.616	26.547	39.112	1.00	64.59	6
ATOM	3045	CG1	VAL	B	176	20.681	27.529	37.943	1.00	62.08	6
ATOM	3046	CG2	VAL	B	176	21.866	26.645	39.964	1.00	64.50	6
ATOM	3047	C	VAL	B	176	18.139	26.760	39.088	1.00	66.92	6
ATOM	3048	O	VAL	B	176	17.723	25.682	38.657	1.00	68.14	8
ATOM	3049	N	THR	B	177	17.555	27.920	38.816	1.00	68.01	7
ATOM	3050	CA	THR	B	177	16.393	27.988	37.939	1.00	70.52	6
ATOM	3051	CB	THR	B	177	15.087	28.139	38.744	1.00	69.59	6
ATOM	3052	OG1	THR	B	177	15.203	29.253	39.638	1.00	70.12	8
ATOM	3053	CG2	THR	B	177	14.821	26.885	39.544	1.00	68.35	6
ATOM	3054	C	THR	B	177	16.537	29.173	36.984	1.00	72.66	6
ATOM	3055	O	THR	B	177	17.095	30.220	37.356	1.00	74.08	8
ATOM	3056	N	GLN	B	178	16.049	29.002	35.757	1.00	73.01	7
ATOM	3057	CA	GLN	B	178	16.121	30.057	34.756	1.00	74.26	6
ATOM	3058	CB	GLN	B	178	17.006	29.619	33.594	1.00	76.29	6
ATOM	3059	CG	GLN	B	178	18.090	28.628	33.984	1.00	79.92	6
ATOM	3060	CD	GLN	B	178	19.227	28.575	32.959	1.00	83.13	6
ATOM	3061	OE1	GLN	B	178	18.993	28.495	31.731	1.00	83.91	8
ATOM	3062	NE2	GLN	B	178	20.469	28.616	33.458	1.00	82.82	7
ATOM	3063	C	GLN	B	178	14.725	30.354	34.232	1.00	73.95	6
ATOM	3064	O	GLN	B	178	14.041	29.454	33.752	1.00	75.30	8
ATOM	3065	N	LYS	B	179	14.306	31.611	34.310	1.00	73.25	7
ATOM	3066	CA	LYS	B	179	12.978	31.995	33.837	1.00	72.86	6
ATOM	3067	CB	LYS	B	179	12.076	32.307	35.030	1.00	75.19	6
ATOM	3068	CG	LYS	B	179	12.196	31.282	36.160	1.00	78.55	6
ATOM	3069	CD	LYS	B	179	11.456	31.735	37.428	1.00	80.12	6
ATOM	3070	CE	LYS	B	179	11.845	30.874	38.631	1.00	80.51	6
ATOM	3071	NZ	LYS	B	179	13.320	30.987	38.927	1.00	81.19	7
ATOM	3072	C	LYS	B	179	13.101	33.232	32.961	1.00	70.68	6
ATOM	3073	O	LYS	B	179	13.411	34.311	33.455	1.00	70.88	8
ATOM	3074	N	LYS	B	180	12.852	33.090	31.665	1.00	68.28	7
ATOM	3075	CA	LYS	B	180	12.970	34.242	30.776	1.00	68.69	6
ATOM	3076	CB	LYS	B	180	12.873	33.792	29.305	1.00	66.36	6
ATOM	3077	CG	LYS	B	180	11.517	33.383	28.831	1.00	61.57	6
ATOM	3078	CD	LYS	B	180	10.763	34.578	28.296	1.00	62.84	6
ATOM	3079	CE	LYS	B	180	11.419	35.168	27.058	1.00	63.27	6
ATOM	3080	NZ	LYS	B	180	11.317	34.295	25.857	1.00	64.69	7
ATOM	3081	C	LYS	B	180	11.914	35.297	31.096	1.00	69.36	6
ATOM	3082	O	LYS	B	180	11.131	35.112	32.019	1.00	70.64	8
ATOM	3083	N	ASN	B	181	11.922	36.416	30.366	1.00	69.86	7
ATOM	3084	CA	ASN	B	181	10.927	37.473	30.560	1.00	70.42	6
ATOM	3085	CB	ASN	B	181	10.755	37.816	32.052	1.00	71.53	6
ATOM	3086	CG	ASN	B	181	12.058	38.021	32.760	1.00	71.03	6
ATOM	3087	OD1	ASN	B	181	12.935	38.731	32.267	1.00	71.52	8
ATOM	3088	ND2	ASN	B	181	12.195	37.412	33.940	1.00	71.36	7
ATOM	3089	C	ASN	B	181	11.125	38.768	29.779	1.00	70.25	6
ATOM	3090	O	ASN	B	181	12.104	39.478	29.975	1.00	70.25	8
ATOM	3091	N	SER	B	182	10.162	39.078	28.911	1.00	70.77	7
ATOM	3092	CA	SER	B	182	10.203	40.297	28.105	1.00	70.64	6
ATOM	3093	CB	SER	B	182	9.107	40.262	27.045	1.00	70.47	6
ATOM	3094	OG	SER	B	182	9.267	41.327	26.122	1.00	71.28	8
ATOM	3095	C	SER	B	182	9.997	41.500	29.024	1.00	70.77	6
ATOM	3096	O	SER	B	182	9.429	41.359	30.095	1.00	72.80	8
ATOM	3097	N	VAL	B	183	10.442	42.680	28.600	1.00	71.20	7
ATOM	3098	CA	VAL	B	183	10.334	43.887	29.425	1.00	70.43	6
ATOM	3099	CB	VAL	B	183	11.337	43.826	30.630	1.00	68.47	6
ATOM	3100	CG1	VAL	B	183	12.636	43.178	30.202	1.00	68.72	6

ATOM	3101	CG2	VAL	B	183	11.625	45.230	31.148	1.00	67.78	6
ATOM	3102	C	VAL	B	183	10.590	45.189	28.659	1.00	70.59	6
ATOM	3103	O	VAL	B	183	11.522	45.282	27.853	1.00	71.25	8
ATOM	3104	N	THR	B	184	9.761	46.195	28.911	1.00	70.21	7
ATOM	3105	CA	THR	B	184	9.949	47.480	28.250	1.00	71.59	6
ATOM	3106	CB	THR	B	184	8.610	48.062	27.711	1.00	70.78	6
ATOM	3107	OG1	THR	B	184	8.065	47.183	26.721	1.00	69.37	8
ATOM	3108	CG2	THR	B	184	8.836	49.431	27.074	1.00	69.81	6
ATOM	3109	C	THR	B	184	10.558	48.447	29.271	1.00	73.13	6
ATOM	3110	O	THR	B	184	10.240	48.384	30.467	1.00	73.23	8
ATOM	3111	N	TYR	B	185	11.449	49.319	28.806	1.00	74.37	7
ATOM	3112	CA	TYR	B	185	12.085	50.287	29.689	1.00	76.17	6
ATOM	3113	CB	TYR	B	185	13.614	50.134	29.663	1.00	77.19	6
ATOM	3114	CG	TYR	B	185	14.076	48.723	29.912	1.00	78.36	6
ATOM	3115	CD1	TYR	B	185	13.942	47.745	28.928	1.00	78.94	6
ATOM	3116	CE1	TYR	B	185	14.298	46.417	29.178	1.00	80.41	6
ATOM	3117	CD2	TYR	B	185	14.584	48.344	31.154	1.00	79.09	6
ATOM	3118	CE2	TYR	B	185	14.944	47.013	31.413	1.00	79.41	6
ATOM	3119	CZ	TYR	B	185	14.796	46.054	30.424	1.00	79.27	6
ATOM	3120	OH	TYR	B	185	15.119	44.731	30.677	1.00	79.15	8
ATOM	3121	C	TYR	B	185	11.713	51.670	29.209	1.00	76.81	6
ATOM	3122	O	TYR	B	185	11.669	51.927	28.003	1.00	76.75	8
ATOM	3123	N	SER	B	186	11.445	52.563	30.152	1.00	78.68	7
ATOM	3124	CA	SER	B	186	11.078	53.941	29.810	1.00	80.00	6
ATOM	3125	CB	SER	B	186	11.002	54.795	31.089	1.00	80.19	6
ATOM	3126	OG	SER	B	186	12.160	54.610	31.902	1.00	79.86	8
ATOM	3127	C	SER	B	186	12.100	54.539	28.832	1.00	80.21	6
ATOM	3128	O	SER	B	186	11.745	55.296	27.923	1.00	79.15	8
ATOM	3129	N	CYS	B	187	13.364	54.171	29.025	1.00	80.45	7
ATOM	3130	CA	CYS	B	187	14.459	54.653	28.189	1.00	80.85	6
ATOM	3131	C	CYS	B	187	14.259	54.260	26.772	1.00	81.01	6
ATOM	3132	O	CYS	B	187	14.510	55.018	25.838	1.00	80.34	8
ATOM	3133	CB	CYS	B	187	15.787	53.993	28.574	1.00	81.53	6
ATOM	3134	SG	CYS	B	187	15.913	52.165	28.268	1.00	84.25	16
ATOM	3135	N	CYS	B	188	13.791	53.035	26.637	1.00	82.80	7
ATOM	3136	CA	CYS	B	188	13.712	52.411	25.339	1.00	83.26	6
ATOM	3137	C	CYS	B	188	12.352	51.851	24.849	1.00	82.46	6
ATOM	3138	O	CYS	B	188	11.733	50.977	25.491	1.00	82.70	8
ATOM	3139	CB	CYS	B	188	14.811	51.336	25.365	1.00	82.41	6
ATOM	3140	SG	CYS	B	188	16.353	51.824	26.282	1.00	83.49	16
ATOM	3141	N	PRO	B	189	11.891	52.346	23.679	1.00	81.48	7
ATOM	3142	CD	PRO	B	189	12.734	53.291	22.910	1.00	81.13	6
ATOM	3143	CA	PRO	B	189	10.652	52.037	22.938	1.00	79.97	6
ATOM	3144	CB	PRO	B	189	10.977	52.510	21.517	1.00	80.12	6
ATOM	3145	CG	PRO	B	189	11.825	53.725	21.766	1.00	80.41	6
ATOM	3146	C	PRO	B	189	10.133	50.585	22.941	1.00	78.77	6
ATOM	3147	O	PRO	B	189	9.063	50.303	23.490	1.00	78.66	8
ATOM	3148	N	GLU	B	190	10.878	49.671	22.313	1.00	77.68	7
ATOM	3149	CA	GLU	B	190	10.473	48.254	22.219	1.00	73.96	6
ATOM	3150	CB	GLU	B	190	11.214	47.570	21.075	1.00	75.24	6
ATOM	3151	CG	GLU	B	190	11.578	48.475	19.908	1.00	77.67	6
ATOM	3152	CD	GLU	B	190	10.414	48.680	18.950	1.00	79.11	6
ATOM	3153	OE1	GLU	B	190	9.731	47.672	18.617	1.00	77.05	8
ATOM	3154	OE2	GLU	B	190	10.200	49.845	18.526	1.00	79.84	8
ATOM	3155	C	GLU	B	190	10.779	47.482	23.494	1.00	71.49	6
ATOM	3156	O	GLU	B	190	11.317	48.038	24.460	1.00	71.14	8
ATOM	3157	N	ALA	B	191	10.455	46.191	23.483	1.00	68.33	7
ATOM	3158	CA	ALA	B	191	10.708	45.331	24.638	1.00	66.03	6
ATOM	3159	CB	ALA	B	191	9.554	44.340	24.801	1.00	65.95	6
ATOM	3160	C	ALA	B	191	12.035	44.570	24.489	1.00	64.66	6
ATOM	3161	O	ALA	B	191	12.439	44.225	23.374	1.00	63.36	8

ATOM	3162	N	TYR	B	192	12.704	44.306	25.608	1.00	62.75	7
ATOM	3163	CA	TYR	B	192	13.969	43.574	25.572	1.00	61.63	6
ATOM	3164	CB	TYR	B	192	15.134	44.468	26.010	1.00	59.80	6
ATOM	3165	CG	TYR	B	192	15.465	45.538	25.010	1.00	59.56	6
ATOM	3166	CD1	TYR	B	192	14.786	46.754	25.005	1.00	59.46	6
ATOM	3167	CE1	TYR	B	192	15.055	47.728	24.036	1.00	60.27	6
ATOM	3168	CD2	TYR	B	192	16.426	45.315	24.027	1.00	60.64	6
ATOM	3169	CE2	TYR	B	192	16.705	46.274	23.057	1.00	60.97	6
ATOM	3170	CZ	TYR	B	192	16.017	47.480	23.064	1.00	61.60	6
ATOM	3171	OH	TYR	B	192	16.290	48.431	22.101	1.00	60.81	8
ATOM	3172	C	TYR	B	192	13.948	42.302	26.426	1.00	62.58	6
ATOM	3173	O	TYR	B	192	14.047	42.349	27.668	1.00	62.03	8
ATOM	3174	N	GLU	B	193	13.834	41.166	25.738	1.00	62.66	7
ATOM	3175	CA	GLU	B	193	13.794	39.852	26.384	1.00	62.77	6
ATOM	3176	CB	GLU	B	193	13.521	38.742	25.352	1.00	61.29	6
ATOM	3177	CG	GLU	B	193	12.153	38.831	24.681	1.00	61.98	6
ATOM	3178	CD	GLU	B	193	11.858	37.636	23.775	1.00	62.41	6
ATOM	3179	OE1	GLU	B	193	12.059	36.486	24.228	1.00	62.14	8
ATOM	3180	OE2	GLU	B	193	11.411	37.838	22.621	1.00	62.38	8
ATOM	3181	C	GLU	B	193	15.105	39.552	27.091	1.00	61.37	6
ATOM	3182	O	GLU	B	193	16.166	40.019	26.666	1.00	63.09	8
ATOM	3183	N	ASP	B	194	15.026	38.772	28.165	1.00	58.46	7
ATOM	3184	CA	ASP	B	194	16.207	38.395	28.914	1.00	57.68	6
ATOM	3185	CB	ASP	B	194	16.699	39.560	29.794	1.00	58.80	6
ATOM	3186	CG	ASP	B	194	15.806	39.809	31.006	1.00	61.20	6
ATOM	3187	OD1	ASP	B	194	15.115	40.864	31.030	1.00	63.41	8
ATOM	3188	OD2	ASP	B	194	15.804	38.955	31.930	1.00	59.40	8
ATOM	3189	C	ASP	B	194	15.914	37.177	29.772	1.00	56.01	6
ATOM	3190	O	ASP	B	194	14.789	36.956	30.171	1.00	55.53	8
ATOM	3191	N	VAL	B	195	16.943	36.385	30.036	1.00	55.28	7
ATOM	3192	CA	VAL	B	195	16.819	35.199	30.860	1.00	54.79	6
ATOM	3193	CB	VAL	B	195	17.662	34.053	30.300	1.00	53.86	6
ATOM	3194	CG1	VAL	B	195	17.695	32.895	31.285	1.00	51.98	6
ATOM	3195	CG2	VAL	B	195	17.112	33.631	28.968	1.00	53.24	6
ATOM	3196	C	VAL	B	195	17.334	35.522	32.248	1.00	56.42	6
ATOM	3197	O	VAL	B	195	18.451	36.003	32.407	1.00	58.47	8
ATOM	3198	N	GLU	B	196	16.525	35.261	33.261	1.00	58.06	7
ATOM	3199	CA	GLU	B	196	16.942	35.526	34.624	1.00	58.06	6
ATOM	3200	CB	GLU	B	196	15.808	36.168	35.393	1.00	59.44	6
ATOM	3201	CG	GLU	B	196	16.168	36.535	36.811	1.00	64.02	6
ATOM	3202	CD	GLU	B	196	14.983	37.131	37.561	1.00	65.27	6
ATOM	3203	OE1	GLU	B	196	14.414	38.137	37.081	1.00	65.41	8
ATOM	3204	OE2	GLU	B	196	14.625	36.591	38.631	1.00	68.06	8
ATOM	3205	C	GLU	B	196	17.310	34.199	35.252	1.00	57.73	6
ATOM	3206	O	GLU	B	196	16.495	33.285	35.291	1.00	60.64	8
ATOM	3207	N	VAL	B	197	18.543	34.084	35.722	1.00	56.14	7
ATOM	3208	CA	VAL	B	197	18.999	32.854	36.338	1.00	54.69	6
ATOM	3209	CB	VAL	B	197	20.358	32.405	35.757	1.00	52.53	6
ATOM	3210	CG1	VAL	B	197	20.807	31.107	36.404	1.00	50.11	6
ATOM	3211	CG2	VAL	B	197	20.241	32.229	34.264	1.00	51.73	6
ATOM	3212	C	VAL	B	197	19.154	33.106	37.819	1.00	56.80	6
ATOM	3213	O	VAL	B	197	19.817	34.057	38.226	1.00	57.91	8
ATOM	3214	N	SER	B	198	18.539	32.258	38.631	1.00	58.59	7
ATOM	3215	CA	SER	B	198	18.626	32.421	40.071	1.00	58.65	6
ATOM	3216	CB	SER	B	198	17.235	32.308	40.703	1.00	59.34	6
ATOM	3217	OG	SER	B	198	16.426	33.407	40.320	1.00	59.29	8
ATOM	3218	C	SER	B	198	19.556	31.385	40.651	1.00	57.58	6
ATOM	3219	O	SER	B	198	19.340	30.188	40.505	1.00	58.41	8
ATOM	3220	N	LEU	B	199	20.599	31.857	41.310	1.00	57.49	7
ATOM	3221	CA	LEU	B	199	21.569	30.963	41.904	1.00	58.89	6
ATOM	3222	CB	LEU	B	199	23.000	31.437	41.622	1.00	58.76	6

ATOM	3223	CG	LEU	B	199	24.108	30.670	42.358	1.00	59.80	6
ATOM	3224	CD1	LEU	B	199	24.135	29.209	41.927	1.00	60.58	6
ATOM	3225	CD2	LEU	B	199	25.446	31.304	42.063	1.00	60.42	6
ATOM	3226	C	LEU	B	199	21.369	30.885	43.395	1.00	60.51	6
ATOM	3227	O	LEU	B	199	21.759	31.788	44.136	1.00	61.67	8
ATOM	3228	N	ASN	B	200	20.754	29.801	43.838	1.00	60.15	7
ATOM	3229	CA	ASN	B	200	20.539	29.607	45.252	1.00	57.57	6
ATOM	3230	CB	ASN	B	200	19.188	28.919	45.499	1.00	60.95	6
ATOM	3231	CG	ASN	B	200	18.936	28.642	46.968	1.00	62.80	6
ATOM	3232	OD1	ASN	B	200	19.167	29.504	47.820	1.00	65.10	8
ATOM	3233	ND2	ASN	B	200	18.465	27.443	47.275	1.00	59.90	7
ATOM	3234	C	ASN	B	200	21.691	28.736	45.712	1.00	55.80	6
ATOM	3235	O	ASN	B	200	21.793	27.569	45.325	1.00	56.54	8
ATOM	3236	N	PHE	B	201	22.561	29.316	46.527	1.00	53.98	7
ATOM	3237	CA	PHE	B	201	23.725	28.615	47.042	1.00	53.98	6
ATOM	3238	CB	PHE	B	201	24.960	28.975	46.226	1.00	53.35	6
ATOM	3239	CG	PHE	B	201	25.418	30.404	46.418	1.00	51.26	6
ATOM	3240	CD1	PHE	B	201	26.633	30.690	47.050	1.00	50.15	6
ATOM	3241	CD2	PHE	B	201	24.615	31.472	46.000	1.00	50.67	6
ATOM	3242	CE1	PHE	B	201	27.038	32.015	47.264	1.00	45.58	6
ATOM	3243	CE2	PHE	B	201	25.016	32.799	46.213	1.00	47.69	6
ATOM	3244	CZ	PHE	B	201	26.227	33.062	46.845	1.00	46.26	6
ATOM	3245	C	PHE	B	201	23.943	29.080	48.456	1.00	55.95	6
ATOM	3246	O	PHE	B	201	23.275	30.017	48.912	1.00	56.39	8
ATOM	3247	N	ARG	B	202	24.896	28.443	49.132	1.00	56.81	7
ATOM	3248	CA	ARG	B	202	25.223	28.793	50.506	1.00	60.77	6
ATOM	3249	CB	ARG	B	202	24.255	28.104	51.460	1.00	64.25	6
ATOM	3250	CG	ARG	B	202	24.491	26.625	51.497	1.00	66.78	6
ATOM	3251	CD	ARG	B	202	23.494	25.893	52.344	1.00	70.08	6
ATOM	3252	NE	ARG	B	202	23.768	24.454	52.333	1.00	72.69	7
ATOM	3253	CZ	ARG	B	202	22.945	23.528	52.825	1.00	73.67	6
ATOM	3254	NH1	ARG	B	202	21.781	23.884	53.375	1.00	74.01	7
ATOM	3255	NH2	ARG	B	202	23.281	22.245	52.760	1.00	73.29	7
ATOM	3256	C	ARG	B	202	26.635	28.328	50.843	1.00	61.67	6
ATOM	3257	O	ARG	B	202	27.181	27.450	50.183	1.00	62.10	8
ATOM	3258	N	LYS	B	203	27.225	28.918	51.875	1.00	62.58	7
ATOM	3259	CA	LYS	B	203	28.549	28.505	52.298	1.00	62.87	6
ATOM	3260	CB	LYS	B	203	29.067	29.417	53.399	1.00	62.83	6
ATOM	3261	CG	LYS	B	203	30.400	28.995	53.967	1.00	62.29	6
ATOM	3262	CD	LYS	B	203	30.765	29.871	55.141	1.00	65.39	6
ATOM	3263	CE	LYS	B	203	32.135	29.519	55.689	1.00	67.38	6
ATOM	3264	NZ	LYS	B	203	33.232	29.772	54.695	1.00	70.43	7
ATOM	3265	C	LYS	B	203	28.387	27.101	52.854	1.00	64.30	6
ATOM	3266	O	LYS	B	203	27.318	26.736	53.371	1.00	65.43	8
ATOM	3267	N	LYS	B	204	29.446	26.312	52.745	1.00	66.12	7
ATOM	3268	CA	LYS	B	204	29.417	24.955	53.246	1.00	67.10	6
ATOM	3269	CB	LYS	B	204	30.701	24.223	52.860	1.00	63.37	6
ATOM	3270	CG	LYS	B	204	30.745	23.853	51.379	1.00	60.21	6
ATOM	3271	CD	LYS	B	204	31.940	22.966	51.055	1.00	58.61	6
ATOM	3272	CE	LYS	B	204	31.955	22.553	49.582	1.00	57.79	6
ATOM	3273	NZ	LYS	B	204	33.202	21.808	49.238	1.00	53.82	7
ATOM	3274	C	LYS	B	204	29.293	25.081	54.745	1.00	70.90	6
ATOM	3275	O	LYS	B	204	29.893	25.989	55.339	1.00	72.60	8
ATOM	3276	N	GLY	B	205	28.489	24.192	55.342	1.00	74.01	7
ATOM	3277	CA	GLY	B	205	28.260	24.197	56.783	1.00	74.37	6
ATOM	3278	C	GLY	B	205	29.305	23.430	57.576	1.00	75.59	6
ATOM	3279	OT1	GLY	B	205	30.276	22.932	56.958	1.00	75.56	8
ATOM	3280	OT2	GLY	B	205	29.163	23.331	58.822	1.00	76.47	8
ATOM	3281	CB	PHE	C	1	16.639	48.183	2.177	1.00	71.30	6
ATOM	3282	CG	PHE	C	1	17.365	49.162	1.297	1.00	73.66	6
ATOM	3283	CD1	PHE	C	1	18.546	48.805	0.647	1.00	74.99	6

ATOM	3284	CD2	PHE	C	1	16.889	50.471	1.160	1.00	75.46	6
ATOM	3285	CE1	PHE	C	1	19.257	49.743	-0.138	1.00	77.68	6
ATOM	3286	CE2	PHE	C	1	17.590	51.421	0.380	1.00	76.94	6
ATOM	3287	CZ	PHE	C	1	18.779	51.054	-0.271	1.00	77.37	6
ATOM	3288	C	PHE	C	1	16.469	45.841	2.896	1.00	69.30	6
ATOM	3289	O	PHE	C	1	15.487	45.976	3.637	1.00	68.12	8
ATOM	3290	N	PHE	C	1	15.624	46.515	0.608	1.00	67.59	7
ATOM	3291	CA	PHE	C	1	16.651	46.733	1.669	1.00	69.36	6
ATOM	3292	N	ASP	C	2	17.421	44.940	3.123	1.00	69.61	7
ATOM	3293	CA	ASP	C	2	17.373	44.071	4.298	1.00	68.32	6
ATOM	3294	CB	ASP	C	2	17.364	42.592	3.882	1.00	69.98	6
ATOM	3295	CG	ASP	C	2	18.729	42.092	3.426	1.00	71.56	6
ATOM	3296	OD1	ASP	C	2	19.586	41.867	4.316	1.00	71.73	8
ATOM	3297	OD2	ASP	C	2	18.936	41.926	2.187	1.00	72.36	8
ATOM	3298	C	ASP	C	2	18.615	44.399	5.116	1.00	66.00	6
ATOM	3299	O	ASP	C	2	19.617	44.865	4.562	1.00	67.56	8
ATOM	3300	N	ARG	C	3	18.550	44.165	6.423	1.00	62.29	7
ATOM	3301	CA	ARG	C	3	19.663	44.455	7.320	1.00	59.37	6
ATOM	3302	CB	ARG	C	3	19.515	43.661	8.604	1.00	56.89	6
ATOM	3303	CG	ARG	C	3	18.280	44.017	9.387	1.00	55.35	6
ATOM	3304	CD	ARG	C	3	18.177	43.172	10.640	1.00	57.70	6
ATOM	3305	NE	ARG	C	3	16.947	43.437	11.378	1.00	60.36	7
ATOM	3306	CZ	ARG	C	3	16.714	44.540	12.084	1.00	62.92	6
ATOM	3307	NH1	ARG	C	3	17.623	45.503	12.166	1.00	62.53	7
ATOM	3308	NH2	ARG	C	3	15.554	44.689	12.700	1.00	64.87	7
ATOM	3309	C	ARG	C	3	21.060	44.236	6.749	1.00	59.30	6
ATOM	3310	O	ARG	C	3	21.970	45.008	7.051	1.00	61.36	8
ATOM	3311	N	ALA	C	4	21.257	43.215	5.920	1.00	57.54	7
ATOM	3312	CA	ALA	C	4	22.595	43.023	5.379	1.00	55.37	6
ATOM	3313	CB	ALA	C	4	22.686	41.727	4.610	1.00	53.55	6
ATOM	3314	C	ALA	C	4	22.947	44.186	4.478	1.00	54.97	6
ATOM	3315	O	ALA	C	4	24.020	44.764	4.603	1.00	55.12	8
ATOM	3316	N	ASP	C	5	22.034	44.534	3.575	1.00	56.24	7
ATOM	3317	CA	ASP	C	5	22.265	45.632	2.646	1.00	56.25	6
ATOM	3318	CB	ASP	C	5	21.081	45.795	1.680	1.00	58.72	6
ATOM	3319	CG	ASP	C	5	20.773	44.529	0.906	1.00	62.35	6
ATOM	3320	OD1	ASP	C	5	21.715	43.900	0.364	1.00	63.21	8
ATOM	3321	OD2	ASP	C	5	19.574	44.171	0.834	1.00	65.38	8
ATOM	3322	C	ASP	C	5	22.471	46.935	3.406	1.00	55.27	6
ATOM	3323	O	ASP	C	5	23.294	47.764	3.020	1.00	54.31	8
ATOM	3324	N	ILE	C	6	21.732	47.110	4.495	1.00	53.55	7
ATOM	3325	CA	ILE	C	6	21.840	48.339	5.270	1.00	54.16	6
ATOM	3326	CB	ILE	C	6	20.713	48.456	6.311	1.00	54.45	6
ATOM	3327	CG2	ILE	C	6	20.811	49.793	7.021	1.00	52.65	6
ATOM	3328	CG1	ILE	C	6	19.352	48.344	5.612	1.00	56.53	6
ATOM	3329	CD1	ILE	C	6	18.146	48.530	6.524	1.00	56.74	6
ATOM	3330	C	ILE	C	6	23.178	48.475	5.972	1.00	52.95	6
ATOM	3331	O	ILE	C	6	23.872	49.487	5.818	1.00	53.74	8
ATOM	3332	N	LEU	C	7	23.543	47.455	6.741	1.00	51.30	7
ATOM	3333	CA	LEU	C	7	24.814	47.462	7.460	1.00	49.62	6
ATOM	3334	CB	LEU	C	7	24.931	46.194	8.293	1.00	47.45	6
ATOM	3335	CG	LEU	C	7	23.912	46.136	9.429	1.00	47.62	6
ATOM	3336	CD1	LEU	C	7	23.819	44.743	10.014	1.00	48.73	6
ATOM	3337	CD2	LEU	C	7	24.321	47.122	10.486	1.00	47.41	6
ATOM	3338	C	LEU	C	7	25.970	47.559	6.465	1.00	49.71	6
ATOM	3339	O	LEU	C	7	26.951	48.269	6.677	1.00	47.57	8
ATOM	3340	N	TYR	C	8	25.827	46.845	5.361	1.00	52.00	7
ATOM	3341	CA	TYR	C	8	26.830	46.838	4.318	1.00	53.34	6
ATOM	3342	CB	TYR	C	8	26.367	45.961	3.167	1.00	53.82	6
ATOM	3343	CG	TYR	C	8	27.335	45.969	2.020	1.00	57.66	6
ATOM	3344	CD1	TYR	C	8	28.552	45.289	2.106	1.00	58.72	6

ATOM	3345	CE1	TYR	C	8	29.467	45.315	1.045	1.00	60.33	6
ATOM	3346	CD2	TYR	C	8	27.051	46.679	0.851	1.00	58.73	6
ATOM	3347	CE2	TYR	C	8	27.957	46.714	-0.211	1.00	60.05	6
ATOM	3348	CZ	TYR	C	8	29.162	46.027	-0.107	1.00	60.68	6
ATOM	3349	OH	TYR	C	8	30.045	46.045	-1.163	1.00	62.86	8
ATOM	3350	C	TYR	C	8	27.134	48.235	3.790	1.00	54.25	6
ATOM	3351	O	TYR	C	8	28.298	48.589	3.614	1.00	55.00	8
ATOM	3352	N	ASN	C	9	26.092	49.015	3.516	1.00	53.76	7
ATOM	3353	CA	ASN	C	9	26.283	50.369	3.013	1.00	55.35	6
ATOM	3354	CB	ASN	C	9	24.941	51.005	2.660	1.00	59.27	6
ATOM	3355	CG	ASN	C	9	24.299	50.372	1.433	1.00	61.31	6
ATOM	3356	OD1	ASN	C	9	24.907	49.531	0.758	1.00	61.18	8
ATOM	3357	ND2	ASN	C	9	23.068	50.778	1.136	1.00	62.69	7
ATOM	3358	C	ASN	C	9	27.003	51.233	4.034	1.00	54.14	6
ATOM	3359	O	ASN	C	9	28.001	51.877	3.722	1.00	54.09	8
ATOM	3360	N	ILE	C	10	26.494	51.240	5.258	1.00	54.05	7
ATOM	3361	CA	ILE	C	10	27.107	52.014	6.330	1.00	54.35	6
ATOM	3362	CB	ILE	C	10	26.399	51.757	7.668	1.00	53.88	6
ATOM	3363	CG2	ILE	C	10	27.141	52.453	8.784	1.00	52.27	6
ATOM	3364	CG1	ILE	C	10	24.956	52.257	7.595	1.00	53.43	6
ATOM	3365	CD1	ILE	C	10	24.114	51.860	8.769	1.00	51.08	6
ATOM	3366	C	ILE	C	10	28.580	51.635	6.479	1.00	55.70	6
ATOM	3367	O	ILE	C	10	29.452	52.497	6.609	1.00	56.88	8
ATOM	3368	N	ARG	C	11	28.844	50.337	6.456	1.00	56.11	7
ATOM	3369	CA	ARG	C	11	30.194	49.827	6.579	1.00	57.74	6
ATOM	3370	CB	ARG	C	11	30.161	48.307	6.466	1.00	61.80	6
ATOM	3371	CG	ARG	C	11	31.495	47.629	6.644	1.00	67.28	6
ATOM	3372	CD	ARG	C	11	31.879	47.631	8.102	1.00	75.61	6
ATOM	3373	NE	ARG	C	11	32.848	46.586	8.419	1.00	82.91	7
ATOM	3374	CZ	ARG	C	11	32.779	45.333	7.957	1.00	86.49	6
ATOM	3375	NH1	ARG	C	11	31.785	44.963	7.140	1.00	87.62	7
ATOM	3376	NH2	ARG	C	11	33.689	44.436	8.331	1.00	87.96	7
ATOM	3377	C	ARG	C	11	31.099	50.388	5.490	1.00	57.06	6
ATOM	3378	O	ARG	C	11	32.198	50.865	5.758	1.00	57.56	8
ATOM	3379	N	GLN	C	12	30.617	50.333	4.255	1.00	57.22	7
ATOM	3380	CA	GLN	C	12	31.377	50.781	3.093	1.00	56.59	6
ATOM	3381	CB	GLN	C	12	30.783	50.169	1.829	1.00	56.62	6
ATOM	3382	CG	GLN	C	12	31.795	49.448	0.976	1.00	58.01	6
ATOM	3383	CD	GLN	C	12	32.113	48.101	1.532	1.00	58.10	6
ATOM	3384	OE1	GLN	C	12	31.215	47.289	1.704	1.00	59.91	8
ATOM	3385	NE2	GLN	C	12	33.384	47.846	1.824	1.00	57.19	7
ATOM	3386	C	GLN	C	12	31.505	52.278	2.872	1.00	56.02	6
ATOM	3387	O	GLN	C	12	32.424	52.728	2.208	1.00	54.27	8
ATOM	3388	N	THR	C	13	30.589	53.054	3.423	1.00	58.04	7
ATOM	3389	CA	THR	C	13	30.631	54.492	3.213	1.00	59.72	6
ATOM	3390	CB	THR	C	13	29.302	54.985	2.653	1.00	58.83	6
ATOM	3391	OG1	THR	C	13	28.253	54.622	3.559	1.00	55.46	8
ATOM	3392	CG2	THR	C	13	29.043	54.374	1.277	1.00	59.29	6
ATOM	3393	C	THR	C	13	30.944	55.316	4.459	1.00	61.81	6
ATOM	3394	O	THR	C	13	31.317	56.492	4.364	1.00	62.06	8
ATOM	3395	N	SER	C	14	30.794	54.705	5.627	1.00	62.55	7
ATOM	3396	CA	SER	C	14	31.053	55.421	6.865	1.00	62.19	6
ATOM	3397	CB	SER	C	14	30.549	54.612	8.056	1.00	62.76	6
ATOM	3398	OG	SER	C	14	30.476	55.435	9.209	1.00	64.16	8
ATOM	3399	C	SER	C	14	32.521	55.779	7.074	1.00	61.03	6
ATOM	3400	O	SER	C	14	33.422	55.098	6.577	1.00	61.70	8
ATOM	3401	N	ARG	C	15	32.735	56.863	7.816	1.00	58.93	7
ATOM	3402	CA	ARG	C	15	34.064	57.367	8.127	1.00	57.11	6
ATOM	3403	CB	ARG	C	15	34.383	58.576	7.247	1.00	57.80	6
ATOM	3404	CG	ARG	C	15	34.388	58.261	5.748	1.00	59.34	6
ATOM	3405	CD	ARG	C	15	35.114	59.331	4.968	1.00	61.90	6

ATOM	3406	NE	ARG	C	15	36.475	59.479	5.475	1.00	64.09	7
ATOM	3407	CZ	ARG	C	15	37.287	60.488	5.180	1.00	63.60	6
ATOM	3408	NH1	ARG	C	15	36.873	61.450	4.375	1.00	62.16	7
ATOM	3409	NH2	ARG	C	15	38.516	60.526	5.688	1.00	66.26	7
ATOM	3410	C	ARG	C	15	34.081	57.753	9.598	1.00	54.80	6
ATOM	3411	O	ARG	C	15	33.736	58.874	9.969	1.00	54.31	8
ATOM	3412	N	PRO	C	16	34.483	56.811	10.460	1.00	53.16	7
ATOM	3413	CD	PRO	C	16	34.921	55.451	10.106	1.00	49.32	6
ATOM	3414	CA	PRO	C	16	34.547	57.012	11.911	1.00	51.93	6
ATOM	3415	CB	PRO	C	16	35.072	55.668	12.429	1.00	49.26	6
ATOM	3416	CG	PRO	C	16	34.647	54.702	11.387	1.00	48.93	6
ATOM	3417	C	PRO	C	16	35.420	58.172	12.356	1.00	51.62	6
ATOM	3418	O	PRO	C	16	35.266	58.663	13.468	1.00	52.27	8
ATOM	3419	N	ASP	C	17	36.337	58.608	11.501	1.00	51.78	7
ATOM	3420	CA	ASP	C	17	37.219	59.706	11.863	1.00	54.16	6
ATOM	3421	CB	ASP	C	17	38.597	59.526	11.209	1.00	59.36	6
ATOM	3422	CG	ASP	C	17	39.421	58.411	11.859	1.00	64.02	6
ATOM	3423	OD1	ASP	C	17	39.200	58.134	13.067	1.00	64.61	8
ATOM	3424	OD2	ASP	C	17	40.299	57.824	11.170	1.00	64.76	8
ATOM	3425	C	ASP	C	17	36.680	61.080	11.499	1.00	53.77	6
ATOM	3426	O	ASP	C	17	37.350	62.088	11.736	1.00	54.82	8
ATOM	3427	N	VAL	C	18	35.473	61.129	10.944	1.00	53.02	7
ATOM	3428	CA	VAL	C	18	34.902	62.398	10.528	1.00	53.40	6
ATOM	3429	CB	VAL	C	18	34.699	62.421	9.003	1.00	53.89	6
ATOM	3430	CG1	VAL	C	18	34.194	63.785	8.563	1.00	53.62	6
ATOM	3431	CG2	VAL	C	18	36.013	62.087	8.308	1.00	52.31	6
ATOM	3432	C	VAL	C	18	33.589	62.771	11.201	1.00	54.75	6
ATOM	3433	O	VAL	C	18	32.573	62.097	11.046	1.00	54.30	8
ATOM	3434	N	ILE	C	19	33.634	63.870	11.944	1.00	56.30	7
ATOM	3435	CA	ILE	C	19	32.480	64.401	12.662	1.00	55.34	6
ATOM	3436	CB	ILE	C	19	32.934	65.631	13.519	1.00	54.46	6
ATOM	3437	CG2	ILE	C	19	33.362	66.777	12.618	1.00	53.28	6
ATOM	3438	CG1	ILE	C	19	31.827	66.078	14.467	1.00	53.52	6
ATOM	3439	CD1	ILE	C	19	32.318	67.022	15.525	1.00	50.20	6
ATOM	3440	C	ILE	C	19	31.392	64.784	11.644	1.00	56.25	6
ATOM	3441	O	ILE	C	19	31.675	65.474	10.653	1.00	56.64	8
ATOM	3442	N	PRO	C	20	30.142	64.318	11.861	1.00	55.95	7
ATOM	3443	CD	PRO	C	20	29.756	63.451	12.978	1.00	55.72	6
ATOM	3444	CA	PRO	C	20	28.980	64.574	10.996	1.00	57.07	6
ATOM	3445	CB	PRO	C	20	27.912	63.627	11.540	1.00	55.92	6
ATOM	3446	CG	PRO	C	20	28.673	62.639	12.349	1.00	57.30	6
ATOM	3447	C	PRO	C	20	28.500	66.023	11.035	1.00	59.85	6
ATOM	3448	O	PRO	C	20	27.326	66.290	11.270	1.00	58.63	8
ATOM	3449	N	THR	C	21	29.416	66.947	10.782	1.00	64.15	7
ATOM	3450	CA	THR	C	21	29.123	68.370	10.797	1.00	68.52	6
ATOM	3451	CB	THR	C	21	30.421	69.169	11.046	1.00	68.47	6
ATOM	3452	OG1	THR	C	21	30.496	69.477	12.440	1.00	70.47	8
ATOM	3453	CG2	THR	C	21	30.470	70.455	10.216	1.00	69.90	6
ATOM	3454	C	THR	C	21	28.424	68.913	9.555	1.00	72.31	6
ATOM	3455	O	THR	C	21	28.826	68.631	8.412	1.00	71.25	8
ATOM	3456	N	GLN	C	22	27.384	69.709	9.805	1.00	76.61	7
ATOM	3457	CA	GLN	C	22	26.599	70.346	8.747	1.00	80.67	6
ATOM	3458	CB	GLN	C	22	25.112	70.087	8.972	1.00	81.49	6
ATOM	3459	CG	GLN	C	22	24.749	68.606	9.029	1.00	82.93	6
ATOM	3460	CD	GLN	C	22	23.534	68.351	9.900	1.00	83.25	6
ATOM	3461	OE1	GLN	C	22	23.566	68.595	11.120	1.00	84.14	8
ATOM	3462	NE2	GLN	C	22	22.452	67.867	9.285	1.00	83.14	7
ATOM	3463	C	GLN	C	22	26.865	71.846	8.814	1.00	83.04	6
ATOM	3464	O	GLN	C	22	26.382	72.523	9.730	1.00	83.36	8
ATOM	3465	N	ARG	C	23	27.635	72.357	7.849	1.00	85.46	7
ATOM	3466	CA	ARG	C	23	27.985	73.783	7.802	1.00	86.39	6

ATOM	3467	CB	ARG	C	23	26.722	74.654	7.771	1.00	87.20	6
ATOM	3468	CG	ARG	C	23	26.050	74.710	6.393	1.00	89.96	6
ATOM	3469	CD	ARG	C	23	24.797	73.834	6.297	1.00	90.96	6
ATOM	3470	NE	ARG	C	23	24.282	73.771	4.920	1.00	93.30	7
ATOM	3471	CZ	ARG	C	23	23.996	74.830	4.145	1.00	94.77	6
ATOM	3472	NH1	ARG	C	23	24.167	76.083	4.591	1.00	94.25	7
ATOM	3473	NH2	ARG	C	23	23.537	74.640	2.905	1.00	94.32	7
ATOM	3474	C	ARG	C	23	28.828	74.134	9.013	1.00	85.61	6
ATOM	3475	O	ARG	C	23	29.599	73.302	9.495	1.00	85.98	8
ATOM	3476	N	ASP	C	24	28.700	75.358	9.503	1.00	85.83	7
ATOM	3477	CA	ASP	C	24	29.462	75.755	10.685	1.00	86.66	6
ATOM	3478	CB	ASP	C	24	29.625	77.283	10.785	1.00	90.61	6
ATOM	3479	CG	ASP	C	24	29.385	78.002	9.458	1.00	92.74	6
ATOM	3480	OD1	ASP	C	24	30.108	77.704	8.471	1.00	93.41	8
ATOM	3481	OD2	ASP	C	24	28.468	78.868	9.418	1.00	93.68	8
ATOM	3482	C	ASP	C	24	28.679	75.280	11.907	1.00	85.20	6
ATOM	3483	O	ASP	C	24	29.053	75.591	13.052	1.00	85.29	8
ATOM	3484	N	ARG	C	25	27.587	74.553	11.660	1.00	82.29	7
ATOM	3485	CA	ARG	C	25	26.761	74.039	12.742	1.00	79.75	6
ATOM	3486	CB	ARG	C	25	25.422	73.522	12.210	1.00	82.55	6
ATOM	3487	CG	ARG	C	25	24.428	74.588	11.781	1.00	86.91	6
ATOM	3488	CD	ARG	C	25	23.026	73.964	11.594	1.00	91.01	6
ATOM	3489	NE	ARG	C	25	22.007	74.963	11.252	1.00	94.97	7
ATOM	3490	CZ	ARG	C	25	20.702	74.705	11.146	1.00	96.54	6
ATOM	3491	NH1	ARG	C	25	20.253	73.471	11.356	1.00	97.65	7
ATOM	3492	NH2	ARG	C	25	19.844	75.679	10.837	1.00	96.40	7
ATOM	3493	C	ARG	C	25	27.456	72.906	13.490	1.00	76.53	6
ATOM	3494	O	ARG	C	25	28.004	71.987	12.876	1.00	78.25	8
ATOM	3495	N	PRO	C	26	27.449	72.963	14.829	1.00	72.39	7
ATOM	3496	CD	PRO	C	26	27.074	74.126	15.647	1.00	71.70	6
ATOM	3497	CA	PRO	C	26	28.073	71.935	15.660	1.00	68.13	6
ATOM	3498	CB	PRO	C	26	28.087	72.574	17.050	1.00	69.12	6
ATOM	3499	CG	PRO	C	26	28.066	74.039	16.770	1.00	69.98	6
ATOM	3500	C	PRO	C	26	27.183	70.706	15.639	1.00	64.71	6
ATOM	3501	O	PRO	C	26	26.010	70.795	15.275	1.00	63.13	8
ATOM	3502	N	VAL	C	27	27.735	69.560	16.019	1.00	61.55	7
ATOM	3503	CA	VAL	C	27	26.937	68.349	16.081	1.00	57.92	6
ATOM	3504	CB	VAL	C	27	27.805	67.073	15.948	1.00	56.85	6
ATOM	3505	CG1	VAL	C	27	27.038	65.860	16.439	1.00	54.71	6
ATOM	3506	CG2	VAL	C	27	28.197	66.872	14.502	1.00	54.24	6
ATOM	3507	C	VAL	C	27	26.301	68.400	17.452	1.00	56.84	6
ATOM	3508	O	VAL	C	27	26.987	68.621	18.450	1.00	57.02	8
ATOM	3509	N	ALA	C	28	24.989	68.228	17.506	1.00	56.11	7
ATOM	3510	CA	ALA	C	28	24.302	68.262	18.783	1.00	54.82	6
ATOM	3511	CB	ALA	C	28	22.896	68.775	18.600	1.00	55.72	6
ATOM	3512	C	ALA	C	28	24.282	66.879	19.424	1.00	54.45	6
ATOM	3513	O	ALA	C	28	23.579	65.972	18.964	1.00	54.53	8
ATOM	3514	N	VAL	C	29	25.067	66.742	20.488	1.00	53.25	7
ATOM	3515	CA	VAL	C	29	25.191	65.503	21.235	1.00	51.65	6
ATOM	3516	CB	VAL	C	29	26.676	65.113	21.450	1.00	50.25	6
ATOM	3517	CG1	VAL	C	29	26.770	63.846	22.297	1.00	47.03	6
ATOM	3518	CG2	VAL	C	29	27.358	64.921	20.108	1.00	50.21	6
ATOM	3519	C	VAL	C	29	24.549	65.670	22.595	1.00	52.02	6
ATOM	3520	O	VAL	C	29	24.833	66.615	23.320	1.00	51.40	8
ATOM	3521	N	SER	C	30	23.669	64.745	22.932	1.00	53.81	7
ATOM	3522	CA	SER	C	30	23.012	64.785	24.214	1.00	55.39	6
ATOM	3523	CB	SER	C	30	21.495	64.666	24.034	1.00	54.53	6
ATOM	3524	OG	SER	C	30	21.159	63.462	23.373	1.00	56.88	8
ATOM	3525	C	SER	C	30	23.566	63.614	25.013	1.00	55.69	6
ATOM	3526	O	SER	C	30	23.688	62.504	24.503	1.00	56.19	8
ATOM	3527	N	VAL	C	31	23.916	63.888	26.261	1.00	56.76	7

ATOM	3528	CA	VAL	C	31	24.466	62.893	27.174	1.00	57.06	6
ATOM	3529	CB	VAL	C	31	25.871	63.301	27.640	1.00	57.34	6
ATOM	3530	CG1	VAL	C	31	26.543	62.141	28.354	1.00	57.65	6
ATOM	3531	CG2	VAL	C	31	26.674	63.784	26.467	1.00	58.89	6
ATOM	3532	C	VAL	C	31	23.585	62.791	28.415	1.00	57.25	6
ATOM	3533	O	VAL	C	31	23.152	63.806	28.979	1.00	57.25	8
ATOM	3534	N	SER	C	32	23.339	61.569	28.855	1.00	56.49	7
ATOM	3535	CA	SER	C	32	22.505	61.356	30.024	1.00	57.63	6
ATOM	3536	CB	SER	C	32	21.045	61.182	29.589	1.00	59.80	6
ATOM	3537	OG	SER	C	32	20.220	60.763	30.667	1.00	63.17	8
ATOM	3538	C	SER	C	32	22.958	60.123	30.781	1.00	57.81	6
ATOM	3539	O	SER	C	32	22.860	58.998	30.271	1.00	60.21	8
ATOM	3540	N	LEU	C	33	23.448	60.317	31.997	1.00	56.08	7
ATOM	3541	CA	LEU	C	33	23.895	59.182	32.801	1.00	55.73	6
ATOM	3542	CB	LEU	C	33	25.021	59.581	33.752	1.00	53.14	6
ATOM	3543	CG	LEU	C	33	26.240	60.219	33.105	1.00	52.98	6
ATOM	3544	CD1	LEU	C	33	27.353	60.346	34.127	1.00	51.17	6
ATOM	3545	CD2	LEU	C	33	26.680	59.374	31.933	1.00	53.34	6
ATOM	3546	C	LEU	C	33	22.752	58.629	33.624	1.00	56.29	6
ATOM	3547	O	LEU	C	33	21.976	59.392	34.193	1.00	57.63	8
ATOM	3548	N	LYS	C	34	22.642	57.303	33.664	1.00	54.96	7
ATOM	3549	CA	LYS	C	34	21.616	56.643	34.447	1.00	55.26	6
ATOM	3550	CB	LYS	C	34	20.710	55.790	33.563	1.00	58.99	6
ATOM	3551	CG	LYS	C	34	20.053	56.544	32.414	1.00	63.56	6
ATOM	3552	CD	LYS	C	34	19.098	57.649	32.897	1.00	68.99	6
ATOM	3553	CE	LYS	C	34	18.499	58.434	31.705	1.00	71.13	6
ATOM	3554	NZ	LYS	C	34	17.528	59.497	32.120	1.00	71.58	7
ATOM	3555	C	LYS	C	34	22.410	55.756	35.369	1.00	53.96	6
ATOM	3556	O	LYS	C	34	23.034	54.806	34.922	1.00	54.63	8
ATOM	3557	N	PHE	C	35	22.410	56.064	36.657	1.00	53.24	7
ATOM	3558	CA	PHE	C	35	23.190	55.260	37.579	1.00	51.26	6
ATOM	3559	CB	PHE	C	35	23.427	56.032	38.864	1.00	49.55	6
ATOM	3560	CG	PHE	C	35	24.291	57.226	38.662	1.00	48.89	6
ATOM	3561	CD1	PHE	C	35	23.745	58.428	38.239	1.00	48.34	6
ATOM	3562	CD2	PHE	C	35	25.669	57.133	38.814	1.00	50.53	6
ATOM	3563	CE1	PHE	C	35	24.553	59.526	37.967	1.00	47.39	6
ATOM	3564	CE2	PHE	C	35	26.488	58.228	38.542	1.00	50.75	6
ATOM	3565	CZ	PHE	C	35	25.925	59.424	38.118	1.00	49.19	6
ATOM	3566	C	PHE	C	35	22.608	53.899	37.849	1.00	50.23	6
ATOM	3567	O	PHE	C	35	21.418	53.754	38.078	1.00	50.29	8
ATOM	3568	N	ILE	C	36	23.478	52.901	37.795	1.00	49.55	7
ATOM	3569	CA	ILE	C	36	23.095	51.519	37.997	1.00	47.28	6
ATOM	3570	CB	ILE	C	36	23.658	50.632	36.883	1.00	46.86	6
ATOM	3571	CG2	ILE	C	36	23.173	49.223	37.055	1.00	44.45	6
ATOM	3572	CG1	ILE	C	36	23.252	51.192	35.521	1.00	46.79	6
ATOM	3573	CD1	ILE	C	36	21.754	51.310	35.328	1.00	48.67	6
ATOM	3574	C	ILE	C	36	23.619	50.999	39.308	1.00	46.88	6
ATOM	3575	O	ILE	C	36	23.052	50.074	39.866	1.00	48.98	8
ATOM	3576	N	ASN	C	37	24.711	51.578	39.799	1.00	45.50	7
ATOM	3577	CA	ASN	C	37	25.271	51.124	41.061	1.00	44.80	6
ATOM	3578	CB	ASN	C	37	25.738	49.678	40.919	1.00	44.35	6
ATOM	3579	CG	ASN	C	37	25.685	48.919	42.226	1.00	47.95	6
ATOM	3580	OD1	ASN	C	37	26.077	49.424	43.285	1.00	47.36	8
ATOM	3581	ND2	ASN	C	37	25.209	47.688	42.157	1.00	50.05	7
ATOM	3582	C	ASN	C	37	26.430	51.985	41.573	1.00	44.84	6
ATOM	3583	O	ASN	C	37	27.089	52.678	40.810	1.00	42.36	8
ATOM	3584	N	ILE	C	38	26.654	51.939	42.882	1.00	45.30	7
ATOM	3585	CA	ILE	C	38	27.735	52.671	43.518	1.00	46.27	6
ATOM	3586	CB	ILE	C	38	27.186	53.759	44.434	1.00	44.46	6
ATOM	3587	CG2	ILE	C	38	28.319	54.433	45.178	1.00	42.73	6
ATOM	3588	CG1	ILE	C	38	26.418	54.770	43.584	1.00	42.70	6

ATOM	3589	CD1	ILE	C	38	25.630	55.758	44.343	1.00	40.81	6
ATOM	3590	C	ILE	C	38	28.432	51.585	44.306	1.00	49.67	6
ATOM	3591	O	ILE	C	38	27.890	51.083	45.281	1.00	53.17	8
ATOM	3592	N	LEU	C	39	29.636	51.228	43.872	1.00	51.33	7
ATOM	3593	CA	LEU	C	39	30.378	50.125	44.468	1.00	53.07	6
ATOM	3594	CB	LEU	C	39	31.113	49.384	43.353	1.00	53.88	6
ATOM	3595	CG	LEU	C	39	30.167	49.000	42.215	1.00	55.35	6
ATOM	3596	CD1	LEU	C	39	30.932	48.308	41.115	1.00	54.78	6
ATOM	3597	CD2	LEU	C	39	29.053	48.097	42.760	1.00	54.41	6
ATOM	3598	C	LEU	C	39	31.334	50.367	45.619	1.00	53.89	6
ATOM	3599	O	LEU	C	39	31.386	49.567	46.558	1.00	53.73	8
ATOM	3600	N	GLU	C	40	32.124	51.426	45.536	1.00	54.34	7
ATOM	3601	CA	GLU	C	40	33.058	51.714	46.602	1.00	56.97	6
ATOM	3602	CB	GLU	C	40	34.446	51.211	46.271	1.00	59.79	6
ATOM	3603	CG	GLU	C	40	34.555	49.711	46.147	1.00	67.48	6
ATOM	3604	CD	GLU	C	40	35.996	49.266	45.979	1.00	70.43	6
ATOM	3605	OE1	GLU	C	40	36.647	49.719	44.998	1.00	71.96	8
ATOM	3606	OE2	GLU	C	40	36.471	48.476	46.832	1.00	71.19	8
ATOM	3607	C	GLU	C	40	33.125	53.192	46.823	1.00	57.35	6
ATOM	3608	O	GLU	C	40	33.163	53.975	45.886	1.00	58.85	8
ATOM	3609	N	VAL	C	41	33.132	53.572	48.084	1.00	57.50	7
ATOM	3610	CA	VAL	C	41	33.202	54.964	48.440	1.00	56.50	6
ATOM	3611	CB	VAL	C	41	31.845	55.447	49.000	1.00	57.37	6
ATOM	3612	CG1	VAL	C	41	31.972	56.832	49.567	1.00	56.32	6
ATOM	3613	CG2	VAL	C	41	30.797	55.437	47.894	1.00	57.94	6
ATOM	3614	C	VAL	C	41	34.289	55.098	49.486	1.00	55.27	6
ATOM	3615	O	VAL	C	41	34.502	54.200	50.300	1.00	54.09	8
ATOM	3616	N	ASN	C	42	34.994	56.216	49.433	1.00	55.74	7
ATOM	3617	CA	ASN	C	42	36.053	56.504	50.379	1.00	56.05	6
ATOM	3618	CB	ASN	C	42	37.418	56.169	49.787	1.00	53.93	6
ATOM	3619	CG	ASN	C	42	38.509	56.155	50.833	1.00	53.86	6
ATOM	3620	OD1	ASN	C	42	38.622	57.075	51.634	1.00	54.42	8
ATOM	3621	ND2	ASN	C	42	39.325	55.110	50.828	1.00	54.04	7
ATOM	3622	C	ASN	C	42	35.947	57.994	50.635	1.00	58.42	6
ATOM	3623	O	ASN	C	42	36.322	58.806	49.786	1.00	58.83	8
ATOM	3624	N	GLU	C	43	35.408	58.348	51.801	1.00	60.55	7
ATOM	3625	CA	GLU	C	43	35.242	59.744	52.163	1.00	61.17	6
ATOM	3626	CB	GLU	C	43	34.269	59.874	53.327	1.00	63.37	6
ATOM	3627	CG	GLU	C	43	33.932	61.318	53.646	1.00	67.39	6
ATOM	3628	CD	GLU	C	43	32.773	61.463	54.616	1.00	68.69	6
ATOM	3629	OE1	GLU	C	43	32.494	62.613	55.019	1.00	69.27	8
ATOM	3630	OE2	GLU	C	43	32.142	60.444	54.964	1.00	68.84	8
ATOM	3631	C	GLU	C	43	36.571	60.391	52.524	1.00	60.37	6
ATOM	3632	O	GLU	C	43	36.706	61.611	52.459	1.00	59.71	8
ATOM	3633	N	ILE	C	44	37.544	59.567	52.903	1.00	59.67	7
ATOM	3634	CA	ILE	C	44	38.874	60.051	53.254	1.00	60.12	6
ATOM	3635	CB	ILE	C	44	39.727	58.944	53.908	1.00	60.72	6
ATOM	3636	CG2	ILE	C	44	41.124	59.469	54.194	1.00	61.61	6
ATOM	3637	CG1	ILE	C	44	39.081	58.470	55.206	1.00	62.18	6
ATOM	3638	CD1	ILE	C	44	39.142	59.479	56.325	1.00	63.46	6
ATOM	3639	C	ILE	C	44	39.617	60.514	51.998	1.00	59.74	6
ATOM	3640	O	ILE	C	44	40.255	61.569	51.988	1.00	60.88	8
ATOM	3641	N	THR	C	45	39.540	59.710	50.944	1.00	57.16	7
ATOM	3642	CA	THR	C	45	40.221	60.022	49.698	1.00	54.13	6
ATOM	3643	CB	THR	C	45	40.819	58.743	49.056	1.00	52.62	6
ATOM	3644	OG1	THR	C	45	39.776	57.810	48.773	1.00	52.62	8
ATOM	3645	CG2	THR	C	45	41.812	58.106	49.985	1.00	52.65	6
ATOM	3646	C	THR	C	45	39.325	60.706	48.675	1.00	51.85	6
ATOM	3647	O	THR	C	45	39.801	61.196	47.664	1.00	51.94	8
ATOM	3648	N	ASN	C	46	38.029	60.736	48.933	1.00	51.51	7
ATOM	3649	CA	ASN	C	46	37.106	61.367	48.002	1.00	52.39	6

ATOM	3650	CB	ASN	C	46	37.420	62.856	47.890	1.00	54.02	6
ATOM	3651	CG	ASN	C	46	36.525	63.703	48.766	1.00	56.29	6
ATOM	3652	OD1	ASN	C	46	36.877	64.821	49.132	1.00	59.35	8
ATOM	3653	ND2	ASN	C	46	35.357	63.182	49.093	1.00	53.30	7
ATOM	3654	C	ASN	C	46	37.143	60.711	46.618	1.00	52.56	6
ATOM	3655	O	ASN	C	46	37.269	61.376	45.587	1.00	51.60	8
ATOM	3656	N	GLU	C	47	37.013	59.392	46.610	1.00	51.63	7
ATOM	3657	CA	GLU	C	47	37.023	58.633	45.376	1.00	50.56	6
ATOM	3658	CB	GLU	C	47	38.307	57.805	45.300	1.00	49.50	6
ATOM	3659	CG	GLU	C	47	39.566	58.650	45.210	1.00	49.79	6
ATOM	3660	CD	GLU	C	47	40.823	57.810	45.227	1.00	51.38	6
ATOM	3661	OE1	GLU	C	47	40.741	56.621	44.860	1.00	52.93	8
ATOM	3662	OE2	GLU	C	47	41.892	58.339	45.595	1.00	51.30	8
ATOM	3663	C	GLU	C	47	35.793	57.734	45.314	1.00	48.78	6
ATOM	3664	O	GLU	C	47	35.403	57.133	46.300	1.00	48.46	8
ATOM	3665	N	VAL	C	48	35.178	57.654	44.147	1.00	47.95	7
ATOM	3666	CA	VAL	C	48	33.998	56.834	43.993	1.00	49.71	6
ATOM	3667	CB	VAL	C	48	32.768	57.701	43.736	1.00	50.43	6
ATOM	3668	CG1	VAL	C	48	31.549	56.834	43.578	1.00	53.94	6
ATOM	3669	CG2	VAL	C	48	32.567	58.645	44.869	1.00	52.35	6
ATOM	3670	C	VAL	C	48	34.130	55.838	42.850	1.00	49.77	6
ATOM	3671	O	VAL	C	48	34.686	56.146	41.802	1.00	49.93	8
ATOM	3672	N	ASP	C	49	33.615	54.636	43.068	1.00	49.86	7
ATOM	3673	CA	ASP	C	49	33.646	53.595	42.061	1.00	49.59	6
ATOM	3674	CB	ASP	C	49	34.261	52.331	42.644	1.00	51.71	6
ATOM	3675	CG	ASP	C	49	34.714	51.366	41.580	1.00	51.64	6
ATOM	3676	OD1	ASP	C	49	33.992	51.233	40.581	1.00	50.25	8
ATOM	3677	OD2	ASP	C	49	35.777	50.736	41.748	1.00	51.89	8
ATOM	3678	C	ASP	C	49	32.181	53.382	41.728	1.00	49.00	6
ATOM	3679	O	ASP	C	49	31.437	52.818	42.524	1.00	51.14	8
ATOM	3680	N	VAL	C	50	31.770	53.840	40.551	1.00	48.30	7
ATOM	3681	CA	VAL	C	50	30.374	53.757	40.147	1.00	48.89	6
ATOM	3682	CB	VAL	C	50	29.755	55.185	40.167	1.00	51.49	6
ATOM	3683	CG1	VAL	C	50	30.212	55.964	38.944	1.00	50.49	6
ATOM	3684	CG2	VAL	C	50	28.248	55.120	40.223	1.00	53.32	6
ATOM	3685	C	VAL	C	50	30.130	53.122	38.771	1.00	47.56	6
ATOM	3686	O	VAL	C	50	31.012	53.080	37.928	1.00	49.11	8
ATOM	3687	N	VAL	C	51	28.917	52.621	38.574	1.00	44.81	7
ATOM	3688	CA	VAL	C	51	28.484	52.003	37.324	1.00	43.09	6
ATOM	3689	CB	VAL	C	51	28.003	50.542	37.539	1.00	41.28	6
ATOM	3690	CG1	VAL	C	51	27.355	50.017	36.267	1.00	37.45	6
ATOM	3691	CG2	VAL	C	51	29.157	49.659	37.953	1.00	36.77	6
ATOM	3692	C	VAL	C	51	27.300	52.817	36.781	1.00	44.98	6
ATOM	3693	O	VAL	C	51	26.385	53.163	37.522	1.00	46.72	8
ATOM	3694	N	PHE	C	52	27.299	53.113	35.490	1.00	44.48	7
ATOM	3695	CA	PHE	C	52	26.206	53.883	34.937	1.00	45.00	6
ATOM	3696	CB	PHE	C	52	26.469	55.352	35.210	1.00	44.94	6
ATOM	3697	CG	PHE	C	52	27.729	55.857	34.587	1.00	44.74	6
ATOM	3698	CD1	PHE	C	52	27.735	56.327	33.278	1.00	44.14	6
ATOM	3699	CD2	PHE	C	52	28.921	55.841	35.299	1.00	44.43	6
ATOM	3700	CE1	PHE	C	52	28.908	56.771	32.690	1.00	45.23	6
ATOM	3701	CE2	PHE	C	52	30.102	56.284	34.722	1.00	41.52	6
ATOM	3702	CZ	PHE	C	52	30.098	56.751	33.415	1.00	42.14	6
ATOM	3703	C	PHE	C	52	26.048	53.663	33.443	1.00	47.73	6
ATOM	3704	O	PHE	C	52	26.932	53.102	32.798	1.00	49.84	8
ATOM	3705	N	TRP	C	53	24.918	54.099	32.895	1.00	46.73	7
ATOM	3706	CA	TRP	C	53	24.684	53.985	31.471	1.00	47.02	6
ATOM	3707	CB	TRP	C	53	23.251	53.595	31.175	1.00	46.36	6
ATOM	3708	CG	TRP	C	53	22.915	52.221	31.552	1.00	48.76	6
ATOM	3709	CD2	TRP	C	53	21.615	51.636	31.534	1.00	50.65	6
ATOM	3710	CE2	TRP	C	53	21.748	50.311	32.002	1.00	49.66	6

ATOM	3711	CE3	TRP	C	53	20.342	52.106	31.170	1.00	51.64	6
ATOM	3712	CD1	TRP	C	53	23.765	51.259	32.008	1.00	48.94	6
ATOM	3713	NE1	TRP	C	53	23.073	50.107	32.284	1.00	48.58	7
ATOM	3714	CZ2	TRP	C	53	20.659	49.448	32.120	1.00	50.24	6
ATOM	3715	CZ3	TRP	C	53	19.258	51.250	31.286	1.00	51.60	6
ATOM	3716	CH2	TRP	C	53	19.424	49.935	31.759	1.00	52.14	6
ATOM	3717	C	TRP	C	53	24.940	55.339	30.862	1.00	48.39	6
ATOM	3718	O	TRP	C	53	24.234	56.290	31.156	1.00	50.70	8
ATOM	3719	N	GLN	C	54	25.946	55.429	30.010	1.00	49.71	7
ATOM	3720	CA	GLN	C	54	26.265	56.691	29.378	1.00	50.29	6
ATOM	3721	CB	GLN	C	54	27.759	56.749	29.053	1.00	50.27	6
ATOM	3722	CG	GLN	C	54	28.231	58.111	28.587	1.00	54.00	6
ATOM	3723	CD	GLN	C	54	29.710	58.344	28.853	1.00	55.07	6
ATOM	3724	OE1	GLN	C	54	30.172	58.241	29.988	1.00	53.42	8
ATOM	3725	NE2	GLN	C	54	30.458	58.667	27.805	1.00	57.05	7
ATOM	3726	C	GLN	C	54	25.415	56.797	28.125	1.00	50.70	6
ATOM	3727	O	GLN	C	54	25.886	56.617	27.004	1.00	52.15	8
ATOM	3728	N	GLN	C	55	24.138	57.069	28.345	1.00	51.37	7
ATOM	3729	CA	GLN	C	55	23.169	57.205	27.272	1.00	54.41	6
ATOM	3730	CB	GLN	C	55	21.786	57.326	27.897	1.00	57.18	6
ATOM	3731	CG	GLN	C	55	20.667	57.648	26.948	1.00	64.94	6
ATOM	3732	CD	GLN	C	55	19.313	57.472	27.617	1.00	70.65	6
ATOM	3733	OE1	GLN	C	55	19.154	57.760	28.817	1.00	73.87	8
ATOM	3734	NE2	GLN	C	55	18.325	56.997	26.849	1.00	72.08	7
ATOM	3735	C	GLN	C	55	23.509	58.419	26.396	1.00	53.13	6
ATOM	3736	O	GLN	C	55	23.296	59.569	26.779	1.00	54.85	8
ATOM	3737	N	THR	C	56	24.044	58.148	25.211	1.00	50.27	7
ATOM	3738	CA	THR	C	56	24.455	59.193	24.290	1.00	48.20	6
ATOM	3739	CB	THR	C	56	25.916	59.019	23.905	1.00	47.97	6
ATOM	3740	OG1	THR	C	56	26.693	58.795	25.085	1.00	51.04	8
ATOM	3741	CG2	THR	C	56	26.431	60.243	23.219	1.00	46.01	6
ATOM	3742	C	THR	C	56	23.633	59.162	23.023	1.00	49.71	6
ATOM	3743	O	THR	C	56	23.216	58.095	22.568	1.00	49.78	8
ATOM	3744	N	THR	C	57	23.393	60.340	22.454	1.00	49.24	7
ATOM	3745	CA	THR	C	57	22.619	60.436	21.221	1.00	49.62	6
ATOM	3746	CB	THR	C	57	21.122	60.592	21.501	1.00	49.45	6
ATOM	3747	OG1	THR	C	57	20.640	59.440	22.206	1.00	49.55	8
ATOM	3748	CG2	THR	C	57	20.368	60.722	20.191	1.00	51.01	6
ATOM	3749	C	THR	C	57	23.057	61.608	20.368	1.00	48.68	6
ATOM	3750	O	THR	C	57	23.423	62.649	20.888	1.00	51.05	8
ATOM	3751	N	TRP	C	58	23.033	61.428	19.056	1.00	45.80	7
ATOM	3752	CA	TRP	C	58	23.415	62.487	18.145	1.00	45.33	6
ATOM	3753	CB	TRP	C	58	24.934	62.702	18.146	1.00	44.23	6
ATOM	3754	CG	TRP	C	58	25.733	61.584	17.556	1.00	45.68	6
ATOM	3755	CD2	TRP	C	58	26.221	60.428	18.241	1.00	43.51	6
ATOM	3756	CE2	TRP	C	58	26.896	59.642	17.296	1.00	41.95	6
ATOM	3757	CE3	TRP	C	58	26.150	59.983	19.566	1.00	44.75	6
ATOM	3758	CD1	TRP	C	58	26.120	61.453	16.264	1.00	41.99	6
ATOM	3759	NE1	TRP	C	58	26.818	60.292	16.097	1.00	43.07	7
ATOM	3760	CZ2	TRP	C	58	27.498	58.436	17.625	1.00	42.44	6
ATOM	3761	CZ3	TRP	C	58	26.748	58.778	19.894	1.00	45.66	6
ATOM	3762	CH2	TRP	C	58	27.414	58.020	18.926	1.00	44.08	6
ATOM	3763	C	TRP	C	58	22.915	62.107	16.772	1.00	46.80	6
ATOM	3764	O	TRP	C	58	22.315	61.054	16.603	1.00	45.26	8
ATOM	3765	N	SER	C	59	23.157	62.959	15.788	1.00	50.21	7
ATOM	3766	CA	SER	C	59	22.663	62.684	14.452	1.00	53.47	6
ATOM	3767	CB	SER	C	59	21.536	63.657	14.128	1.00	54.42	6
ATOM	3768	OG	SER	C	59	20.707	63.146	13.104	1.00	59.88	8
ATOM	3769	C	SER	C	59	23.733	62.752	13.376	1.00	54.85	6
ATOM	3770	O	SER	C	59	24.541	63.682	13.343	1.00	54.12	8
ATOM	3771	N	ASP	C	60	23.727	61.745	12.503	1.00	57.21	7

ATOM	3772	CA	ASP	C	60	24.677	61.646	11.396	1.00	59.27	6
ATOM	3773	CB	ASP	C	60	25.680	60.517	11.650	1.00	59.62	6
ATOM	3774	CG	ASP	C	60	26.786	60.472	10.615	1.00	61.35	6
ATOM	3775	OD1	ASP	C	60	26.553	60.894	9.462	1.00	60.03	8
ATOM	3776	OD2	ASP	C	60	27.890	59.996	10.957	1.00	62.69	8
ATOM	3777	C	ASP	C	60	23.842	61.317	10.172	1.00	61.10	6
ATOM	3778	O	ASP	C	60	23.493	60.163	9.940	1.00	61.72	8
ATOM	3779	N	ARG	C	61	23.509	62.338	9.396	1.00	63.66	7
ATOM	3780	CA	ARG	C	61	22.689	62.153	8.201	1.00	65.73	6
ATOM	3781	CB	ARG	C	61	22.276	63.516	7.628	1.00	68.89	6
ATOM	3782	CG	ARG	C	61	21.106	64.221	8.348	1.00	74.08	6
ATOM	3783	CD	ARG	C	61	20.624	65.417	7.517	1.00	79.55	6
ATOM	3784	NE	ARG	C	61	19.438	66.085	8.059	1.00	84.63	7
ATOM	3785	CZ	ARG	C	61	18.810	67.101	7.457	1.00	87.07	6
ATOM	3786	NH1	ARG	C	61	19.257	67.572	6.291	1.00	88.09	7
ATOM	3787	NH2	ARG	C	61	17.721	67.636	8.005	1.00	87.40	7
ATOM	3788	C	ARG	C	61	23.322	61.310	7.083	1.00	64.92	6
ATOM	3789	O	ARG	C	61	22.604	60.783	6.225	1.00	65.71	8
ATOM	3790	N	THR	C	62	24.648	61.176	7.078	1.00	62.18	7
ATOM	3791	CA	THR	C	62	25.301	60.393	6.038	1.00	60.64	6
ATOM	3792	CB	THR	C	62	26.840	60.568	6.056	1.00	61.65	6
ATOM	3793	OG1	THR	C	62	27.389	59.999	7.256	1.00	63.35	8
ATOM	3794	CG2	THR	C	62	27.207	62.045	5.983	1.00	61.52	6
ATOM	3795	C	THR	C	62	24.970	58.917	6.211	1.00	60.11	6
ATOM	3796	O	THR	C	62	25.303	58.095	5.354	1.00	61.77	8
ATOM	3797	N	LEU	C	63	24.313	58.592	7.321	1.00	58.17	7
ATOM	3798	CA	LEU	C	63	23.919	57.219	7.621	1.00	57.53	6
ATOM	3799	CB	LEU	C	63	24.079	56.929	9.111	1.00	54.69	6
ATOM	3800	CG	LEU	C	63	25.442	57.142	9.750	1.00	55.50	6
ATOM	3801	CD1	LEU	C	63	25.327	56.938	11.263	1.00	54.27	6
ATOM	3802	CD2	LEU	C	63	26.449	56.178	9.139	1.00	55.93	6
ATOM	3803	C	LEU	C	63	22.455	56.977	7.242	1.00	58.42	6
ATOM	3804	O	LEU	C	63	22.010	55.830	7.147	1.00	58.94	8
ATOM	3805	N	ALA	C	64	21.707	58.055	7.037	1.00	58.80	7
ATOM	3806	CA	ALA	C	64	20.291	57.928	6.703	1.00	61.86	6
ATOM	3807	CB	ALA	C	64	19.666	59.310	6.522	1.00	61.89	6
ATOM	3808	C	ALA	C	64	20.081	57.087	5.450	1.00	63.09	6
ATOM	3809	O	ALA	C	64	20.840	57.179	4.481	1.00	63.27	8
ATOM	3810	N	TRP	C	65	19.055	56.249	5.485	1.00	65.02	7
ATOM	3811	CA	TRP	C	65	18.749	55.381	4.355	1.00	66.31	6
ATOM	3812	CB	TRP	C	65	19.329	53.989	4.600	1.00	64.14	6
ATOM	3813	CG	TRP	C	65	18.597	53.208	5.687	1.00	62.22	6
ATOM	3814	CD2	TRP	C	65	18.962	53.110	7.074	1.00	57.97	6
ATOM	3815	CE2	TRP	C	65	18.025	52.247	7.694	1.00	56.42	6
ATOM	3816	CE3	TRP	C	65	19.985	53.666	7.848	1.00	55.52	6
ATOM	3817	CD1	TRP	C	65	17.475	52.430	5.533	1.00	60.23	6
ATOM	3818	NE1	TRP	C	65	17.131	51.849	6.734	1.00	57.79	7
ATOM	3819	CZ2	TRP	C	65	18.088	51.926	9.049	1.00	55.30	6
ATOM	3820	CZ3	TRP	C	65	20.047	53.350	9.195	1.00	56.61	6
ATOM	3821	CH2	TRP	C	65	19.102	52.484	9.784	1.00	56.47	6
ATOM	3822	C	TRP	C	65	17.238	55.287	4.252	1.00	68.58	6
ATOM	3823	O	TRP	C	65	16.540	55.365	5.268	1.00	67.72	8
ATOM	3824	N	ASN	C	66	16.728	55.113	3.037	1.00	72.17	7
ATOM	3825	CA	ASN	C	66	15.283	55.011	2.882	1.00	75.21	6
ATOM	3826	CB	ASN	C	66	14.863	55.013	1.408	1.00	77.34	6
ATOM	3827	CG	ASN	C	66	13.355	55.190	1.244	1.00	79.16	6
ATOM	3828	OD1	ASN	C	66	12.845	55.261	0.119	1.00	80.81	8
ATOM	3829	ND2	ASN	C	66	12.633	55.267	2.374	1.00	77.07	7
ATOM	3830	C	ASN	C	66	14.802	53.730	3.532	1.00	74.77	6
ATOM	3831	O	ASN	C	66	15.431	52.675	3.383	1.00	75.31	8
ATOM	3832	N	SER	C	67	13.685	53.816	4.244	1.00	73.52	7

ATOM	3833	CA	SER	C	67	13.166	52.647	4.920	1.00	73.52	6
ATOM	3834	CB	SER	C	67	13.451	52.759	6.411	1.00	72.63	6
ATOM	3835	OG	SER	C	67	12.985	53.994	6.914	1.00	70.04	8
ATOM	3836	C	SER	C	67	11.684	52.469	4.702	1.00	75.29	6
ATOM	3837	O	SER	C	67	11.010	51.788	5.493	1.00	75.31	8
ATOM	3838	N	SER	C	68	11.165	53.077	3.639	1.00	77.57	7
ATOM	3839	CA	SER	C	68	9.739	52.957	3.356	1.00	78.39	6
ATOM	3840	CB	SER	C	68	9.327	53.874	2.187	1.00	77.79	6
ATOM	3841	OG	SER	C	68	10.010	53.570	0.983	1.00	77.16	8
ATOM	3842	C	SER	C	68	9.398	51.498	3.051	1.00	78.91	6
ATOM	3843	O	SER	C	68	8.242	51.165	2.802	1.00	78.88	8
ATOM	3844	N	HIS	C	69	10.415	50.634	3.090	1.00	80.17	7
ATOM	3845	CA	HIS	C	69	10.252	49.197	2.824	1.00	81.55	6
ATOM	3846	CB	HIS	C	69	10.307	48.935	1.319	1.00	84.67	6
ATOM	3847	CG	HIS	C	69	9.327	49.755	0.542	1.00	88.75	6
ATOM	3848	CD2	HIS	C	69	8.119	49.436	0.014	1.00	89.38	6
ATOM	3849	ND1	HIS	C	69	9.479	51.115	0.359	1.00	89.98	7
ATOM	3850	CE1	HIS	C	69	8.405	51.600	-0.239	1.00	91.29	6
ATOM	3851	NE2	HIS	C	69	7.564	50.602	-0.458	1.00	91.72	7
ATOM	3852	C	HIS	C	69	11.363	48.406	3.514	1.00	80.62	6
ATOM	3853	O	HIS	C	69	11.740	47.318	3.072	1.00	79.15	8
ATOM	3854	N	SER	C	70	11.867	48.961	4.614	1.00	79.62	7
ATOM	3855	CA	SER	C	70	12.950	48.341	5.355	1.00	77.30	6
ATOM	3856	CB	SER	C	70	14.262	48.818	4.739	1.00	77.47	6
ATOM	3857	OG	SER	C	70	14.107	48.991	3.336	1.00	74.00	8
ATOM	3858	C	SER	C	70	12.880	48.746	6.836	1.00	76.56	6
ATOM	3859	O	SER	C	70	12.168	49.686	7.193	1.00	77.11	8
ATOM	3860	N	PRO	C	71	13.587	48.014	7.726	1.00	76.29	7
ATOM	3861	CD	PRO	C	71	14.305	46.733	7.544	1.00	75.52	6
ATOM	3862	CA	PRO	C	71	13.538	48.401	9.143	1.00	74.74	6
ATOM	3863	CB	PRO	C	71	14.366	47.322	9.843	1.00	75.26	6
ATOM	3864	CG	PRO	C	71	14.241	46.124	8.936	1.00	75.64	6
ATOM	3865	C	PRO	C	71	14.202	49.771	9.235	1.00	73.61	6
ATOM	3866	O	PRO	C	71	15.042	50.125	8.401	1.00	72.22	8
ATOM	3867	N	ASP	C	72	13.828	50.537	10.247	1.00	72.60	7
ATOM	3868	CA	ASP	C	72	14.377	51.869	10.414	1.00	70.96	6
ATOM	3869	CB	ASP	C	72	13.277	52.795	10.899	1.00	75.25	6
ATOM	3870	CG	ASP	C	72	11.919	52.353	10.415	1.00	78.33	6
ATOM	3871	OD1	ASP	C	72	11.633	52.512	9.199	1.00	79.88	8
ATOM	3872	OD2	ASP	C	72	11.150	51.821	11.256	1.00	79.56	8
ATOM	3873	C	ASP	C	72	15.519	51.835	11.411	1.00	68.36	6
ATOM	3874	O	ASP	C	72	16.046	52.887	11.799	1.00	66.88	8
ATOM	3875	N	GLN	C	73	15.883	50.625	11.838	1.00	63.81	7
ATOM	3876	CA	GLN	C	73	17.001	50.485	12.756	1.00	61.20	6
ATOM	3877	CB	GLN	C	73	16.537	50.494	14.191	1.00	61.12	6
ATOM	3878	CG	GLN	C	73	16.121	51.802	14.749	1.00	62.71	6
ATOM	3879	CD	GLN	C	73	15.665	51.603	16.163	1.00	64.60	6
ATOM	3880	OE1	GLN	C	73	14.784	50.779	16.421	1.00	67.49	8
ATOM	3881	NE2	GLN	C	73	16.267	52.329	17.099	1.00	66.00	7
ATOM	3882	C	GLN	C	73	17.842	49.232	12.583	1.00	59.70	6
ATOM	3883	O	GLN	C	73	17.350	48.167	12.213	1.00	61.26	8
ATOM	3884	N	VAL	C	74	19.122	49.369	12.893	1.00	56.05	7
ATOM	3885	CA	VAL	C	74	20.050	48.260	12.825	1.00	52.11	6
ATOM	3886	CB	VAL	C	74	20.736	48.177	11.454	1.00	52.42	6
ATOM	3887	CG1	VAL	C	74	19.732	47.788	10.397	1.00	51.61	6
ATOM	3888	CG2	VAL	C	74	21.376	49.507	11.112	1.00	52.96	6
ATOM	3889	C	VAL	C	74	21.095	48.498	13.891	1.00	50.29	6
ATOM	3890	O	VAL	C	74	21.277	49.626	14.332	1.00	49.79	8
ATOM	3891	N	SER	C	75	21.754	47.431	14.323	1.00	48.56	7
ATOM	3892	CA	SER	C	75	22.809	47.533	15.318	1.00	45.56	6
ATOM	3893	CB	SER	C	75	22.784	46.337	16.257	1.00	43.40	6

ATOM	3894	OG	SER	C	75	21.818	46.521	17.269	1.00	43.99	8
ATOM	3895	C	SER	C	75	24.146	47.611	14.595	1.00	44.84	6
ATOM	3896	O	SER	C	75	24.519	46.703	13.858	1.00	47.60	8
ATOM	3897	N	VAL	C	76	24.858	48.712	14.811	1.00	43.51	7
ATOM	3898	CA	VAL	C	76	26.140	48.941	14.165	1.00	42.84	6
ATOM	3899	CB	VAL	C	76	26.122	50.273	13.412	1.00	41.76	6
ATOM	3900	CG1	VAL	C	76	27.441	50.504	12.741	1.00	42.71	6
ATOM	3901	CG2	VAL	C	76	25.003	50.279	12.403	1.00	40.70	6
ATOM	3902	C	VAL	C	76	27.294	48.961	15.153	1.00	42.64	6
ATOM	3903	O	VAL	C	76	27.194	49.542	16.227	1.00	45.77	8
ATOM	3904	N	PRO	C	77	28.409	48.313	14.812	1.00	41.78	7
ATOM	3905	CD	PRO	C	77	28.644	47.345	13.737	1.00	41.15	6
ATOM	3906	CA	PRO	C	77	29.532	48.326	15.748	1.00	41.64	6
ATOM	3907	CB	PRO	C	77	30.527	47.370	15.108	1.00	40.47	6
ATOM	3908	CG	PRO	C	77	29.654	46.432	14.379	1.00	42.43	6
ATOM	3909	C	PRO	C	77	30.074	49.746	15.860	1.00	41.29	6
ATOM	3910	O	PRO	C	77	30.123	50.489	14.881	1.00	38.61	8
ATOM	3911	N	ILE	C	78	30.469	50.111	17.070	1.00	41.82	7
ATOM	3912	CA	ILE	C	78	31.000	51.433	17.359	1.00	41.93	6
ATOM	3913	CB	ILE	C	78	31.439	51.489	18.837	1.00	42.16	6
ATOM	3914	CG2	ILE	C	78	32.370	52.634	19.107	1.00	42.14	6
ATOM	3915	CG1	ILE	C	78	30.193	51.601	19.696	1.00	44.77	6
ATOM	3916	CD1	ILE	C	78	29.251	52.676	19.216	1.00	44.16	6
ATOM	3917	C	ILE	C	78	32.149	51.813	16.450	1.00	42.57	6
ATOM	3918	O	ILE	C	78	32.287	52.963	16.063	1.00	45.18	8
ATOM	3919	N	SER	C	79	32.963	50.829	16.100	1.00	43.18	7
ATOM	3920	CA	SER	C	79	34.120	51.030	15.241	1.00	43.52	6
ATOM	3921	CB	SER	C	79	34.969	49.768	15.242	1.00	43.74	6
ATOM	3922	OG	SER	C	79	34.189	48.637	14.910	1.00	43.50	8
ATOM	3923	C	SER	C	79	33.810	51.415	13.804	1.00	43.41	6
ATOM	3924	O	SER	C	79	34.698	51.838	13.082	1.00	44.10	8
ATOM	3925	N	SER	C	80	32.562	51.264	13.380	1.00	43.62	7
ATOM	3926	CA	SER	C	80	32.180	51.604	12.012	1.00	44.83	6
ATOM	3927	CB	SER	C	80	31.260	50.534	11.441	1.00	44.21	6
ATOM	3928	OG	SER	C	80	31.915	49.284	11.380	1.00	52.55	8
ATOM	3929	C	SER	C	80	31.482	52.956	11.908	1.00	46.57	6
ATOM	3930	O	SER	C	80	31.050	53.355	10.829	1.00	46.16	8
ATOM	3931	N	LEU	C	81	31.366	53.649	13.035	1.00	46.49	7
ATOM	3932	CA	LEU	C	81	30.720	54.952	13.080	1.00	45.86	6
ATOM	3933	CB	LEU	C	81	29.467	54.891	13.935	1.00	45.00	6
ATOM	3934	CG	LEU	C	81	28.421	53.827	13.653	1.00	46.58	6
ATOM	3935	CD1	LEU	C	81	27.488	53.701	14.839	1.00	45.04	6
ATOM	3936	CD2	LEU	C	81	27.667	54.198	12.405	1.00	47.69	6
ATOM	3937	C	LEU	C	81	31.645	55.973	13.718	1.00	46.18	6
ATOM	3938	O	LEU	C	81	32.636	55.613	14.355	1.00	50.36	8
ATOM	3939	N	TRP	C	82	31.323	57.249	13.536	1.00	43.58	7
ATOM	3940	CA	TRP	C	82	32.086	58.303	14.161	1.00	39.79	6
ATOM	3941	CB	TRP	C	82	31.860	59.639	13.463	1.00	41.96	6
ATOM	3942	CG	TRP	C	82	32.342	60.817	14.278	1.00	44.12	6
ATOM	3943	CD2	TRP	C	82	31.577	61.569	15.230	1.00	44.19	6
ATOM	3944	CE2	TRP	C	82	32.453	62.504	15.823	1.00	43.39	6
ATOM	3945	CE3	TRP	C	82	30.234	61.540	15.645	1.00	44.58	6
ATOM	3946	CD1	TRP	C	82	33.611	61.318	14.327	1.00	43.74	6
ATOM	3947	NE1	TRP	C	82	33.686	62.327	15.252	1.00	44.54	7
ATOM	3948	CZ2	TRP	C	82	32.033	63.405	16.809	1.00	42.68	6
ATOM	3949	CZ3	TRP	C	82	29.818	62.430	16.623	1.00	43.22	6
ATOM	3950	CH2	TRP	C	82	30.717	63.352	17.195	1.00	43.77	6
ATOM	3951	C	TRP	C	82	31.426	58.348	15.514	1.00	40.00	6
ATOM	3952	O	TRP	C	82	30.219	58.174	15.619	1.00	39.36	8
ATOM	3953	N	VAL	C	83	32.201	58.574	16.557	1.00	40.23	7
ATOM	3954	CA	VAL	C	83	31.626	58.649	17.887	1.00	39.34	6

ATOM	3955	CB	VAL	C	83	31.891	57.325	18.657	1.00	38.82	6
ATOM	3956	CG1	VAL	C	83	31.587	57.479	20.109	1.00	39.50	6
ATOM	3957	CG2	VAL	C	83	31.021	56.219	18.087	1.00	38.81	6
ATOM	3958	C	VAL	C	83	32.205	59.860	18.624	1.00	40.30	6
ATOM	3959	O	VAL	C	83	33.365	60.222	18.428	1.00	41.45	8
ATOM	3960	N	PRO	C	84	31.386	60.528	19.451	1.00	38.82	7
ATOM	3961	CD	PRO	C	84	29.948	60.288	19.644	1.00	40.83	6
ATOM	3962	CA	PRO	C	84	31.812	61.698	20.220	1.00	36.19	6
ATOM	3963	CB	PRO	C	84	30.580	62.022	21.058	1.00	37.66	6
ATOM	3964	CG	PRO	C	84	29.479	61.609	20.201	1.00	39.39	6
ATOM	3965	C	PRO	C	84	32.999	61.358	21.098	1.00	34.25	6
ATOM	3966	O	PRO	C	84	32.987	60.351	21.788	1.00	35.16	8
ATOM	3967	N	ASP	C	85	34.016	62.206	21.093	1.00	33.39	7
ATOM	3968	CA	ASP	C	85	35.192	61.949	21.909	1.00	34.67	6
ATOM	3969	CB	ASP	C	85	36.423	62.588	21.270	1.00	35.95	6
ATOM	3970	CG	ASP	C	85	36.260	64.056	21.046	1.00	35.70	6
ATOM	3971	OD1	ASP	C	85	35.159	64.468	20.662	1.00	34.85	8
ATOM	3972	OD2	ASP	C	85	37.234	64.798	21.238	1.00	38.52	8
ATOM	3973	C	ASP	C	85	35.005	62.452	23.326	1.00	36.34	6
ATOM	3974	O	ASP	C	85	35.806	63.229	23.841	1.00	39.41	8
ATOM	3975	N	LEU	C	86	33.941	61.978	23.962	1.00	36.11	7
ATOM	3976	CA	LEU	C	86	33.609	62.385	25.315	1.00	36.00	6
ATOM	3977	CB	LEU	C	86	32.208	61.904	25.678	1.00	35.07	6
ATOM	3978	CG	LEU	C	86	31.089	62.464	24.806	1.00	36.71	6
ATOM	3979	CD1	LEU	C	86	29.752	61.912	25.240	1.00	31.87	6
ATOM	3980	CD2	LEU	C	86	31.112	63.974	24.910	1.00	35.41	6
ATOM	3981	C	LEU	C	86	34.585	61.870	26.337	1.00	36.89	6
ATOM	3982	O	LEU	C	86	35.147	60.795	26.189	1.00	38.19	8
ATOM	3983	N	ALA	C	87	34.773	62.648	27.391	1.00	38.71	7
ATOM	3984	CA	ALA	C	87	35.672	62.268	28.461	1.00	38.06	6
ATOM	3985	CB	ALA	C	87	37.045	62.838	28.200	1.00	35.59	6
ATOM	3986	C	ALA	C	87	35.119	62.799	29.772	1.00	38.10	6
ATOM	3987	O	ALA	C	87	34.586	63.891	29.815	1.00	37.91	8
ATOM	3988	N	ALA	C	88	35.217	62.013	30.833	1.00	39.52	7
ATOM	3989	CA	ALA	C	88	34.756	62.448	32.147	1.00	40.05	6
ATOM	3990	CB	ALA	C	88	34.356	61.250	33.005	1.00	40.30	6
ATOM	3991	C	ALA	C	88	35.939	63.169	32.771	1.00	41.63	6
ATOM	3992	O	ALA	C	88	36.912	62.545	33.195	1.00	41.71	8
ATOM	3993	N	TYR	C	89	35.852	64.492	32.799	1.00	42.71	7
ATOM	3994	CA	TYR	C	89	36.904	65.350	33.330	1.00	41.60	6
ATOM	3995	CB	TYR	C	89	36.368	66.775	33.459	1.00	43.41	6
ATOM	3996	CG	TYR	C	89	35.976	67.422	32.149	1.00	48.68	6
ATOM	3997	CD1	TYR	C	89	35.321	68.653	32.129	1.00	51.90	6
ATOM	3998	CE1	TYR	C	89	34.991	69.284	30.920	1.00	53.01	6
ATOM	3999	CD2	TYR	C	89	36.290	66.830	30.929	1.00	48.32	6
ATOM	4000	CE2	TYR	C	89	35.966	67.449	29.726	1.00	52.45	6
ATOM	4001	CZ	TYR	C	89	35.318	68.678	29.730	1.00	53.45	6
ATOM	4002	OH	TYR	C	89	35.017	69.305	28.545	1.00	56.75	8
ATOM	4003	C	TYR	C	89	37.527	64.914	34.657	1.00	40.68	6
ATOM	4004	O	TYR	C	89	38.727	65.075	34.863	1.00	39.21	8
ATOM	4005	N	ASN	C	90	36.725	64.364	35.562	1.00	39.53	7
ATOM	4006	CA	ASN	C	90	37.265	63.952	36.848	1.00	39.15	6
ATOM	4007	CB	ASN	C	90	36.476	64.603	37.989	1.00	38.99	6
ATOM	4008	CG	ASN	C	90	34.995	64.290	37.944	1.00	38.22	6
ATOM	4009	OD1	ASN	C	90	34.355	64.378	36.902	1.00	37.33	8
ATOM	4010	ND2	ASN	C	90	34.443	63.939	39.090	1.00	39.59	7
ATOM	4011	C	ASN	C	90	37.343	62.448	37.033	1.00	41.22	6
ATOM	4012	O	ASN	C	90	37.354	61.946	38.153	1.00	42.78	8
ATOM	4013	N	ALA	C	91	37.400	61.733	35.915	1.00	42.37	7
ATOM	4014	CA	ALA	C	91	37.528	60.292	35.928	1.00	40.71	6
ATOM	4015	CB	ALA	C	91	37.346	59.733	34.521	1.00	41.88	6

ATOM	4016	C	ALA	C	91	38.939	60.033	36.435	1.00	39.96	6
ATOM	4017	O	ALA	C	91	39.898	60.664	36.007	1.00	35.60	8
ATOM	4018	N	ILE	C	92	39.040	59.093	37.356	1.00	41.49	7
ATOM	4019	CA	ILE	C	92	40.292	58.731	37.993	1.00	43.20	6
ATOM	4020	CB	ILE	C	92	40.020	58.594	39.511	1.00	47.77	6
ATOM	4021	CG2	ILE	C	92	39.923	57.130	39.921	1.00	48.36	6
ATOM	4022	CG1	ILE	C	92	41.093	59.293	40.316	1.00	50.98	6
ATOM	4023	CD1	ILE	C	92	40.903	59.036	41.812	1.00	55.36	6
ATOM	4024	C	ILE	C	92	40.861	57.416	37.403	1.00	41.81	6
ATOM	4025	O	ILE	C	92	41.973	56.992	37.720	1.00	40.19	8
ATOM	4026	N	SER	C	93	40.080	56.781	36.541	1.00	39.24	7
ATOM	4027	CA	SER	C	93	40.470	55.534	35.913	1.00	39.09	6
ATOM	4028	CB	SER	C	93	39.892	54.356	36.685	1.00	39.19	6
ATOM	4029	OG	SER	C	93	38.479	54.310	36.541	1.00	39.34	8
ATOM	4030	C	SER	C	93	39.839	55.579	34.546	1.00	37.69	6
ATOM	4031	O	SER	C	93	38.987	56.404	34.311	1.00	39.27	8
ATOM	4032	N	LYS	C	94	40.251	54.717	33.632	1.00	37.58	7
ATOM	4033	CA	LYS	C	94	39.612	54.737	32.330	1.00	40.65	6
ATOM	4034	CB	LYS	C	94	40.560	54.256	31.228	1.00	41.66	6
ATOM	4035	CG	LYS	C	94	41.383	53.024	31.520	1.00	46.32	6
ATOM	4036	CD	LYS	C	94	42.502	52.902	30.485	1.00	48.62	6
ATOM	4037	CE	LYS	C	94	41.962	53.091	29.069	1.00	47.90	6
ATOM	4038	NZ	LYS	C	94	42.999	52.929	28.024	1.00	48.05	7
ATOM	4039	C	LYS	C	94	38.321	53.926	32.359	1.00	40.78	6
ATOM	4040	O	LYS	C	94	38.102	53.094	33.234	1.00	42.52	8
ATOM	4041	N	PRO	C	95	37.434	54.178	31.404	1.00	41.55	7
ATOM	4042	CD	PRO	C	95	37.555	55.150	30.312	1.00	42.12	6
ATOM	4043	CA	PRO	C	95	36.153	53.479	31.335	1.00	41.34	6
ATOM	4044	CB	PRO	C	95	35.439	54.166	30.177	1.00	41.08	6
ATOM	4045	CG	PRO	C	95	36.125	55.476	30.058	1.00	42.87	6
ATOM	4046	C	PRO	C	95	36.256	52.000	31.102	1.00	40.86	6
ATOM	4047	O	PRO	C	95	36.941	51.563	30.189	1.00	41.65	8
ATOM	4048	N	GLU	C	96	35.581	51.228	31.940	1.00	40.55	7
ATOM	4049	CA	GLU	C	96	35.560	49.791	31.766	1.00	41.10	6
ATOM	4050	CB	GLU	C	96	35.684	49.050	33.104	1.00	43.71	6
ATOM	4051	CG	GLU	C	96	35.762	47.521	32.954	1.00	49.85	6
ATOM	4052	CD	GLU	C	96	35.912	46.768	34.286	1.00	54.35	6
ATOM	4053	OE1	GLU	C	96	36.282	47.404	35.302	1.00	58.62	8
ATOM	4054	OE2	GLU	C	96	35.682	45.534	34.316	1.00	52.48	8
ATOM	4055	C	GLU	C	96	34.190	49.553	31.168	1.00	39.91	6
ATOM	4056	O	GLU	C	96	33.200	49.478	31.894	1.00	40.62	8
ATOM	4057	N	VAL	C	97	34.133	49.483	29.841	1.00	35.73	7
ATOM	4058	CA	VAL	C	97	32.876	49.249	29.153	1.00	34.27	6
ATOM	4059	CB	VAL	C	97	33.006	49.541	27.660	1.00	31.66	6
ATOM	4060	CG1	VAL	C	97	31.686	49.333	26.968	1.00	34.09	6
ATOM	4061	CG2	VAL	C	97	33.437	50.963	27.470	1.00	30.22	6
ATOM	4062	C	VAL	C	97	32.481	47.801	29.382	1.00	34.55	6
ATOM	4063	O	VAL	C	97	33.167	46.891	28.949	1.00	35.63	8
ATOM	4064	N	LEU	C	98	31.362	47.607	30.072	1.00	35.35	7
ATOM	4065	CA	LEU	C	98	30.868	46.286	30.433	1.00	34.12	6
ATOM	4066	CB	LEU	C	98	30.098	46.377	31.752	1.00	33.63	6
ATOM	4067	CG	LEU	C	98	30.741	47.049	32.961	1.00	35.44	6
ATOM	4068	CD1	LEU	C	98	29.694	47.352	33.989	1.00	37.77	6
ATOM	4069	CD2	LEU	C	98	31.806	46.166	33.538	1.00	34.23	6
ATOM	4070	C	LEU	C	98	29.965	45.641	29.404	1.00	36.94	6
ATOM	4071	O	LEU	C	98	29.640	44.464	29.524	1.00	39.49	8
ATOM	4072	N	THR	C	99	29.567	46.398	28.389	1.00	36.94	7
ATOM	4073	CA	THR	C	99	28.642	45.881	27.393	1.00	36.72	6
ATOM	4074	CB	THR	C	99	27.317	46.674	27.450	1.00	36.81	6
ATOM	4075	OG1	THR	C	99	27.574	48.076	27.259	1.00	40.25	8
ATOM	4076	CG2	THR	C	99	26.648	46.474	28.792	1.00	34.14	6

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ATOM   4077  C   THR C  99      29.154  45.895  25.965  1.00 37.65   6
ATOM   4078  O   THR C  99      30.147  46.549  25.664  1.00 37.93   8
ATOM   4079  N   PRO C 100      28.497  45.134  25.073  1.00 37.89   7
ATOM   4080  CD  PRO C 100      27.443  44.145  25.364  1.00 40.71   6
ATOM   4081  CA  PRO C 100      28.874  45.065  23.667  1.00 37.03   6
ATOM   4082  CB  PRO C 100      27.716  44.298  23.046  1.00 37.46   6
ATOM   4083  CG  PRO C 100      27.402  43.316  24.094  1.00 38.27   6
ATOM   4084  C   PRO C 100      28.963  46.476  23.139  1.00 38.41   6
ATOM   4085  O   PRO C 100      28.082  47.297  23.390  1.00 39.24   8
ATOM   4086  N   GLN C 101      30.026  46.772  22.412  1.00 38.06   7
ATOM   4087  CA  GLN C 101      30.169  48.113  21.893  1.00 39.24   6
ATOM   4088  CB  GLN C 101      31.639  48.479  21.827  1.00 38.35   6
ATOM   4089  CG  GLN C 101      32.140  48.846  23.195  1.00 43.58   6
ATOM   4090  CD  GLN C 101      33.633  48.822  23.291  1.00 47.06   6
ATOM   4091  OE1 GLN C 101      34.315  49.497  22.533  1.00 51.61   8
ATOM   4092  NE2 GLN C 101      34.160  48.041  24.227  1.00 48.13   7
ATOM   4093  C   GLN C 101      29.471  48.333  20.571  1.00 38.37   6
ATOM   4094  O   GLN C 101      30.095  48.620  19.554  1.00 36.55   8
ATOM   4095  N   LEU C 102      28.148  48.198  20.627  1.00 40.04   7
ATOM   4096  CA  LEU C 102      27.263  48.373  19.478  1.00 40.82   6
ATOM   4097  CB  LEU C 102      26.376  47.143  19.289  1.00 38.65   6
ATOM   4098  CG  LEU C 102      27.061  45.791  19.163  1.00 40.16   6
ATOM   4099  CD1 LEU C 102      26.015  44.708  18.994  1.00 37.69   6
ATOM   4100  CD2 LEU C 102      27.991  45.815  17.981  1.00 39.89   6
ATOM   4101  C   LEU C 102      26.362  49.583  19.685  1.00 40.48   6
ATOM   4102  O   LEU C 102      25.940  49.880  20.800  1.00 39.50   8
ATOM   4103  N   ALA C 103      26.072  50.280  18.603  1.00 40.58   7
ATOM   4104  CA  ALA C 103      25.203  51.434  18.674  1.00 42.17   6
ATOM   4105  CB  ALA C 103      25.879  52.646  18.054  1.00 43.90   6
ATOM   4106  C   ALA C 103      23.950  51.087  17.904  1.00 43.55   6
ATOM   4107  O   ALA C 103      23.905  50.092  17.189  1.00 44.89   8
ATOM   4108  N   ARG C 104      22.930  51.916  18.048  1.00 45.38   7
ATOM   4109  CA  ARG C 104      21.674  51.689  17.359  1.00 46.54   6
ATOM   4110  CB  ARG C 104      20.549  51.665  18.381  1.00 46.10   6
ATOM   4111  CG  ARG C 104      19.292  51.040  17.879  1.00 47.91   6
ATOM   4112  CD  ARG C 104      19.457  49.560  17.559  1.00 45.29   6
ATOM   4113  NE  ARG C 104      18.188  49.059  17.035  1.00 46.68   7
ATOM   4114  CZ  ARG C 104      17.927  47.792  16.761  1.00 46.66   6
ATOM   4115  NH1 ARG C 104      18.850  46.866  16.954  1.00 47.05   7
ATOM   4116  NH2 ARG C 104      16.733  47.452  16.308  1.00 48.97   7
ATOM   4117  C   ARG C 104      21.491  52.830  16.367  1.00 46.82   6
ATOM   4118  O   ARG C 104      21.550  53.999  16.738  1.00 49.29   8
ATOM   4119  N   VAL C 105      21.296  52.501  15.098  1.00 47.65   7
ATOM   4120  CA  VAL C 105      21.138  53.543  14.092  1.00 47.99   6
ATOM   4121  CB  VAL C 105      22.200  53.426  12.980  1.00 46.29   6
ATOM   4122  CG1 VAL C 105      22.080  54.588  12.021  1.00 44.96   6
ATOM   4123  CG2 VAL C 105      23.583  53.386  13.580  1.00 42.95   6
ATOM   4124  C   VAL C 105      19.769  53.519  13.444  1.00 50.20   6
ATOM   4125  O   VAL C 105      19.340  52.497  12.904  1.00 50.01   8
ATOM   4126  N   VAL C 106      19.097  54.666  13.506  1.00 51.90   7
ATOM   4127  CA  VAL C 106      17.767  54.836  12.933  1.00 53.33   6
ATOM   4128  CB  VAL C 106      16.947  55.840  13.758  1.00 51.93   6
ATOM   4129  CG1 VAL C 106      15.503  55.825  13.306  1.00 49.94   6
ATOM   4130  CG2 VAL C 106      17.060  55.504  15.222  1.00 50.56   6
ATOM   4131  C   VAL C 106      17.899  55.347  11.497  1.00 53.76   6
ATOM   4132  O   VAL C 106      18.782  56.151  11.203  1.00 52.33   8
ATOM   4133  N   SER C 107      17.016  54.889  10.615  1.00 54.08   7
ATOM   4134  CA  SER C 107      17.066  55.275   9.208  1.00 56.13   6
ATOM   4135  CB  SER C 107      15.835  54.734   8.487  1.00 56.67   6
ATOM   4136  OG  SER C 107      14.672  54.943   9.268  1.00 59.41   8
ATOM   4137  C   SER C 107      17.228  56.762   8.895  1.00 56.30   6
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ATOM	4138	O	SER	C	107	17.678	57.129	7.797	1.00	55.13	8
ATOM	4139	N	ASP	C	108	16.879	57.619	9.849	1.00	56.72	7
ATOM	4140	CA	ASP	C	108	16.999	59.064	9.632	1.00	58.46	6
ATOM	4141	CB	ASP	C	108	15.875	59.807	10.353	1.00	59.64	6
ATOM	4142	CG	ASP	C	108	15.998	59.735	11.856	1.00	60.59	6
ATOM	4143	OD1	ASP	C	108	16.432	58.693	12.378	1.00	61.80	8
ATOM	4144	OD2	ASP	C	108	15.643	60.724	12.520	1.00	63.04	8
ATOM	4145	C	ASP	C	108	18.345	59.648	10.054	1.00	58.38	6
ATOM	4146	O	ASP	C	108	18.513	60.859	10.068	1.00	58.33	8
ATOM	4147	N	GLY	C	109	19.299	58.785	10.396	1.00	59.41	7
ATOM	4148	CA	GLY	C	109	20.618	59.246	10.786	1.00	58.66	6
ATOM	4149	C	GLY	C	109	20.802	59.467	12.271	1.00	59.58	6
ATOM	4150	O	GLY	C	109	21.868	59.926	12.695	1.00	59.07	8
ATOM	4151	N	GLU	C	110	19.775	59.165	13.064	1.00	59.04	7
ATOM	4152	CA	GLU	C	110	19.871	59.325	14.508	1.00	59.38	6
ATOM	4153	CB	GLU	C	110	18.481	59.327	15.141	1.00	62.39	6
ATOM	4154	CG	GLU	C	110	18.386	60.020	16.513	1.00	66.23	6
ATOM	4155	CD	GLU	C	110	18.717	61.520	16.441	1.00	70.42	6
ATOM	4156	OE1	GLU	C	110	18.640	62.107	15.333	1.00	69.27	8
ATOM	4157	OE2	GLU	C	110	19.047	62.117	17.493	1.00	72.25	8
ATOM	4158	C	GLU	C	110	20.677	58.141	15.038	1.00	59.61	6
ATOM	4159	O	GLU	C	110	20.467	56.995	14.623	1.00	60.95	8
ATOM	4160	N	VAL	C	111	21.600	58.419	15.953	1.00	57.63	7
ATOM	4161	CA	VAL	C	111	22.444	57.379	16.535	1.00	55.43	6
ATOM	4162	CB	VAL	C	111	23.926	57.620	16.200	1.00	55.71	6
ATOM	4163	CG1	VAL	C	111	24.783	56.511	16.788	1.00	53.14	6
ATOM	4164	CG2	VAL	C	111	24.105	57.706	14.686	1.00	56.04	6
ATOM	4165	C	VAL	C	111	22.308	57.337	18.048	1.00	54.63	6
ATOM	4166	O	VAL	C	111	22.328	58.373	18.706	1.00	53.67	8
ATOM	4167	N	LEU	C	112	22.171	56.137	18.596	1.00	53.09	7
ATOM	4168	CA	LEU	C	112	22.050	55.992	20.034	1.00	53.62	6
ATOM	4169	CB	LEU	C	112	20.638	55.548	20.420	1.00	56.64	6
ATOM	4170	CG	LEU	C	112	19.380	56.011	19.657	1.00	60.85	6
ATOM	4171	CD1	LEU	C	112	19.439	57.490	19.341	1.00	62.41	6
ATOM	4172	CD2	LEU	C	112	19.244	55.207	18.374	1.00	62.32	6
ATOM	4173	C	LEU	C	112	23.053	54.963	20.542	1.00	53.28	6
ATOM	4174	O	LEU	C	112	23.024	53.807	20.134	1.00	54.91	8
ATOM	4175	N	TYR	C	113	23.943	55.389	21.429	1.00	50.87	7
ATOM	4176	CA	TYR	C	113	24.947	54.502	22.003	1.00	47.87	6
ATOM	4177	CB	TYR	C	113	26.362	54.924	21.560	1.00	44.85	6
ATOM	4178	CG	TYR	C	113	27.500	54.099	22.134	1.00	40.84	6
ATOM	4179	CD1	TYR	C	113	27.428	52.716	22.181	1.00	39.92	6
ATOM	4180	CE1	TYR	C	113	28.481	51.956	22.679	1.00	39.26	6
ATOM	4181	CD2	TYR	C	113	28.663	54.710	22.602	1.00	41.11	6
ATOM	4182	CE2	TYR	C	113	29.720	53.962	23.100	1.00	40.68	6
ATOM	4183	CZ	TYR	C	113	29.625	52.583	23.138	1.00	41.46	6
ATOM	4184	OH	TYR	C	113	30.667	51.831	23.649	1.00	40.70	8
ATOM	4185	C	TYR	C	113	24.805	54.611	23.508	1.00	48.03	6
ATOM	4186	O	TYR	C	113	25.002	55.673	24.089	1.00	47.83	8
ATOM	4187	N	MET	C	114	24.457	53.508	24.146	1.00	48.88	7
ATOM	4188	CA	MET	C	114	24.283	53.519	25.583	1.00	49.26	6
ATOM	4189	CB	MET	C	114	22.809	53.375	25.910	1.00	53.64	6
ATOM	4190	CG	MET	C	114	22.494	53.558	27.370	1.00	58.33	6
ATOM	4191	SD	MET	C	114	20.864	52.927	27.696	1.00	67.34	16
ATOM	4192	CE	MET	C	114	19.859	54.330	27.098	1.00	65.99	6
ATOM	4193	C	MET	C	114	25.055	52.393	26.244	1.00	47.94	6
ATOM	4194	O	MET	C	114	24.485	51.360	26.579	1.00	48.32	8
ATOM	4195	N	PRO	C	115	26.364	52.576	26.440	1.00	47.40	7
ATOM	4196	CD	PRO	C	115	27.181	53.711	25.976	1.00	49.35	6
ATOM	4197	CA	PRO	C	115	27.207	51.556	27.066	1.00	48.05	6
ATOM	4198	CB	PRO	C	115	28.591	51.903	26.545	1.00	48.90	6

ATOM	4199	CG	PRO	C	115	28.548	53.398	26.559	1.00	48.59	6
ATOM	4200	C	PRO	C	115	27.153	51.636	28.585	1.00	48.68	6
ATOM	4201	O	PRO	C	115	26.976	52.720	29.142	1.00	48.78	8
ATOM	4202	N	SER	C	116	27.291	50.493	29.249	1.00	47.05	7
ATOM	4203	CA	SER	C	116	27.292	50.481	30.699	1.00	45.85	6
ATOM	4204	CB	SER	C	116	26.746	49.178	31.248	1.00	45.70	6
ATOM	4205	OG	SER	C	116	26.731	49.228	32.667	1.00	46.59	8
ATOM	4206	C	SER	C	116	28.743	50.607	31.097	1.00	47.30	6
ATOM	4207	O	SER	C	116	29.568	49.794	30.695	1.00	48.38	8
ATOM	4208	N	ILE	C	117	29.058	51.622	31.892	1.00	45.86	7
ATOM	4209	CA	ILE	C	117	30.437	51.849	32.293	1.00	41.61	6
ATOM	4210	CB	ILE	C	117	30.926	53.210	31.749	1.00	39.60	6
ATOM	4211	CG2	ILE	C	117	32.325	53.499	32.230	1.00	38.47	6
ATOM	4212	CG1	ILE	C	117	30.876	53.208	30.225	1.00	38.60	6
ATOM	4213	CD1	ILE	C	117	31.025	54.563	29.619	1.00	34.54	6
ATOM	4214	C	ILE	C	117	30.708	51.830	33.796	1.00	42.04	6
ATOM	4215	O	ILE	C	117	29.948	52.390	34.587	1.00	42.87	8
ATOM	4216	N	ARG	C	118	31.787	51.158	34.182	1.00	40.79	7
ATOM	4217	CA	ARG	C	118	32.210	51.162	35.568	1.00	40.35	6
ATOM	4218	CB	ARG	C	118	32.607	49.782	36.060	1.00	37.23	6
ATOM	4219	CG	ARG	C	118	33.172	49.866	37.455	1.00	36.55	6
ATOM	4220	CD	ARG	C	118	33.277	48.538	38.156	1.00	39.03	6
ATOM	4221	NE	ARG	C	118	33.874	48.693	39.483	1.00	39.42	7
ATOM	4222	CZ	ARG	C	118	33.882	47.756	40.424	1.00	39.50	6
ATOM	4223	NH1	ARG	C	118	33.326	46.574	40.208	1.00	40.01	7
ATOM	4224	NH2	ARG	C	118	34.434	48.012	41.594	1.00	40.75	7
ATOM	4225	C	ARG	C	118	33.440	52.065	35.545	1.00	41.99	6
ATOM	4226	O	ARG	C	118	34.322	51.881	34.722	1.00	43.88	8
ATOM	4227	N	GLN	C	119	33.514	53.040	36.436	1.00	42.79	7
ATOM	4228	CA	GLN	C	119	34.649	53.947	36.408	1.00	43.05	6
ATOM	4229	CB	GLN	C	119	34.439	54.914	35.252	1.00	41.88	6
ATOM	4230	CG	GLN	C	119	35.502	55.939	35.034	1.00	41.06	6
ATOM	4231	CD	GLN	C	119	35.281	56.668	33.732	1.00	41.03	6
ATOM	4232	OE1	GLN	C	119	34.148	56.899	33.331	1.00	40.46	8
ATOM	4233	NE2	GLN	C	119	36.363	57.039	33.066	1.00	43.78	7
ATOM	4234	C	GLN	C	119	34.786	54.685	37.728	1.00	43.66	6
ATOM	4235	O	GLN	C	119	33.803	54.937	38.397	1.00	45.00	8
ATOM	4236	N	ARG	C	120	36.008	55.018	38.113	1.00	44.71	7
ATOM	4237	CA	ARG	C	120	36.210	55.722	39.369	1.00	48.39	6
ATOM	4238	CB	ARG	C	120	37.414	55.169	40.107	1.00	51.11	6
ATOM	4239	CG	ARG	C	120	37.325	53.696	40.397	1.00	56.82	6
ATOM	4240	CD	ARG	C	120	38.116	53.386	41.641	1.00	64.45	6
ATOM	4241	NE	ARG	C	120	37.375	53.650	42.886	1.00	68.42	7
ATOM	4242	CZ	ARG	C	120	37.903	54.231	43.969	1.00	68.95	6
ATOM	4243	NH1	ARG	C	120	39.169	54.631	43.967	1.00	66.80	7
ATOM	4244	NH2	ARG	C	120	37.177	54.373	45.076	1.00	69.05	7
ATOM	4245	C	ARG	C	120	36.388	57.215	39.168	1.00	48.49	6
ATOM	4246	O	ARG	C	120	36.937	57.660	38.161	1.00	48.13	8
ATOM	4247	N	PHE	C	121	35.916	57.992	40.133	1.00	47.70	7
ATOM	4248	CA	PHE	C	121	36.013	59.437	40.035	1.00	47.31	6
ATOM	4249	CB	PHE	C	121	34.649	60.045	39.719	1.00	43.68	6
ATOM	4250	CG	PHE	C	121	34.022	59.489	38.504	1.00	43.63	6
ATOM	4251	CD1	PHE	C	121	33.365	58.275	38.549	1.00	42.29	6
ATOM	4252	CD2	PHE	C	121	34.104	60.165	37.301	1.00	44.87	6
ATOM	4253	CE1	PHE	C	121	32.793	57.741	37.410	1.00	44.63	6
ATOM	4254	CE2	PHE	C	121	33.539	59.643	36.160	1.00	45.50	6
ATOM	4255	CZ	PHE	C	121	32.878	58.425	36.213	1.00	45.14	6
ATOM	4256	C	PHE	C	121	36.535	60.098	41.280	1.00	46.67	6
ATOM	4257	O	PHE	C	121	36.528	59.525	42.359	1.00	47.10	8
ATOM	4258	N	SER	C	122	36.984	61.328	41.098	1.00	47.71	7
ATOM	4259	CA	SER	C	122	37.469	62.150	42.187	1.00	49.70	6

ATOM	4260	CB	SER	C	122	38.799	62.808	41.809	1.00	51.31	6
ATOM	4261	OG	SER	C	122	39.240	63.688	42.829	1.00	51.16	8
ATOM	4262	C	SER	C	122	36.387	63.213	42.365	1.00	50.12	6
ATOM	4263	O	SER	C	122	36.169	64.050	41.489	1.00	49.00	8
ATOM	4264	N	CYS	C	123	35.687	63.156	43.488	1.00	50.55	7
ATOM	4265	CA	CYS	C	123	34.636	64.112	43.754	1.00	52.50	6
ATOM	4266	C	CYS	C	123	34.356	64.198	45.246	1.00	54.52	6
ATOM	4267	O	CYS	C	123	34.998	63.514	46.043	1.00	54.24	8
ATOM	4268	CB	CYS	C	123	33.377	63.709	42.993	1.00	53.16	6
ATOM	4269	SG	CYS	C	123	32.811	62.031	43.374	1.00	51.95	16
ATOM	4270	N	ASP	C	124	33.389	65.037	45.622	1.00	56.86	7
ATOM	4271	CA	ASP	C	124	33.047	65.215	47.034	1.00	58.55	6
ATOM	4272	CB	ASP	C	124	32.265	66.514	47.252	1.00	58.22	6
ATOM	4273	CG	ASP	C	124	32.506	67.105	48.634	1.00	58.91	6
ATOM	4274	OD1	ASP	C	124	32.703	66.338	49.589	1.00	58.22	8
ATOM	4275	OD2	ASP	C	124	32.500	68.341	48.777	1.00	62.67	8
ATOM	4276	C	ASP	C	124	32.246	64.055	47.601	1.00	58.49	6
ATOM	4277	O	ASP	C	124	31.098	63.837	47.229	1.00	58.26	8
ATOM	4278	N	VAL	C	125	32.868	63.320	48.513	1.00	59.01	7
ATOM	4279	CA	VAL	C	125	32.232	62.175	49.152	1.00	60.88	6
ATOM	4280	CB	VAL	C	125	33.224	60.983	49.243	1.00	59.28	6
ATOM	4281	CG1	VAL	C	125	32.601	59.838	49.983	1.00	56.75	6
ATOM	4282	CG2	VAL	C	125	33.639	60.552	47.856	1.00	58.31	6
ATOM	4283	C	VAL	C	125	31.740	62.530	50.565	1.00	63.26	6
ATOM	4284	O	VAL	C	125	30.892	61.833	51.143	1.00	63.90	8
ATOM	4285	N	SER	C	126	32.267	63.616	51.122	1.00	63.98	7
ATOM	4286	CA	SER	C	126	31.878	64.026	52.464	1.00	64.49	6
ATOM	4287	CB	SER	C	126	32.464	65.400	52.793	1.00	63.93	6
ATOM	4288	OG	SER	C	126	31.972	66.381	51.898	1.00	61.34	8
ATOM	4289	C	SER	C	126	30.364	64.061	52.614	1.00	64.90	6
ATOM	4290	O	SER	C	126	29.654	64.603	51.766	1.00	64.08	8
ATOM	4291	N	GLY	C	127	29.871	63.458	53.689	1.00	66.05	7
ATOM	4292	CA	GLY	C	127	28.442	63.458	53.929	1.00	68.25	6
ATOM	4293	C	GLY	C	127	27.742	62.201	53.467	1.00	69.88	6
ATOM	4294	O	GLY	C	127	26.546	62.040	53.679	1.00	70.57	8
ATOM	4295	N	VAL	C	128	28.480	61.297	52.839	1.00	71.23	7
ATOM	4296	CA	VAL	C	128	27.871	60.065	52.366	1.00	72.78	6
ATOM	4297	CB	VAL	C	128	28.890	59.124	51.690	1.00	72.13	6
ATOM	4298	CG1	VAL	C	128	29.282	59.670	50.361	1.00	75.47	6
ATOM	4299	CG2	VAL	C	128	30.104	58.940	52.585	1.00	70.24	6
ATOM	4300	C	VAL	C	128	27.223	59.242	53.466	1.00	74.00	6
ATOM	4301	O	VAL	C	128	26.090	58.770	53.316	1.00	73.73	8
ATOM	4302	N	ASP	C	129	27.946	59.063	54.567	1.00	75.39	7
ATOM	4303	CA	ASP	C	129	27.440	58.222	55.628	1.00	77.33	6
ATOM	4304	CB	ASP	C	129	28.490	58.040	56.721	1.00	77.51	6
ATOM	4305	CG	ASP	C	129	28.304	56.729	57.486	1.00	78.34	6
ATOM	4306	OD1	ASP	C	129	29.328	56.051	57.770	1.00	78.50	8
ATOM	4307	OD2	ASP	C	129	27.132	56.377	57.803	1.00	77.23	8
ATOM	4308	C	ASP	C	129	26.114	58.634	56.235	1.00	78.98	6
ATOM	4309	O	ASP	C	129	25.497	57.832	56.948	1.00	79.11	8
ATOM	4310	N	THR	C	130	25.645	59.851	55.948	1.00	79.48	7
ATOM	4311	CA	THR	C	130	24.365	60.250	56.521	1.00	80.50	6
ATOM	4312	CB	THR	C	130	24.447	60.229	58.077	1.00	83.19	6
ATOM	4313	OG1	THR	C	130	25.829	60.140	58.472	1.00	82.84	8
ATOM	4314	CG2	THR	C	130	23.618	59.035	58.670	1.00	83.96	6
ATOM	4315	C	THR	C	130	23.705	61.566	56.146	1.00	79.50	6
ATOM	4316	O	THR	C	130	24.362	62.536	55.760	1.00	78.71	8
ATOM	4317	N	GLU	C	131	22.382	61.553	56.307	1.00	79.39	7
ATOM	4318	CA	GLU	C	131	21.486	62.700	56.114	1.00	79.61	6
ATOM	4319	CB	GLU	C	131	21.981	63.893	56.961	1.00	82.70	6
ATOM	4320	CG	GLU	C	131	21.680	63.772	58.471	1.00	85.13	6

ATOM	4321	CD	GLU	C	131	22.642	64.580	59.335	1.00 86.47	6
ATOM	4322	OE1	GLU	C	131	22.862	65.788	59.024	1.00 87.43	8
ATOM	4323	OE2	GLU	C	131	23.168	63.998	60.320	1.00 85.12	8
ATOM	4324	C	GLU	C	131	21.207	63.185	54.715	1.00 77.86	6
ATOM	4325	O	GLU	C	131	20.460	62.560	53.955	1.00 76.34	8
ATOM	4326	N	SER	C	132	21.771	64.355	54.428	1.00 76.46	7
ATOM	4327	CA	SER	C	132	21.652	64.995	53.136	1.00 75.54	6
ATOM	4328	CB	SER	C	132	21.941	66.495	53.290	1.00 76.21	6
ATOM	4329	OG	SER	C	132	23.233	66.719	53.841	1.00 78.77	8
ATOM	4330	C	SER	C	132	22.673	64.318	52.205	1.00 74.37	6
ATOM	4331	O	SER	C	132	22.799	64.675	51.026	1.00 74.56	8
ATOM	4332	N	GLY	C	133	23.392	63.338	52.764	1.00 72.74	7
ATOM	4333	CA	GLY	C	133	24.389	62.591	52.019	1.00 70.01	6
ATOM	4334	C	GLY	C	133	25.435	63.449	51.337	1.00 68.98	6
ATOM	4335	O	GLY	C	133	25.636	64.615	51.686	1.00 69.00	8
ATOM	4336	N	ALA	C	134	26.107	62.859	50.355	1.00 66.70	7
ATOM	4337	CA	ALA	C	134	27.131	63.563	49.609	1.00 64.10	6
ATOM	4338	CB	ALA	C	134	28.394	62.723	49.531	1.00 63.57	6
ATOM	4339	C	ALA	C	134	26.641	63.899	48.212	1.00 62.41	6
ATOM	4340	O	ALA	C	134	25.640	63.360	47.737	1.00 60.16	8
ATOM	4341	N	THR	C	135	27.347	64.826	47.573	1.00 62.33	7
ATOM	4342	CA	THR	C	135	27.023	65.237	46.211	1.00 62.11	6
ATOM	4343	CB	THR	C	135	26.431	66.642	46.166	1.00 61.79	6
ATOM	4344	OG1	THR	C	135	25.253	66.675	46.980	1.00 65.07	8
ATOM	4345	CG2	THR	C	135	26.057	67.007	44.746	1.00 60.95	6
ATOM	4346	C	THR	C	135	28.292	65.181	45.375	1.00 60.85	6
ATOM	4347	O	THR	C	135	29.181	66.040	45.473	1.00 61.27	8
ATOM	4348	N	CYS	C	136	28.368	64.128	44.574	1.00 58.77	7
ATOM	4349	CA	CYS	C	136	29.499	63.891	43.712	1.00 56.58	6
ATOM	4350	C	CYS	C	136	29.140	64.393	42.325	1.00 56.26	6
ATOM	4351	O	CYS	C	136	28.197	63.907	41.710	1.00 56.21	8
ATOM	4352	CB	CYS	C	136	29.794	62.396	43.698	1.00 54.70	6
ATOM	4353	SG	CYS	C	136	31.010	61.882	42.454	1.00 52.66	16
ATOM	4354	N	ARG	C	137	29.874	65.386	41.843	1.00 55.40	7
ATOM	4355	CA	ARG	C	137	29.605	65.938	40.520	1.00 55.61	6
ATOM	4356	CB	ARG	C	137	29.698	67.466	40.537	1.00 56.53	6
ATOM	4357	CG	ARG	C	137	28.713	68.135	41.462	1.00 61.72	6
ATOM	4358	CD	ARG	C	137	29.231	69.491	41.947	1.00 65.19	6
ATOM	4359	NE	ARG	C	137	28.632	69.871	43.236	1.00 69.78	7
ATOM	4360	CZ	ARG	C	137	27.352	70.221	43.412	1.00 71.88	6
ATOM	4361	NH1	ARG	C	137	26.504	70.256	42.384	1.00 74.24	7
ATOM	4362	NH2	ARG	C	137	26.908	70.522	44.626	1.00 70.49	7
ATOM	4363	C	ARG	C	137	30.604	65.392	39.522	1.00 55.23	6
ATOM	4364	O	ARG	C	137	31.807	65.381	39.773	1.00 57.26	8
ATOM	4365	N	ILE	C	138	30.095	64.948	38.385	1.00 52.01	7
ATOM	4366	CA	ILE	C	138	30.922	64.398	37.333	1.00 50.01	6
ATOM	4367	CB	ILE	C	138	30.529	62.928	37.061	1.00 49.70	6
ATOM	4368	CG2	ILE	C	138	31.361	62.360	35.933	1.00 47.04	6
ATOM	4369	CG1	ILE	C	138	30.703	62.090	38.327	1.00 48.47	6
ATOM	4370	CD1	ILE	C	138	30.080	60.706	38.225	1.00 46.09	6
ATOM	4371	C	ILE	C	138	30.693	65.222	36.070	1.00 48.82	6
ATOM	4372	O	ILE	C	138	29.571	65.322	35.597	1.00 46.40	8
ATOM	4373	N	LYS	C	139	31.752	65.814	35.529	1.00 49.18	7
ATOM	4374	CA	LYS	C	139	31.634	66.614	34.309	1.00 52.75	6
ATOM	4375	CB	LYS	C	139	32.364	67.950	34.464	1.00 54.78	6
ATOM	4376	CG	LYS	C	139	31.952	68.737	35.697	1.00 59.35	6
ATOM	4377	CD	LYS	C	139	32.477	70.168	35.669	1.00 60.96	6
ATOM	4378	CE	LYS	C	139	31.780	71.019	34.594	1.00 62.06	6
ATOM	4379	NZ	LYS	C	139	32.316	72.419	34.559	1.00 59.27	7
ATOM	4380	C	LYS	C	139	32.218	65.886	33.106	1.00 52.07	6
ATOM	4381	O	LYS	C	139	33.364	65.446	33.143	1.00 52.64	8

ATOM	4382	N	ILE	C	140	31.441	65.761	32.036	1.00	51.29	7
ATOM	4383	CA	ILE	C	140	31.938	65.091	30.842	1.00	50.15	6
ATOM	4384	CB	ILE	C	140	31.404	63.613	30.769	1.00	51.22	6
ATOM	4385	CG2	ILE	C	140	31.536	62.955	32.134	1.00	52.05	6
ATOM	4386	CG1	ILE	C	140	29.930	63.555	30.393	1.00	49.11	6
ATOM	4387	CD1	ILE	C	140	29.307	62.187	30.676	1.00	49.89	6
ATOM	4388	C	ILE	C	140	31.624	65.861	29.560	1.00	47.99	6
ATOM	4389	O	ILE	C	140	30.515	66.323	29.365	1.00	50.04	8
ATOM	4390	N	GLY	C	141	32.620	66.025	28.701	1.00	46.57	7
ATOM	4391	CA	GLY	C	141	32.414	66.732	27.447	1.00	46.87	6
ATOM	4392	C	GLY	C	141	33.453	66.323	26.416	1.00	46.66	6
ATOM	4393	O	GLY	C	141	34.359	65.565	26.739	1.00	46.42	8
ATOM	4394	N	SER	C	142	33.329	66.804	25.180	1.00	45.19	7
ATOM	4395	CA	SER	C	142	34.303	66.474	24.140	1.00	41.98	6
ATOM	4396	CB	SER	C	142	33.974	67.165	22.828	1.00	40.96	6
ATOM	4397	OG	SER	C	142	35.062	67.057	21.943	1.00	34.78	8
ATOM	4398	C	SER	C	142	35.698	66.885	24.551	1.00	43.33	6
ATOM	4399	O	SER	C	142	35.915	67.956	25.115	1.00	45.01	8
ATOM	4400	N	TRP	C	143	36.655	66.028	24.256	1.00	43.12	7
ATOM	4401	CA	TRP	C	143	38.025	66.300	24.622	1.00	42.98	6
ATOM	4402	CB	TRP	C	143	38.768	64.982	24.819	1.00	41.57	6
ATOM	4403	CG	TRP	C	143	40.125	65.141	25.446	1.00	39.54	6
ATOM	4404	CD2	TRP	C	143	40.394	65.420	26.820	1.00	36.50	6
ATOM	4405	CE2	TRP	C	143	41.795	65.481	26.967	1.00	35.30	6
ATOM	4406	CE3	TRP	C	143	39.584	65.625	27.943	1.00	36.55	6
ATOM	4407	CD1	TRP	C	143	41.345	65.048	24.829	1.00	38.96	6
ATOM	4408	NE1	TRP	C	143	42.353	65.251	25.738	1.00	35.00	7
ATOM	4409	CZ2	TRP	C	143	42.400	65.736	28.192	1.00	34.47	6
ATOM	4410	CZ3	TRP	C	143	40.185	65.878	29.153	1.00	35.28	6
ATOM	4411	CH2	TRP	C	143	41.580	65.931	29.271	1.00	35.16	6
ATOM	4412	C	TRP	C	143	38.767	67.159	23.605	1.00	43.69	6
ATOM	4413	O	TRP	C	143	39.657	67.915	23.962	1.00	46.65	8
ATOM	4414	N	THR	C	144	38.402	67.065	22.338	1.00	42.21	7
ATOM	4415	CA	THR	C	144	39.107	67.834	21.333	1.00	40.90	6
ATOM	4416	CB	THR	C	144	39.839	66.901	20.372	1.00	40.06	6
ATOM	4417	OG1	THR	C	144	38.907	65.976	19.798	1.00	40.17	8
ATOM	4418	CG2	THR	C	144	40.916	66.144	21.106	1.00	38.34	6
ATOM	4419	C	THR	C	144	38.252	68.795	20.520	1.00	43.03	6
ATOM	4420	O	THR	C	144	38.786	69.631	19.795	1.00	43.02	8
ATOM	4421	N	HIS	C	145	36.934	68.687	20.635	1.00	42.41	7
ATOM	4422	CA	HIS	C	145	36.065	69.571	19.885	1.00	45.42	6
ATOM	4423	CB	HIS	C	145	34.994	68.772	19.144	1.00	48.25	6
ATOM	4424	CG	HIS	C	145	35.533	67.873	18.071	1.00	49.32	6
ATOM	4425	CD2	HIS	C	145	36.052	68.154	16.853	1.00	47.20	6
ATOM	4426	ND1	HIS	C	145	35.572	66.500	18.197	1.00	47.13	7
ATOM	4427	CE1	HIS	C	145	36.091	65.976	17.103	1.00	47.99	6
ATOM	4428	NE2	HIS	C	145	36.391	66.958	16.272	1.00	48.34	7
ATOM	4429	C	HIS	C	145	35.394	70.627	20.754	1.00	48.71	6
ATOM	4430	O	HIS	C	145	34.738	70.325	21.746	1.00	47.60	8
ATOM	4431	N	HIS	C	146	35.562	71.883	20.363	1.00	52.53	7
ATOM	4432	CA	HIS	C	146	34.972	72.993	21.094	1.00	53.12	6
ATOM	4433	CB	HIS	C	146	35.777	74.261	20.840	1.00	50.98	6
ATOM	4434	CG	HIS	C	146	35.931	74.586	19.390	1.00	48.89	6
ATOM	4435	CD2	HIS	C	146	35.013	74.755	18.409	1.00	47.83	6
ATOM	4436	ND1	HIS	C	146	37.161	74.776	18.801	1.00	48.82	7
ATOM	4437	CE1	HIS	C	146	36.993	75.049	17.519	1.00	48.32	6
ATOM	4438	NE2	HIS	C	146	35.699	75.043	17.257	1.00	46.12	7
ATOM	4439	C	HIS	C	146	33.524	73.188	20.664	1.00	54.19	6
ATOM	4440	O	HIS	C	146	33.047	72.531	19.736	1.00	54.21	8
ATOM	4441	N	SER	C	147	32.847	74.112	21.341	1.00	56.30	7
ATOM	4442	CA	SER	C	147	31.437	74.418	21.115	1.00	57.23	6

ATOM	4443	CB	SER	C	147	31.055	75.610	21.978	1.00	57.36	6
ATOM	4444	OG	SER	C	147	32.017	76.635	21.828	1.00	59.18	8
ATOM	4445	C	SER	C	147	30.972	74.660	19.682	1.00	57.72	6
ATOM	4446	O	SER	C	147	29.790	74.484	19.375	1.00	57.25	8
ATOM	4447	N	ARG	C	148	31.885	75.065	18.809	1.00	58.23	7
ATOM	4448	CA	ARG	C	148	31.517	75.336	17.424	1.00	60.12	6
ATOM	4449	CB	ARG	C	148	32.555	76.264	16.777	1.00	63.75	6
ATOM	4450	CG	ARG	C	148	32.799	77.567	17.549	1.00	70.83	6
ATOM	4451	CD	ARG	C	148	33.950	78.393	16.946	1.00	77.31	6
ATOM	4452	NE	ARG	C	148	34.422	79.453	17.852	1.00	84.18	7
ATOM	4453	CZ	ARG	C	148	33.696	80.506	18.245	1.00	86.23	6
ATOM	4454	NH1	ARG	C	148	32.447	80.661	17.818	1.00	87.64	7
ATOM	4455	NH2	ARG	C	148	34.213	81.408	19.072	1.00	86.26	7
ATOM	4456	C	ARG	C	148	31.390	74.051	16.601	1.00	59.83	6
ATOM	4457	O	ARG	C	148	30.786	74.053	15.519	1.00	60.30	8
ATOM	4458	N	GLU	C	149	31.954	72.959	17.121	1.00	57.69	7
ATOM	4459	CA	GLU	C	149	31.937	71.677	16.425	1.00	54.67	6
ATOM	4460	CB	GLU	C	149	33.364	71.132	16.321	1.00	52.47	6
ATOM	4461	CG	GLU	C	149	34.395	72.228	16.050	1.00	52.11	6
ATOM	4462	CD	GLU	C	149	35.824	71.718	15.896	1.00	50.20	6
ATOM	4463	OE1	GLU	C	149	36.246	70.852	16.678	1.00	49.43	8
ATOM	4464	OE2	GLU	C	149	36.537	72.203	15.004	1.00	47.62	8
ATOM	4465	C	GLU	C	149	31.043	70.698	17.162	1.00	53.64	6
ATOM	4466	O	GLU	C	149	30.252	69.985	16.552	1.00	53.16	8
ATOM	4467	N	ILE	C	150	31.172	70.667	18.479	1.00	52.16	7
ATOM	4468	CA	ILE	C	150	30.353	69.795	19.289	1.00	51.98	6
ATOM	4469	CB	ILE	C	150	31.157	68.612	19.883	1.00	53.49	6
ATOM	4470	CG2	ILE	C	150	30.361	67.954	21.019	1.00	52.00	6
ATOM	4471	CG1	ILE	C	150	31.450	67.571	18.800	1.00	53.48	6
ATOM	4472	CD1	ILE	C	150	32.235	66.383	19.299	1.00	50.44	6
ATOM	4473	C	ILE	C	150	29.750	70.565	20.446	1.00	53.26	6
ATOM	4474	O	ILE	C	150	30.410	71.389	21.095	1.00	51.01	8
ATOM	4475	N	SER	C	151	28.479	70.280	20.694	1.00	54.99	7
ATOM	4476	CA	SER	C	151	27.749	70.887	21.797	1.00	56.94	6
ATOM	4477	CB	SER	C	151	26.693	71.873	21.280	1.00	54.85	6
ATOM	4478	OG	SER	C	151	25.665	71.221	20.557	1.00	55.92	8
ATOM	4479	C	SER	C	151	27.084	69.717	22.516	1.00	59.00	6
ATOM	4480	O	SER	C	151	26.536	68.820	21.871	1.00	60.03	8
ATOM	4481	N	VAL	C	152	27.172	69.705	23.844	1.00	60.32	7
ATOM	4482	CA	VAL	C	152	26.569	68.651	24.655	1.00	61.16	6
ATOM	4483	CB	VAL	C	152	27.564	68.096	25.694	1.00	60.14	6
ATOM	4484	CG1	VAL	C	152	28.858	67.723	25.009	1.00	61.98	6
ATOM	4485	CG2	VAL	C	152	27.817	69.110	26.775	1.00	61.23	6
ATOM	4486	C	VAL	C	152	25.373	69.237	25.391	1.00	62.82	6
ATOM	4487	O	VAL	C	152	25.379	70.409	25.758	1.00	63.73	8
ATOM	4488	N	ASP	C	153	24.349	68.425	25.614	1.00	65.81	7
ATOM	4489	CA	ASP	C	153	23.147	68.887	26.293	1.00	67.23	6
ATOM	4490	CB	ASP	C	153	22.150	69.377	25.249	1.00	69.19	6
ATOM	4491	CG	ASP	C	153	22.748	70.425	24.320	1.00	72.38	6
ATOM	4492	OD1	ASP	C	153	22.786	71.614	24.718	1.00	72.90	8
ATOM	4493	OD2	ASP	C	153	23.193	70.060	23.201	1.00	75.01	8
ATOM	4494	C	ASP	C	153	22.505	67.776	27.120	1.00	69.10	6
ATOM	4495	O	ASP	C	153	22.504	66.612	26.717	1.00	68.47	8
ATOM	4496	N	PRO	C	154	21.970	68.115	28.304	1.00	70.49	7
ATOM	4497	CD	PRO	C	154	22.282	69.309	29.094	1.00	69.97	6
ATOM	4498	CA	PRO	C	154	21.325	67.098	29.147	1.00	73.18	6
ATOM	4499	CB	PRO	C	154	21.148	67.814	30.477	1.00	70.84	6
ATOM	4500	CG	PRO	C	154	22.300	68.745	30.493	1.00	71.35	6
ATOM	4501	C	PRO	C	154	19.985	66.669	28.522	1.00	77.25	6
ATOM	4502	O	PRO	C	154	19.591	67.183	27.462	1.00	77.76	8
ATOM	4503	N	THR	C	155	19.279	65.744	29.175	1.00	80.57	7

ATOM	4504	CA	THR	C	155	18.010	65.253	28.633	1.00 83.84	6
ATOM	4505	CB	THR	C	155	18.244	63.932	27.837	1.00 83.53	6
ATOM	4506	OG1	THR	C	155	18.609	62.882	28.744	1.00 83.26	8
ATOM	4507	CG2	THR	C	155	19.361	64.105	26.823	1.00 83.08	6
ATOM	4508	C	THR	C	155	16.897	65.001	29.678	1.00 87.74	6
ATOM	4509	O	THR	C	155	16.826	65.677	30.715	1.00 87.94	8
ATOM	4510	N	THR	C	156	16.042	64.012	29.370	1.00 91.72	7
ATOM	4511	CA	THR	C	156	14.882	63.577	30.180	1.00 93.73	6
ATOM	4512	CB	THR	C	156	14.501	62.092	29.877	1.00 93.94	6
ATOM	4513	OG1	THR	C	156	14.249	61.933	28.470	1.00 93.93	8
ATOM	4514	CG2	THR	C	156	13.253	61.681	30.696	1.00 93.29	6
ATOM	4515	C	THR	C	156	15.042	63.695	31.693	1.00 95.32	6
ATOM	4516	O	THR	C	156	15.626	62.817	32.347	1.00 95.61	8
ATOM	4517	N	GLU	C	157	14.490	64.767	32.246	1.00 97.07	7
ATOM	4518	CA	GLU	C	157	14.578	65.011	33.679	1.00 98.94	6
ATOM	4519	CB	GLU	C	157	14.487	66.514	33.942	1.00100.27	6
ATOM	4520	CG	GLU	C	157	15.282	67.359	32.950	1.00102.55	6
ATOM	4521	CD	GLU	C	157	15.113	68.852	33.214	1.00104.54	6
ATOM	4522	OE1	GLU	C	157	13.943	69.322	33.312	1.00105.88	8
ATOM	4523	OE2	GLU	C	157	16.150	69.555	33.327	1.00104.90	8
ATOM	4524	C	GLU	C	157	13.475	64.290	34.465	1.00 99.30	6
ATOM	4525	O	GLU	C	157	13.452	64.337	35.706	1.00 99.77	8
ATOM	4526	N	ASN	C	158	12.557	63.639	33.751	1.00 99.15	7
ATOM	4527	CA	ASN	C	158	11.457	62.919	34.404	1.00 98.32	6
ATOM	4528	CB	ASN	C	158	10.382	62.541	33.374	1.00100.43	6
ATOM	4529	CG	ASN	C	158	9.902	63.736	32.555	1.00101.38	6
ATOM	4530	OD1	ASN	C	158	9.423	64.738	33.112	1.00101.96	8
ATOM	4531	ND2	ASN	C	158	10.026	63.636	31.224	1.00101.40	7
ATOM	4532	C	ASN	C	158	11.991	61.638	35.064	1.00 96.64	6
ATOM	4533	O	ASN	C	158	12.380	61.643	36.239	1.00 96.33	8
ATOM	4534	N	SER	C	159	11.992	60.558	34.283	1.00 93.61	7
ATOM	4535	CA	SER	C	159	12.466	59.237	34.690	1.00 90.35	6
ATOM	4536	CB	SER	C	159	13.541	58.788	33.690	1.00 90.84	6
ATOM	4537	OG	SER	C	159	14.367	59.898	33.320	1.00 90.44	8
ATOM	4538	C	SER	C	159	13.005	59.167	36.123	1.00 88.15	6
ATOM	4539	O	SER	C	159	13.942	59.894	36.481	1.00 88.99	8
ATOM	4540	N	ASP	C	160	12.414	58.302	36.945	1.00 84.53	7
ATOM	4541	CA	ASP	C	160	12.863	58.152	38.330	1.00 80.47	6
ATOM	4542	CB	ASP	C	160	12.232	56.921	38.985	1.00 80.26	6
ATOM	4543	CG	ASP	C	160	12.760	56.683	40.398	1.00 82.12	6
ATOM	4544	OD1	ASP	C	160	12.658	55.536	40.890	1.00 82.78	8
ATOM	4545	OD2	ASP	C	160	13.277	57.644	41.023	1.00 82.17	8
ATOM	4546	C	ASP	C	160	14.380	57.978	38.340	1.00 77.39	6
ATOM	4547	O	ASP	C	160	14.892	57.009	37.768	1.00 75.75	8
ATOM	4548	N	ASP	C	161	15.080	58.910	38.992	1.00 73.66	7
ATOM	4549	CA	ASP	C	161	16.529	58.864	39.072	1.00 71.77	6
ATOM	4550	CB	ASP	C	161	17.060	59.934	40.028	1.00 71.93	6
ATOM	4551	CG	ASP	C	161	16.943	61.330	39.461	1.00 72.28	6
ATOM	4552	OD1	ASP	C	161	17.115	61.486	38.230	1.00 71.71	8
ATOM	4553	OD2	ASP	C	161	16.695	62.270	40.246	1.00 74.13	8
ATOM	4554	C	ASP	C	161	17.118	57.515	39.479	1.00 70.97	6
ATOM	4555	O	ASP	C	161	18.296	57.251	39.222	1.00 73.00	8
ATOM	4556	N	SER	C	162	16.335	56.649	40.105	1.00 68.54	7
ATOM	4557	CA	SER	C	162	16.899	55.366	40.496	1.00 66.65	6
ATOM	4558	CB	SER	C	162	17.085	55.308	42.020	1.00 66.09	6
ATOM	4559	OG	SER	C	162	15.845	55.352	42.698	1.00 66.84	8
ATOM	4560	C	SER	C	162	16.064	54.194	40.019	1.00 65.29	6
ATOM	4561	O	SER	C	162	16.042	53.147	40.646	1.00 65.08	8
ATOM	4562	N	GLU	C	163	15.393	54.357	38.892	1.00 64.69	7
ATOM	4563	CA	GLU	C	163	14.571	53.270	38.398	1.00 66.58	6
ATOM	4564	CB	GLU	C	163	13.543	53.784	37.372	1.00 68.86	6

ATOM	4565	CG	GLU	C	163	14.029	53.942	35.951	1.00 70.35	6
ATOM	4566	CD	GLU	C	163	12.886	54.261	35.000	1.00 73.03	6
ATOM	4567	OE1	GLU	C	163	12.345	55.390	35.065	1.00 75.39	8
ATOM	4568	OE2	GLU	C	163	12.517	53.378	34.193	1.00 72.63	8
ATOM	4569	C	GLU	C	163	15.416	52.145	37.808	1.00 65.46	6
ATOM	4570	O	GLU	C	163	14.902	51.071	37.481	1.00 64.98	8
ATOM	4571	N	TYR	C	164	16.718	52.392	37.675	1.00 65.54	7
ATOM	4572	CA	TYR	C	164	17.647	51.389	37.143	1.00 63.20	6
ATOM	4573	CB	TYR	C	164	18.353	51.894	35.884	1.00 63.41	6
ATOM	4574	CG	TYR	C	164	17.433	52.101	34.716	1.00 65.49	6
ATOM	4575	CD1	TYR	C	164	17.299	53.355	34.119	1.00 66.61	6
ATOM	4576	CE1	TYR	C	164	16.429	53.555	33.046	1.00 68.54	6
ATOM	4577	CD2	TYR	C	164	16.676	51.046	34.216	1.00 68.25	6
ATOM	4578	CE2	TYR	C	164	15.797	51.230	33.144	1.00 70.31	6
ATOM	4579	CZ	TYR	C	164	15.680	52.484	32.562	1.00 70.26	6
ATOM	4580	OH	TYR	C	164	14.832	52.655	31.482	1.00 74.21	8
ATOM	4581	C	TYR	C	164	18.690	51.066	38.184	1.00 61.13	6
ATOM	4582	O	TYR	C	164	19.480	50.147	38.003	1.00 60.53	8
ATOM	4583	N	PHE	C	165	18.687	51.824	39.279	1.00 59.92	7
ATOM	4584	CA	PHE	C	165	19.657	51.622	40.347	1.00 58.58	6
ATOM	4585	CB	PHE	C	165	19.497	52.690	41.425	1.00 56.39	6
ATOM	4586	CG	PHE	C	165	20.717	52.856	42.288	1.00 55.60	6
ATOM	4587	CD1	PHE	C	165	21.904	53.336	41.742	1.00 53.27	6
ATOM	4588	CD2	PHE	C	165	20.692	52.497	43.629	1.00 54.20	6
ATOM	4589	CE1	PHE	C	165	23.049	53.451	42.513	1.00 53.30	6
ATOM	4590	CE2	PHE	C	165	21.835	52.607	44.414	1.00 54.70	6
ATOM	4591	CZ	PHE	C	165	23.018	53.085	43.854	1.00 54.90	6
ATOM	4592	C	PHE	C	165	19.528	50.250	40.974	1.00 58.64	6
ATOM	4593	O	PHE	C	165	18.422	49.749	41.153	1.00 60.35	8
ATOM	4594	N	SER	C	166	20.655	49.631	41.298	1.00 58.50	7
ATOM	4595	CA	SER	C	166	20.614	48.309	41.900	1.00 58.50	6
ATOM	4596	CB	SER	C	166	22.013	47.703	41.996	1.00 58.83	6
ATOM	4597	OG	SER	C	166	21.957	46.391	42.542	1.00 61.34	8
ATOM	4598	C	SER	C	166	20.050	48.473	43.286	1.00 58.49	6
ATOM	4599	O	SER	C	166	20.346	49.454	43.964	1.00 58.40	8
ATOM	4600	N	GLN	C	167	19.249	47.503	43.706	1.00 57.37	7
ATOM	4601	CA	GLN	C	167	18.631	47.545	45.020	1.00 57.17	6
ATOM	4602	CB	GLN	C	167	17.317	46.766	44.994	1.00 59.70	6
ATOM	4603	CG	GLN	C	167	17.467	45.351	44.490	1.00 62.90	6
ATOM	4604	CD	GLN	C	167	16.136	44.696	44.164	1.00 67.19	6
ATOM	4605	OE1	GLN	C	167	15.284	44.519	45.048	1.00 68.37	8
ATOM	4606	NE2	GLN	C	167	15.940	44.334	42.884	1.00 66.77	7
ATOM	4607	C	GLN	C	167	19.548	46.975	46.085	1.00 55.30	6
ATOM	4608	O	GLN	C	167	19.373	47.235	47.271	1.00 53.36	8
ATOM	4609	N	TYR	C	168	20.541	46.211	45.659	1.00 55.00	7
ATOM	4610	CA	TYR	C	168	21.455	45.601	46.609	1.00 55.48	6
ATOM	4611	CB	TYR	C	168	21.845	44.214	46.114	1.00 55.25	6
ATOM	4612	CG	TYR	C	168	20.630	43.413	45.714	1.00 56.93	6
ATOM	4613	CD1	TYR	C	168	20.242	43.315	44.378	1.00 56.29	6
ATOM	4614	CE1	TYR	C	168	19.087	42.640	44.016	1.00 56.50	6
ATOM	4615	CD2	TYR	C	168	19.825	42.809	46.680	1.00 57.12	6
ATOM	4616	CE2	TYR	C	168	18.664	42.133	46.332	1.00 56.97	6
ATOM	4617	CZ	TYR	C	168	18.300	42.054	44.997	1.00 58.82	6
ATOM	4618	OH	TYR	C	168	17.133	41.408	44.640	1.00 61.29	8
ATOM	4619	C	TYR	C	168	22.692	46.431	46.919	1.00 55.31	6
ATOM	4620	O	TYR	C	168	23.582	45.987	47.637	1.00 53.34	8
ATOM	4621	N	SER	C	169	22.733	47.646	46.384	1.00 56.64	7
ATOM	4622	CA	SER	C	169	23.851	48.553	46.620	1.00 58.01	6
ATOM	4623	CB	SER	C	169	23.731	49.786	45.720	1.00 58.39	6
ATOM	4624	OG	SER	C	169	24.745	50.727	46.017	1.00 57.32	8
ATOM	4625	C	SER	C	169	23.860	49.001	48.076	1.00 60.12	6

ATOM	4626	O	SER	C	169	22.803	49.148	48.699	1.00 60.78	8
ATOM	4627	N	ARG	C	170	25.052	49.215	48.621	1.00 59.44	7
ATOM	4628	CA	ARG	C	170	25.174	49.662	49.998	1.00 58.39	6
ATOM	4629	CB	ARG	C	170	26.636	49.602	50.438	1.00 59.12	6
ATOM	4630	CG	ARG	C	170	26.999	48.350	51.195	1.00 61.61	6
ATOM	4631	CD	ARG	C	170	28.466	47.972	51.024	1.00 64.86	6
ATOM	4632	NE	ARG	C	170	29.418	49.012	51.424	1.00 66.40	7
ATOM	4633	CZ	ARG	C	170	30.317	49.556	50.597	1.00 68.28	6
ATOM	4634	NH1	ARG	C	170	30.384	49.165	49.326	1.00 66.23	7
ATOM	4635	NH2	ARG	C	170	31.166	50.480	51.039	1.00 68.62	7
ATOM	4636	C	ARG	C	170	24.668	51.102	50.109	1.00 59.25	6
ATOM	4637	O	ARG	C	170	24.416	51.609	51.215	1.00 59.99	8
ATOM	4638	N	PHE	C	171	24.498	51.759	48.968	1.00 57.06	7
ATOM	4639	CA	PHE	C	171	24.063	53.146	48.982	1.00 56.45	6
ATOM	4640	CB	PHE	C	171	25.131	54.016	48.324	1.00 55.23	6
ATOM	4641	CG	PHE	C	171	26.521	53.719	48.814	1.00 54.51	6
ATOM	4642	CD1	PHE	C	171	27.189	52.568	48.400	1.00 55.98	6
ATOM	4643	CD2	PHE	C	171	27.145	54.559	49.724	1.00 53.29	6
ATOM	4644	CE1	PHE	C	171	28.463	52.257	48.890	1.00 55.09	6
ATOM	4645	CE2	PHE	C	171	28.412	54.258	50.218	1.00 54.24	6
ATOM	4646	CZ	PHE	C	171	29.074	53.102	49.799	1.00 54.89	6
ATOM	4647	C	PHE	C	171	22.732	53.346	48.311	1.00 55.77	6
ATOM	4648	O	PHE	C	171	22.164	52.406	47.761	1.00 55.57	8
ATOM	4649	N	GLU	C	172	22.228	54.569	48.376	1.00 55.26	7
ATOM	4650	CA	GLU	C	172	20.947	54.877	47.760	1.00 58.65	6
ATOM	4651	CB	GLU	C	172	19.806	54.769	48.789	1.00 60.96	6
ATOM	4652	CG	GLU	C	172	19.891	55.739	49.981	1.00 64.19	6
ATOM	4653	CD	GLU	C	172	18.753	55.551	50.992	1.00 64.82	6
ATOM	4654	OE1	GLU	C	172	17.626	55.236	50.557	1.00 65.38	8
ATOM	4655	OE2	GLU	C	172	18.976	55.734	52.216	1.00 64.87	8
ATOM	4656	C	GLU	C	172	21.014	56.279	47.162	1.00 59.71	6
ATOM	4657	O	GLU	C	172	21.815	57.116	47.600	1.00 60.04	8
ATOM	4658	N	ILE	C	173	20.186	56.530	46.154	1.00 58.96	7
ATOM	4659	CA	ILE	C	173	20.182	57.827	45.494	1.00 59.79	6
ATOM	4660	CB	ILE	C	173	20.016	57.687	43.970	1.00 60.17	6
ATOM	4661	CG2	ILE	C	173	19.918	59.071	43.334	1.00 57.73	6
ATOM	4662	CG1	ILE	C	173	21.191	56.896	43.384	1.00 59.23	6
ATOM	4663	CD1	ILE	C	173	21.053	56.663	41.902	1.00 58.26	6
ATOM	4664	C	ILE	C	173	19.088	58.756	45.977	1.00 59.99	6
ATOM	4665	O	ILE	C	173	17.912	58.391	46.021	1.00 57.81	8
ATOM	4666	N	LEU	C	174	19.480	59.972	46.321	1.00 60.93	7
ATOM	4667	CA	LEU	C	174	18.510	60.943	46.782	1.00 62.65	6
ATOM	4668	CB	LEU	C	174	19.164	61.916	47.756	1.00 62.58	6
ATOM	4669	CG	LEU	C	174	19.967	61.213	48.856	1.00 63.64	6
ATOM	4670	CD1	LEU	C	174	20.647	62.264	49.723	1.00 63.25	6
ATOM	4671	CD2	LEU	C	174	19.054	60.303	49.684	1.00 61.62	6
ATOM	4672	C	LEU	C	174	17.985	61.680	45.564	1.00 64.25	6
ATOM	4673	O	LEU	C	174	16.781	61.734	45.329	1.00 65.71	8
ATOM	4674	N	ASP	C	175	18.893	62.223	44.768	1.00 65.23	7
ATOM	4675	CA	ASP	C	175	18.485	62.951	43.576	1.00 66.02	6
ATOM	4676	CB	ASP	C	175	17.949	64.334	43.991	1.00 67.24	6
ATOM	4677	CG	ASP	C	175	17.419	65.160	42.812	1.00 68.54	6
ATOM	4678	OD1	ASP	C	175	16.598	64.650	42.011	1.00 69.53	8
ATOM	4679	OD2	ASP	C	175	17.812	66.338	42.695	1.00 66.59	8
ATOM	4680	C	ASP	C	175	19.651	63.084	42.593	1.00 66.29	6
ATOM	4681	O	ASP	C	175	20.829	63.031	42.980	1.00 66.20	8
ATOM	4682	N	VAL	C	176	19.312	63.237	41.318	1.00 66.07	7
ATOM	4683	CA	VAL	C	176	20.308	63.391	40.267	1.00 65.83	6
ATOM	4684	CB	VAL	C	176	20.426	62.109	39.401	1.00 66.59	6
ATOM	4685	CG1	VAL	C	176	21.382	62.345	38.232	1.00 64.35	6
ATOM	4686	CG2	VAL	C	176	20.900	60.943	40.254	1.00 63.70	6

ATOM	4687	C	VAL	C	176	19.869	64.532	39.368	1.00	67.12	6
ATOM	4688	O	VAL	C	176	18.715	64.589	38.956	1.00	67.64	8
ATOM	4689	N	THR	C	177	20.786	65.447	39.075	1.00	68.63	7
ATOM	4690	CA	THR	C	177	20.482	66.573	38.200	1.00	69.48	6
ATOM	4691	CB	THR	C	177	20.215	67.861	39.004	1.00	69.26	6
ATOM	4692	OG1	THR	C	177	21.310	68.109	39.894	1.00	68.92	8
ATOM	4693	CG2	THR	C	177	18.932	67.718	39.804	1.00	68.40	6
ATOM	4694	C	THR	C	177	21.640	66.813	37.245	1.00	70.44	6
ATOM	4695	O	THR	C	177	22.802	66.641	37.614	1.00	69.76	8
ATOM	4696	N	GLN	C	178	21.312	67.207	36.018	1.00	71.94	7
ATOM	4697	CA	GLN	C	178	22.320	67.470	34.998	1.00	73.43	6
ATOM	4698	CB	GLN	C	178	22.150	66.500	33.831	1.00	76.20	6
ATOM	4699	CG	GLN	C	178	21.560	65.148	34.220	1.00	80.00	6
ATOM	4700	CD	GLN	C	178	21.896	64.046	33.196	1.00	83.21	6
ATOM	4701	OE1	GLN	C	178	21,745	64.237	31.973	1.00	84.40	8
ATOM	4702	NE2	GLN	C	178	22.346	62.889	33.694	1.00	82.90	7
ATOM	4703	C	GLN	C	178	22.149	68.884	34.482	1.00	72.16	6
ATOM	4704	O	GLN	C	178	21.070	69.244	34.044	1.00	72.49	8
ATOM	4705	N	LYS	C	179	23.214	69.675	34.522	1.00	71.74	7
ATOM	4706	CA	LYS	C	179	23.166	71.054	34.048	1.00	71.38	6
ATOM	4707	CB	LYS	C	179	23.205	72.022	35.233	1.00	73.17	6
ATOM	4708	CG	LYS	C	179	22.291	71.610	36.380	1.00	78.41	6
ATOM	4709	CD	LYS	C	179	22.499	72.459	37.644	1.00	79.07	6
ATOM	4710	CE	LYS	C	179	21.814	71.821	38.864	1.00	80.35	6
ATOM	4711	NZ	LYS	C	179	22.363	70.452	39.163	1.00	81.10	7
ATOM	4712	C	LYS	C	179	24.384	71.301	33.176	1.00	70.13	6
ATOM	4713	O	LYS	C	179	25.504	71.353	33.681	1.00	70.65	8
ATOM	4714	N	LYS	C	180	24.180	71.466	31.876	1.00	68.21	7
ATOM	4715	CA	LYS	C	180	25.306	71.719	30.978	1.00	67.25	6
ATOM	4716	CB	LYS	C	180	24.833	71.667	29.519	1.00	67.12	6
ATOM	4717	CG	LYS	C	180	24.008	72.846	29.053	1.00	63.90	6
ATOM	4718	CD	LYS	C	180	24.908	73.920	28.488	1.00	63.70	6
ATOM	4719	CE	LYS	C	180	25.645	73.452	27.223	1.00	63.89	6
ATOM	4720	NZ	LYS	C	180	24.768	73.295	26.013	1.00	62.80	7
ATOM	4721	C	LYS	C	180	25.971	73.075	31.266	1.00	67.33	6
ATOM	4722	O	LYS	C	180	25.552	73.803	32.160	1.00	66.68	8
ATOM	4723	N	ASN	C	181	27.027	73.399	30.528	1.00	67.89	7
ATOM	4724	CA	ASN	C	181	27.698	74.674	30.702	1.00	67.78	6
ATOM	4725	CB	ASN	C	181	27.967	74.948	32.191	1.00	69.90	6
ATOM	4726	CG	ASN	C	181	28.580	73.770	32.916	1.00	70.82	6
ATOM	4727	OD1	ASN	C	181	29.508	73.137	32.422	1.00	73.77	8
ATOM	4728	ND2	ASN	C	181	28.071	73.481	34.109	1.00	70.00	7
ATOM	4729	C	ASN	C	181	28.977	74.884	29.901	1.00	67.29	6
ATOM	4730	O	ASN	C	181	29.937	74.153	30.049	1.00	68.57	8
ATOM	4731	N	SER	C	182	28.978	75.911	29.058	1.00	67.43	7
ATOM	4732	CA	SER	C	182	30.134	76.248	28.233	1.00	66.28	6
ATOM	4733	CB	SER	C	182	29.726	77.290	27.186	1.00	65.32	6
ATOM	4734	OG	SER	C	182	30.731	77.477	26.214	1.00	68.09	8
ATOM	4735	C	SER	C	182	31.230	76.798	29.141	1.00	65.83	6
ATOM	4736	O	SER	C	182	30.941	77.272	30.231	1.00	66.92	8
ATOM	4737	N	VAL	C	183	32.483	76.731	28.698	1.00	65.76	7
ATOM	4738	CA	VAL	C	183	33.613	77.211	29.498	1.00	65.65	6
ATOM	4739	CB	VAL	C	183	33.872	76.264	30.696	1.00	63.98	6
ATOM	4740	CG1	VAL	C	183	33.648	74.843	30.277	1.00	64.03	6
ATOM	4741	CG2	VAL	C	183	35.292	76.442	31.209	1.00	61.75	6
ATOM	4742	C	VAL	C	183	34.925	77.375	28.728	1.00	65.88	6
ATOM	4743	O	VAL	C	183	35.305	76.515	27.944	1.00	65.40	8
ATOM	4744	N	THR	C	184	35.616	78.485	28.957	1.00	66.99	7
ATOM	4745	CA	THR	C	184	36.892	78.722	28.293	1.00	68.57	6
ATOM	4746	CB	THR	C	184	36.995	80.168	27.732	1.00	67.80	6
ATOM	4747	OG1	THR	C	184	35.981	80.369	26.737	1.00	66.40	8

ATOM	4748	CG2	THR	C	184	38.370	80.406	27.094	1.00 66.48	6
ATOM	4749	C	THR	C	184	38.032	78.470	29.292	1.00 70.57	6
ATOM	4750	O	THR	C	184	37.920	78.802	30.482	1.00 70.99	8
ATOM	4751	N	TYR	C	185	39.118	77.869	28.815	1.00 70.74	7
ATOM	4752	CA	TYR	C	185	40.236	77.572	29.683	1.00 71.98	6
ATOM	4753	CB	TYR	C	185	40.555	76.067	29.658	1.00 72.58	6
ATOM	4754	CG	TYR	C	185	39.351	75.195	29.937	1.00 72.59	6
ATOM	4755	CD1	TYR	C	185	38.363	75.011	28.970	1.00 73.55	6
ATOM	4756	CE1	TYR	C	185	37.224	74.258	29.236	1.00 72.54	6
ATOM	4757	CD2	TYR	C	185	39.164	74.597	31.185	1.00 72.27	6
ATOM	4758	CE2	TYR	C	185	38.017	73.839	31.461	1.00 71.72	6
ATOM	4759	CZ	TYR	C	185	37.057	73.678	30.480	1.00 71.73	6
ATOM	4760	OH	TYR	C	185	35.920	72.951	30.732	1.00 71.36	8
ATOM	4761	C	TYR	C	185	41.426	78.355	29.191	1.00 73.72	6
ATOM	4762	O	TYR	C	185	41.625	78.492	27.983	1.00 74.41	8
ATOM	4763	N	SER	C	186	42.220	78.869	30.125	1.00 75.63	7
ATOM	4764	CA	SER	C	186	43.405	79.653	29.772	1.00 77.64	6
ATOM	4765	CB	SER	C	186	44.183	80.015	31.043	1.00 77.47	6
ATOM	4766	OG	SER	C	186	44.398	78.870	31.858	1.00 78.93	8
ATOM	4767	C	SER	C	186	44.300	78.875	28.793	1.00 77.75	6
ATOM	4768	O	SER	C	186	44.926	79.457	27.893	1.00 76.44	8
ATOM	4769	N	CYS	C	187	44.332	77.556	28.977	1.00 78.65	7
ATOM	4770	CA	CYS	C	187	45.116	76.648	28.135	1.00 79.38	6
ATOM	4771	C	CYS	C	187	44.658	76.703	26.715	1.00 79.55	6
ATOM	4772	O	CYS	C	187	45.443	76.687	25.771	1.00 79.09	8
ATOM	4773	CB	CYS	C	187	44.899	75.178	28.529	1.00 79.04	6
ATOM	4774	SG	CYS	C	187	43.205	74.462	28.241	1.00 80.14	16
ATOM	4775	N	CYS	C	188	43.345	76.774	26.589	1.00 80.45	7
ATOM	4776	CA	CYS	C	188	42.727	76.642	25.305	1.00 79.63	6
ATOM	4777	C	CYS	C	188	41.779	77.755	24.835	1.00 79.24	6
ATOM	4778	O	CYS	C	188	40.785	78.065	25.504	1.00 81.46	8
ATOM	4779	CB	CYS	C	188	42.037	75.269	25.365	1.00 79.66	6
ATOM	4780	SG	CYS	C	188	42.984	73.940	26.264	1.00 75.61	16
ATOM	4781	N	PRO	C	189	42.070	78.346	23.656	1.00 77.55	7
ATOM	4782	CD	PRO	C	189	43.222	77.849	22.879	1.00 76.91	6
ATOM	4783	CA	PRO	C	189	41.378	79.431	22.922	1.00 75.67	6
ATOM	4784	CB	PRO	C	189	41.921	79.283	21.502	1.00 75.82	6
ATOM	4785	CG	PRO	C	189	43.328	78.858	21.747	1.00 77.27	6
ATOM	4786	C	PRO	C	189	39.835	79.468	22.927	1.00 73.97	6
ATOM	4787	O	PRO	C	189	39.233	80.403	23.459	1.00 73.90	8
ATOM	4788	N	GLU	C	190	39.201	78.465	22.317	1.00 71.85	7
ATOM	4789	CA	GLU	C	190	37.734	78.404	22.246	1.00 68.61	6
ATOM	4790	CB	GLU	C	190	37.305	77.497	21.099	1.00 70.45	6
ATOM	4791	CG	GLU	C	190	38.277	77.434	19.945	1.00 72.05	6
ATOM	4792	CD	GLU	C	190	38.082	78.554	18.969	1.00 73.59	6
ATOM	4793	OE1	GLU	C	190	36.908	78.876	18.657	1.00 73.46	8
ATOM	4794	OE2	GLU	C	190	39.106	79.100	18.504	1.00 77.52	8
ATOM	4795	C	GLU	C	190	37.084	77.889	23.528	1.00 64.48	6
ATOM	4796	O	GLU	C	190	37.762	77.596	24.501	1.00 64.47	8
ATOM	4797	N	ALA	C	191	35.764	77.765	23.514	1.00 60.72	7
ATOM	4798	CA	ALA	C	191	35.035	77.281	24.679	1.00 60.54	6
ATOM	4799	CB	ALA	C	191	33.755	78.075	24.854	1.00 59.52	6
ATOM	4800	C	ALA	C	191	34.702	75.796	24.554	1.00 60.66	6
ATOM	4801	O	ALA	C	191	34.423	75.306	23.458	1.00 60.77	8
ATOM	4802	N	TYR	C	192	34.717	75.080	25.675	1.00 58.74	7
ATOM	4803	CA	TYR	C	192	34.409	73.653	25.659	1.00 57.24	6
ATOM	4804	CB	TYR	C	192	35.621	72.826	26.109	1.00 55.18	6
ATOM	4805	CG	TYR	C	192	36.737	72.825	25.097	1.00 55.96	6
ATOM	4806	CD1	TYR	C	192	37.694	73.842	25.075	1.00 56.31	6
ATOM	4807	CE1	TYR	C	192	38.680	73.887	24.092	1.00 56.74	6
ATOM	4808	CD2	TYR	C	192	36.800	71.844	24.109	1.00 56.77	6

ATOM	4809	CE2	TYR	C	192	37.785	71.874	23.121	1.00	57.49	6
ATOM	4810	CZ	TYR	C	192	38.720	72.898	23.119	1.00	58.13	6
ATOM	4811	OH	TYR	C	192	39.689	72.918	22.148	1.00	58.55	8
ATOM	4812	C	TYR	C	192	33.204	73.295	26.508	1.00	57.26	6
ATOM	4813	O	TYR	C	192	33.292	73.241	27.736	1.00	57.40	8
ATOM	4814	N	GLU	C	193	32.084	73.042	25.836	1.00	57.28	7
ATOM	4815	CA	GLU	C	193	30.839	72.678	26.506	1.00	58.77	6
ATOM	4816	CB	GLU	C	193	29.681	72.597	25.495	1.00	59.02	6
ATOM	4817	CG	GLU	C	193	29.342	73.912	24.823	1.00	61.64	6
ATOM	4818	CD	GLU	C	193	28.118	73.827	23.945	1.00	63.79	6
ATOM	4819	OE1	GLU	C	193	27.107	73.242	24.411	1.00	66.05	8
ATOM	4820	OE2	GLU	C	193	28.171	74.355	22.805	1.00	63.82	8
ATOM	4821	C	GLU	C	193	30.968	71.336	27.224	1.00	58.56	6
ATOM	4822	O	GLU	C	193	31.749	70.471	26.811	1.00	58.35	8
ATOM	4823	N	ASP	C	194	30.197	71.171	28.296	1.00	57.04	7
ATOM	4824	CA	ASP	C	194	30.215	69.940	29.059	1.00	57.30	6
ATOM	4825	CB	ASP	C	194	31.473	69.849	29.932	1.00	58.11	6
ATOM	4826	CG	ASP	C	194	31.430	70.777	31.141	1.00	58.91	6
ATOM	4827	OD1	ASP	C	194	32.220	71.742	31.172	1.00	57.40	8
ATOM	4828	OD2	ASP	C	194	30.614	70.538	32.060	1.00	58.46	8
ATOM	4829	C	ASP	C	194	28.982	69.848	29.933	1.00	56.78	6
ATOM	4830	O	ASP	C	194	28.411	70.864	30.320	1.00	56.90	8
ATOM	4831	N	VAL	C	195	28.567	68.619	30.223	1.00	55.47	7
ATOM	4832	CA	VAL	C	195	27.404	68.373	31.061	1.00	55.52	6
ATOM	4833	CB	VAL	C	195	26.538	67.236	30.504	1.00	54.50	6
ATOM	4834	CG1	VAL	C	195	25.469	66.841	31.511	1.00	52.44	6
ATOM	4835	CG2	VAL	C	195	25.914	67.671	29.199	1.00	55.96	6
ATOM	4836	C	VAL	C	195	27.874	67.973	32.444	1.00	56.12	6
ATOM	4837	O	VAL	C	195	28.661	67.046	32.602	1.00	56.74	8
ATOM	4838	N	GLU	C	196	27.388	68.675	33.451	1.00	56.91	7
ATOM	4839	CA	GLU	C	196	27.777	68.370	34.816	1.00	57.46	6
ATOM	4840	CB	GLU	C	196	28.051	69.654	35.581	1.00	58.09	6
ATOM	4841	CG	GLU	C	196	28.548	69.445	36.972	1.00	59.59	6
ATOM	4842	CD	GLU	C	196	28.730	70.758	37.700	1.00	62.33	6
ATOM	4843	OE1	GLU	C	196	29.523	71.594	37.229	1.00	62.53	8
ATOM	4844	OE2	GLU	C	196	28.074	70.958	38.746	1.00	65.85	8
ATOM	4845	C	GLU	C	196	26.636	67.627	35.453	1.00	57.05	6
ATOM	4846	O	GLU	C	196	25.517	68.120	35.487	1.00	59.06	8
ATOM	4847	N	VAL	C	197	26.914	66.427	35.938	1.00	56.46	7
ATOM	4848	CA	VAL	C	197	25.889	65.612	36.566	1.00	55.58	6
ATOM	4849	CB	VAL	C	197	25.867	64.179	35.984	1.00	53.38	6
ATOM	4850	CG1	VAL	C	197	24.777	63.360	36.649	1.00	50.20	6
ATOM	4851	CG2	VAL	C	197	25.629	64.239	34.486	1.00	51.56	6
ATOM	4852	C	VAL	C	197	26.199	65.546	38.041	1.00	56.50	6
ATOM	4853	O	VAL	C	197	27.320	65.207	38.430	1.00	58.31	8
ATOM	4854	N	SER	C	198	25.214	65.885	38.866	1.00	57.35	7
ATOM	4855	CA	SER	C	198	25.407	65.857	40.309	1.00	57.08	6
ATOM	4856	CB	SER	C	198	24.867	67.137	40.943	1.00	56.30	6
ATOM	4857	OG	SER	C	198	25.661	68.246	40.565	1.00	55.97	8
ATOM	4858	C	SER	C	198	24.717	64.643	40.886	1.00	57.36	6
ATOM	4859	O	SER	C	198	23.513	64.460	40.731	1.00	58.49	8
ATOM	4860	N	LEU	C	199	25.494	63.791	41.531	1.00	57.83	7
ATOM	4861	CA	LEU	C	199	24.938	62.594	42.120	1.00	57.20	6
ATOM	4862	CB	LEU	C	199	25.824	61.383	41.834	1.00	56.00	6
ATOM	4863	CG	LEU	C	199	25.457	60.110	42.606	1.00	56.43	6
ATOM	4864	CD1	LEU	C	199	24.073	59.627	42.211	1.00	53.65	6
ATOM	4865	CD2	LEU	C	199	26.487	59.050	42.325	1.00	55.64	6
ATOM	4866	C	LEU	C	199	24.818	62.782	43.613	1.00	58.48	6
ATOM	4867	O	LEU	C	199	25.819	62.737	44.337	1.00	59.73	8
ATOM	4868	N	ASN	C	200	23.593	63.012	44.070	1.00	58.64	7
ATOM	4869	CA	ASN	C	200	23.355	63.168	45.489	1.00	58.44	6

ATOM	4870	CB	ASN	C	200	22.285	64.232	45.754	1.00	60.17	6
ATOM	4871	CG	ASN	C	200	21.985	64.387	47.239	1.00	62.50	6
ATOM	4872	OD1	ASN	C	200	22.905	64.419	48.070	1.00	64.15	8
ATOM	4873	ND2	ASN	C	200	20.700	64.480	47.583	1.00	61.21	7
ATOM	4874	C	ASN	C	200	22.898	61.801	45.988	1.00	55.97	6
ATOM	4875	O	ASN	C	200	21.821	61.316	45.627	1.00	54.75	8
ATOM	4876	N	PHE	C	201	23.739	61.181	46.802	1.00	53.51	7
ATOM	4877	CA	PHE	C	201	23.454	59.867	47.330	1.00	53.54	6
ATOM	4878	CB	PHE	C	201	24.169	58.807	46.503	1.00	50.74	6
ATOM	4879	CG	PHE	C	201	25.663	58.820	46.677	1.00	48.36	6
ATOM	4880	CD1	PHE	C	201	26.312	57.763	47.309	1.00	45.72	6
ATOM	4881	CD2	PHE	C	201	26.413	59.912	46.252	1.00	46.85	6
ATOM	4882	CE1	PHE	C	201	27.689	57.794	47.521	1.00	43.95	6
ATOM	4883	CE2	PHE	C	201	27.782	59.955	46.457	1.00	45.93	6
ATOM	4884	CZ	PHE	C	201	28.425	58.889	47.096	1.00	44.09	6
ATOM	4885	C	PHE	C	201	23.979	59.812	48.749	1.00	55.36	6
ATOM	4886	O	PHE	C	201	24.640	60.739	49.210	1.00	53.66	8
ATOM	4887	N	ARG	C	202	23.698	58.702	49.425	1.00	57.35	7
ATOM	4888	CA	ARG	C	202	24.140	58.511	50.792	1.00	59.95	6
ATOM	4889	CB	ARG	C	202	23.192	59.224	51.744	1.00	62.36	6
ATOM	4890	CG	ARG	C	202	21.844	58.529	51.789	1.00	64.26	6
ATOM	4891	CD	ARG	C	202	20.831	59.278	52.610	1.00	67.26	6
ATOM	4892	NE	ARG	C	202	19.555	58.567	52.620	1.00	70.54	7
ATOM	4893	CZ	ARG	C	202	18.430	59.062	53.129	1.00	69.46	6
ATOM	4894	NH1	ARG	C	202	18.420	60.270	53.670	1.00	69.25	7
ATOM	4895	NH2	ARG	C	202	17.315	58.349	53.095	1.00	69.56	7
ATOM	4896	C	ARG	C	202	24.116	57.023	51.119	1.00	60.80	6
ATOM	4897	O	ARG	C	202	23.439	56.231	50.445	1.00	60.45	8
ATOM	4898	N	LYS	C	203	24.860	56.651	52.158	1.00	61.42	7
ATOM	4899	CA	LYS	C	203	24.886	55.270	52.603	1.00	60.82	6
ATOM	4900	CB	LYS	C	203	25.931	55.088	53.703	1.00	59.66	6
ATOM	4901	CG	LYS	C	203	25.988	53.688	54.258	1.00	61.19	6
ATOM	4902	CD	LYS	C	203	26.955	53.617	55.404	1.00	63.27	6
ATOM	4903	CE	LYS	C	203	27.036	52.209	55.947	1.00	66.98	6
ATOM	4904	NZ	LYS	C	203	27.621	51.250	54.945	1.00	68.80	7
ATOM	4905	C	LYS	C	203	23.477	55.037	53.157	1.00	60.81	6
ATOM	4906	O	LYS	C	203	22.878	55.942	53.735	1.00	60.52	8
ATOM	4907	N	LYS	C	204	22.913	53.858	52.944	1.00	60.36	7
ATOM	4908	CA	LYS	C	204	21.584	53.606	53.466	1.00	60.22	6
ATOM	4909	CB	LYS	C	204	21.017	52.329	52.837	1.00	58.64	6
ATOM	4910	CG	LYS	C	204	20.591	52.487	51.381	1.00	55.82	6
ATOM	4911	CD	LYS	C	204	20.445	51.140	50.692	1.00	51.95	6
ATOM	4912	CE	LYS	C	204	19.975	51.298	49.253	1.00	52.70	6
ATOM	4913	NZ	LYS	C	204	19.967	50.027	48.458	1.00	51.76	7
ATOM	4914	C	LYS	C	204	21.742	53.460	54.977	1.00	62.01	6
ATOM	4915	O	LYS	C	204	22.711	52.854	55.440	1.00	63.36	8
ATOM	4916	N	GLY	C	205	20.811	54.022	55.747	1.00	62.55	7
ATOM	4917	CA	GLY	C	205	20.898	53.921	57.202	1.00	62.30	6
ATOM	4918	C	GLY	C	205	19.797	53.078	57.844	1.00	61.75	6
ATOM	4919	OT1	GLY	C	205	18.911	52.614	57.093	1.00	60.18	8
ATOM	4920	OT2	GLY	C	205	19.811	52.879	59.092	1.00	60.86	8
ATOM	4921	CB	PHE	D	1	39.182	71.754	1.648	1.00	71.47	6
ATOM	4922	CG	PHE	D	1	40.239	71.385	0.623	1.00	73.60	6
ATOM	4923	CD1	PHE	D	1	40.122	70.241	-0.169	1.00	75.22	6
ATOM	4924	CD2	PHE	D	1	41.397	72.176	0.493	1.00	73.83	6
ATOM	4925	CE1	PHE	D	1	41.141	69.886	-1.081	1.00	75.00	6
ATOM	4926	CE2	PHE	D	1	42.418	71.835	-0.410	1.00	73.07	6
ATOM	4927	CZ	PHE	D	1	42.289	70.688	-1.199	1.00	74.63	6
ATOM	4928	C	PHE	D	1	37.071	70.999	2.658	1.00	68.35	6
ATOM	4929	O	PHE	D	1	37.607	71.392	3.688	1.00	69.33	8
ATOM	4930	N	PHE	D	1	37.010	72.284	0.515	1.00	69.08	7

ATOM	4931	CA	PHE	D	1	37.756	71.268	1.321	1.00	69.54	6
ATOM	4932	N	ASP	D	2	35.915	70.338	2.678	1.00	67.84	7
ATOM	4933	CA	ASP	D	2	35.253	70.061	3.967	1.00	66.03	6
ATOM	4934	CB	ASP	D	2	33.949	69.266	3.772	1.00	66.47	6
ATOM	4935	CG	ASP	D	2	34.138	68.032	2.928	1.00	68.89	6
ATOM	4936	OD1	ASP	D	2	35.029	67.218	3.287	1.00	68.16	8
ATOM	4937	OD2	ASP	D	2	33.396	67.886	1.912	1.00	70.47	8
ATOM	4938	C	ASP	D	2	36.181	69.310	4.933	1.00	64.63	6
ATOM	4939	O	ASP	D	2	37.378	69.165	4.672	1.00	64.43	8
ATOM	4940	N	ARG	D	3	35.639	68.837	6.049	1.00	62.26	7
ATOM	4941	CA	ARG	D	3	36.461	68.128	7.029	1.00	60.44	6
ATOM	4942	CB	ARG	D	3	35.748	68.078	8.388	1.00	60.90	6
ATOM	4943	CG	ARG	D	3	36.068	69.254	9.302	1.00	60.80	6
ATOM	4944	CD	ARG	D	3	35.185	69.243	10.532	1.00	65.18	6
ATOM	4945	NE	ARG	D	3	35.849	69.838	11.696	1.00	66.90	7
ATOM	4946	CZ	ARG	D	3	36.028	71.141	11.888	1.00	66.63	6
ATOM	4947	NH1	ARG	D	3	35.591	72.031	11.002	1.00	68.16	7
ATOM	4948	NH2	ARG	D	3	36.664	71.553	12.964	1.00	66.33	7
ATOM	4949	C	ARG	D	3	36.831	66.719	6.580	1.00	59.10	6
ATOM	4950	O	ARG	D	3	37.938	66.252	6.845	1.00	57.28	8
ATOM	4951	N	ALA	D	4	35.909	66.050	5.891	1.00	56.67	7
ATOM	4952	CA	ALA	D	4	36.153	64.699	5.414	1.00	53.48	6
ATOM	4953	CB	ALA	D	4	34.938	64.175	4.706	1.00	52.26	6
ATOM	4954	C	ALA	D	4	37.347	64.696	4.479	1.00	53.39	6
ATOM	4955	O	ALA	D	4	38.225	63.851	4.600	1.00	52.40	8
ATOM	4956	N	ASP	D	5	37.381	65.650	3.550	1.00	54.53	7
ATOM	4957	CA	ASP	D	5	38.489	65.756	2.602	1.00	55.71	6
ATOM	4958	CB	ASP	D	5	38.266	66.914	1.627	1.00	58.22	6
ATOM	4959	CG	ASP	D	5	36.938	66.810	0.881	1.00	61.46	6
ATOM	4960	OD1	ASP	D	5	36.605	65.709	0.386	1.00	64.32	8
ATOM	4961	OD2	ASP	D	5	36.227	67.832	0.773	1.00	63.22	8
ATOM	4962	C	ASP	D	5	39.816	65.970	3.326	1.00	54.28	6
ATOM	4963	O	ASP	D	5	40.844	65.440	2.914	1.00	52.86	8
ATOM	4964	N	ILE	D	6	39.787	66.735	4.410	1.00	52.53	7
ATOM	4965	CA	ILE	D	6	41.007	67.003	5.154	1.00	53.69	6
ATOM	4966	CB	ILE	D	6	40.813	68.128	6.191	1.00	55.79	6
ATOM	4967	CG2	ILE	D	6	42.152	68.435	6.877	1.00	54.61	6
ATOM	4968	CG1	ILE	D	6	40.266	69.385	5.499	1.00	55.83	6
ATOM	4969	CD1	ILE	D	6	40.121	70.597	6.400	1.00	55.01	6
ATOM	4970	C	ILE	D	6	41.545	65.775	5.870	1.00	52.43	6
ATOM	4971	O	ILE	D	6	42.711	65.420	5.709	1.00	52.78	8
ATOM	4972	N	LEU	D	7	40.701	65.134	6.666	1.00	51.01	7
ATOM	4973	CA	LEU	D	7	41.111	63.949	7.401	1.00	50.01	6
ATOM	4974	CB	LEU	D	7	39.962	63.459	8.276	1.00	47.85	6
ATOM	4975	CG	LEU	D	7	39.608	64.420	9.408	1.00	46.02	6
ATOM	4976	CD1	LEU	D	7	38.267	64.084	10.010	1.00	48.59	6
ATOM	4977	CD2	LEU	D	7	40.687	64.356	10.440	1.00	45.91	6
ATOM	4978	C	LEU	D	7	41.526	62.871	6.415	1.00	51.80	6
ATOM	4979	O	LEU	D	7	42.507	62.154	6.631	1.00	52.35	8
ATOM	4980	N	TYR	D	8	40.788	62.781	5.315	1.00	52.55	7
ATOM	4981	CA	TYR	D	8	41.060	61.788	4.288	1.00	53.16	6
ATOM	4982	CB	TYR	D	8	40.047	61.936	3.159	1.00	54.45	6
ATOM	4983	CG	TYR	D	8	40.294	61.006	2.006	1.00	57.19	6
ATOM	4984	CD1	TYR	D	8	40.030	59.646	2.120	1.00	57.12	6
ATOM	4985	CE1	TYR	D	8	40.308	58.772	1.069	1.00	60.62	6
ATOM	4986	CD2	TYR	D	8	40.841	61.481	0.810	1.00	58.57	6
ATOM	4987	CE2	TYR	D	8	41.130	60.617	-0.247	1.00	60.35	6
ATOM	4988	CZ	TYR	D	8	40.863	59.264	-0.112	1.00	61.47	6
ATOM	4989	OH	TYR	D	8	41.162	58.403	-1.149	1.00	62.53	8
ATOM	4990	C	TYR	D	8	42.483	61.905	3.735	1.00	53.38	6
ATOM	4991	O	TYR	D	8	43.190	60.907	3.591	1.00	53.74	8

ATOM	4992	N	ASN	D	9	42.900	63.121	3.416	1.00	53.53	7
ATOM	4993	CA	ASN	D	9	44.238	63.329	2.890	1.00	55.79	6
ATOM	4994	CB	ASN	D	9	44.451	64.800	2.509	1.00	59.06	6
ATOM	4995	CG	ASN	D	9	43.588	65.232	1.317	1.00	63.96	6
ATOM	4996	OD1	ASN	D	9	42.912	64.406	0.688	1.00	67.47	8
ATOM	4997	ND2	ASN	D	9	43.612	66.527	1.000	1.00	65.39	7
ATOM	4998	C	ASN	D	9	45.283	62.901	3.907	1.00	55.13	6
ATOM	4999	O	ASN	D	9	46.175	62.117	3.593	1.00	54.15	8
ATOM	5000	N	ILE	D	10	45.167	63.416	5.129	1.00	55.13	7
ATOM	5001	CA	ILE	D	10	46.099	63.077	6.195	1.00	54.61	6
ATOM	5002	CB	ILE	D	10	45.660	63.693	7.534	1.00	54.44	6
ATOM	5003	CG2	ILE	D	10	46.585	63.218	8.651	1.00	53.71	6
ATOM	5004	CG1	ILE	D	10	45.683	65.222	7.435	1.00	52.93	6
ATOM	5005	CD1	ILE	D	10	45.083	65.916	8.605	1.00	47.92	6
ATOM	5006	C	ILE	D	10	46.177	61.566	6.365	1.00	56.15	6
ATOM	5007	O	ILE	D	10	47.258	60.992	6.496	1.00	57.11	8
ATOM	5008	N	ARG	D	11	45.018	60.927	6.363	1.00	56.48	7
ATOM	5009	CA	ARG	D	11	44.938	59.494	6.512	1.00	58.41	6
ATOM	5010	CB	ARG	D	11	43.478	59.070	6.428	1.00	63.58	6
ATOM	5011	CG	ARG	D	11	43.229	57.585	6.631	1.00	70.33	6
ATOM	5012	CD	ARG	D	11	43.398	57.219	8.100	1.00	79.03	6
ATOM	5013	NE	ARG	D	11	42.703	55.980	8.448	1.00	85.37	7
ATOM	5014	CZ	ARG	D	11	41.466	55.685	8.037	1.00	88.61	6
ATOM	5015	NH1	ARG	D	11	40.795	56.548	7.249	1.00	89.11	7
ATOM	5016	NH2	ARG	D	11	40.890	54.545	8.434	1.00	87.93	7
ATOM	5017	C	ARG	D	11	45.721	58.778	5.425	1.00	58.93	6
ATOM	5018	O	ARG	D	11	46.497	57.862	5.698	1.00	58.85	8
ATOM	5019	N	GLN	D	12	45.507	59.211	4.186	1.00	59.05	7
ATOM	5020	CA	GLN	D	12	46.131	58.596	3.024	1.00	57.95	6
ATOM	5021	CB	GLN	D	12	45.345	58.958	1.780	1.00	57.48	6
ATOM	5022	CG	GLN	D	12	44.961	57.767	0.955	1.00	61.67	6
ATOM	5023	CD	GLN	D	12	43.773	57.069	1.525	1.00	61.71	6
ATOM	5024	OE1	GLN	D	12	42.729	57.685	1.698	1.00	64.71	8
ATOM	5025	NE2	GLN	D	12	43.912	55.784	1.831	1.00	59.81	7
ATOM	5026	C	GLN	D	12	47.589	58.926	2.769	1.00	57.99	6
ATOM	5027	O	GLN	D	12	48.280	58.169	2.097	1.00	58.62	8
ATOM	5028	N	THR	D	13	48.070	60.046	3.291	1.00	57.97	7
ATOM	5029	CA	THR	D	13	49.452	60.433	3.042	1.00	58.22	6
ATOM	5030	CB	THR	D	13	49.520	61.855	2.464	1.00	56.90	6
ATOM	5031	OG1	THR	D	13	48.907	62.774	3.377	1.00	53.15	8
ATOM	5032	CG2	THR	D	13	48.808	61.923	1.110	1.00	56.04	6
ATOM	5033	C	THR	D	13	50.361	60.394	4.255	1.00	60.59	6
ATOM	5034	O	THR	D	13	51.589	60.416	4.120	1.00	61.33	8
ATOM	5035	N	SER	D	14	49.762	60.335	5.440	1.00	61.87	7
ATOM	5036	CA	SER	D	14	50.542	60.332	6.669	1.00	61.93	6
ATOM	5037	CB	SER	D	14	49.634	60.613	7.863	1.00	61.53	6
ATOM	5038	OG	SER	D	14	50.417	60.962	8.988	1.00	62.76	8
ATOM	5039	C	SER	D	14	51.323	59.035	6.903	1.00	61.38	6
ATOM	5040	O	SER	D	14	50.922	57.950	6.467	1.00	62.07	8
ATOM	5041	N	ARG	D	15	52.444	59.175	7.596	1.00	59.21	7
ATOM	5042	CA	ARG	D	15	53.317	58.061	7.911	1.00	58.97	6
ATOM	5043	CB	ARG	D	15	54.553	58.087	7.011	1.00	59.72	6
ATOM	5044	CG	ARG	D	15	54.219	57.978	5.528	1.00	62.38	6
ATOM	5045	CD	ARG	D	15	55.455	57.608	4.738	1.00	63.96	6
ATOM	5046	NE	ARG	D	15	56.013	56.364	5.254	1.00	66.53	7
ATOM	5047	CZ	ARG	D	15	57.207	55.873	4.929	1.00	66.36	6
ATOM	5048	NH1	ARG	D	15	57.985	56.528	4.080	1.00	65.36	7
ATOM	5049	NH2	ARG	D	15	57.623	54.721	5.457	1.00	67.99	7
ATOM	5050	C	ARG	D	15	53.724	58.182	9.376	1.00	57.69	6
ATOM	5051	O	ARG	D	15	54.705	58.859	9.715	1.00	57.96	8
ATOM	5052	N	PRO	D	16	52.967	57.517	10.265	1.00	55.24	7

ATOM	5053	CD	PRO	D	16	51.785	56.700	9.935	1.00	51.06	6
ATOM	5054	CA	PRO	D	16	53.200	57.524	11.709	1.00	51.86	6
ATOM	5055	CB	PRO	D	16	52.104	56.602	12.236	1.00	49.85	6
ATOM	5056	CG	PRO	D	16	51.031	56.720	11.226	1.00	51.02	6
ATOM	5057	C	PRO	D	16	54.580	57.066	12.130	1.00	49.97	6
ATOM	5058	O	PRO	D	16	55.034	57.387	13.220	1.00	48.83	8
ATOM	5059	N	ASP	D	17	55.247	56.313	11.270	1.00	50.05	7
ATOM	5060	CA	ASP	D	17	56.568	55.809	11.612	1.00	53.82	6
ATOM	5061	CB	ASP	D	17	56.796	54.419	10.981	1.00	57.43	6
ATOM	5062	CG	ASP	D	17	55.979	53.320	11.666	1.00	63.55	6
ATOM	5063	OD1	ASP	D	17	55.728	53.431	12.892	1.00	63.43	8
ATOM	5064	OD2	ASP	D	17	55.598	52.330	10.985	1.00	66.47	8
ATOM	5065	C	ASP	D	17	57.710	56.733	11.218	1.00	52.72	6
ATOM	5066	O	ASP	D	17	58.875	56.406	11.440	1.00	54.00	8
ATOM	5067	N	VAL	D	18	57.384	57.888	10.653	1.00	50.54	7
ATOM	5068	CA	VAL	D	18	58.418	58.808	10.209	1.00	51.72	6
ATOM	5069	CB	VAL	D	18	58.353	58.992	8.680	1.00	52.70	6
ATOM	5070	CG1	VAL	D	18	59.487	59.869	8.209	1.00	52.67	6
ATOM	5071	CG2	VAL	D	18	58.426	57.642	7.998	1.00	53.16	6
ATOM	5072	C	VAL	D	18	58.402	60.181	10.865	1.00	51.90	6
ATOM	5073	O	VAL	D	18	57.463	60.955	10.716	1.00	50.79	8
ATOM	5074	N	ILE	D	19	59.475	60.473	11.586	1.00	52.81	7
ATOM	5075	CA	ILE	D	19	59.646	61.748	12.280	1.00	54.09	6
ATOM	5076	CB	ILE	D	19	60.960	61.699	13.116	1.00	53.08	6
ATOM	5077	CG2	ILE	D	19	62.168	61.565	12.194	1.00	53.31	6
ATOM	5078	CG1	ILE	D	19	61.074	62.919	14.027	1.00	52.13	6
ATOM	5079	CD1	ILE	D	19	62.157	62.753	15.086	1.00	49.47	6
ATOM	5080	C	ILE	D	19	59.675	62.907	11.255	1.00	56.58	6
ATOM	5081	O	ILE	D	19	60.436	62.877	10.274	1.00	57.79	8
ATOM	5082	N	PRO	D	20	58.833	63.936	11.464	1.00	56.89	7
ATOM	5083	CD	PRO	D	20	57.915	64.059	12.603	1.00	56.43	6
ATOM	5084	CA	PRO	D	20	58.725	65.113	10.587	1.00	58.17	6
ATOM	5085	CB	PRO	D	20	57.505	65.856	11.148	1.00	57.33	6
ATOM	5086	CG	PRO	D	20	56.812	64.848	12.009	1.00	56.81	6
ATOM	5087	C	PRO	D	20	59.985	66.004	10.585	1.00	60.38	6
ATOM	5088	O	PRO	D	20	59.920	67.215	10.802	1.00	57.93	8
ATOM	5089	N	THR	D	21	61.128	65.391	10.329	1.00	64.41	7
ATOM	5090	CA	THR	D	21	62.392	66.106	10.320	1.00	68.99	6
ATOM	5091	CB	THR	D	21	63.546	65.121	10.552	1.00	68.83	6
ATOM	5092	OG1	THR	D	21	63.899	65.152	11.939	1.00	69.74	8
ATOM	5093	CG2	THR	D	21	64.760	65.457	9.688	1.00	69.49	6
ATOM	5094	C	THR	D	21	62.671	66.926	9.067	1.00	73.81	6
ATOM	5095	O	THR	D	21	62.480	66.457	7.936	1.00	75.27	8
ATOM	5096	N	GLN	D	22	63.130	68.157	9.285	1.00	77.41	7
ATOM	5097	CA	GLN	D	22	63.481	69.076	8.203	1.00	81.17	6
ATOM	5098	CB	GLN	D	22	62.791	70.416	8.428	1.00	82.19	6
ATOM	5099	CG	GLN	D	22	61.281	70.306	8.543	1.00	84.72	6
ATOM	5100	CD	GLN	D	22	60.689	71.416	9.409	1.00	86.15	6
ATOM	5101	OE1	GLN	D	22	60.939	71.471	10.623	1.00	85.03	8
ATOM	5102	NE2	GLN	D	22	59.901	72.309	8.789	1.00	86.55	7
ATOM	5103	C	GLN	D	22	65.001	69.262	8.233	1.00	83.27	6
ATOM	5104	O	GLN	D	22	65.538	69.912	9.147	1.00	83.34	8
ATOM	5105	N	ARG	D	23	65.691	68.686	7.243	1.00	85.66	7
ATOM	5106	CA	ARG	D	23	67.159	68.767	7.170	1.00	87.34	6
ATOM	5107	CB	ARG	D	23	67.625	70.231	7.105	1.00	88.19	6
ATOM	5108	CG	ARG	D	23	67.453	70.875	5.742	1.00	89.83	6
ATOM	5109	CD	ARG	D	23	66.246	71.822	5.674	1.00	92.72	6
ATOM	5110	NE	ARG	D	23	65.994	72.293	4.298	1.00	95.59	7
ATOM	5111	CZ	ARG	D	23	66.904	72.868	3.497	1.00	95.46	6
ATOM	5112	NH1	ARG	D	23	68.158	73.068	3.914	1.00	93.60	7
ATOM	5113	NH2	ARG	D	23	66.555	73.226	2.257	1.00	94.84	7

ATOM	5114	C	ARG	D	23	67.768	68.079	8.399	1.00	87.43	6
ATOM	5115	O	ARG	D	23	67.201	67.105	8.907	1.00	88.35	8
ATOM	5116	N	ASP	D	24	68.912	68.570	8.875	1.00	87.68	7
ATOM	5117	CA	ASP	D	24	69.538	67.975	10.055	1.00	86.96	6
ATOM	5118	CB	ASP	D	24	71.041	68.283	10.123	1.00	91.11	6
ATOM	5119	CG	ASP	D	24	71.627	68.719	8.780	1.00	94.40	6
ATOM	5120	OD1	ASP	D	24	71.599	67.908	7.806	1.00	95.87	8
ATOM	5121	OD2	ASP	D	24	72.121	69.881	8.712	1.00	95.25	8
ATOM	5122	C	ASP	D	24	68.864	68.594	11.274	1.00	85.02	6
ATOM	5123	O	ASP	D	24	69.279	68.347	12.414	1.00	83.40	8
ATOM	5124	N	ARG	D	25	67.836	69.409	11.026	1.00	82.95	7
ATOM	5125	CA	ARG	D	25	67.112	70.062	12.111	1.00	81.58	6
ATOM	5126	CB	ARG	D	25	66.218	71.189	11.585	1.00	83.67	6
ATOM	5127	CG	ARG	D	25	66.951	72.455	11.150	1.00	88.52	6
ATOM	5128	CD	ARG	D	25	65.941	73.597	10.942	1.00	92.65	6
ATOM	5129	NE	ARG	D	25	66.579	74.866	10.584	1.00	96.29	7
ATOM	5130	CZ	ARG	D	25	65.928	76.024	10.463	1.00	98.03	6
ATOM	5131	NH1	ARG	D	25	64.608	76.073	10.673	1.00	98.35	7
ATOM	5132	NH2	ARG	D	25	66.597	77.136	10.142	1.00	98.69	7
ATOM	5133	C	ARG	D	25	66.241	69.091	12.901	1.00	78.66	6
ATOM	5134	O	ARG	D	25	65.480	68.303	12.325	1.00	79.51	8
ATOM	5135	N	PRO	D	26	66.353	69.127	14.237	1.00	74.94	7
ATOM	5136	CD	PRO	D	26	67.383	69.831	15.020	1.00	73.76	6
ATOM	5137	CA	PRO	D	26	65.562	68.252	15.101	1.00	71.13	6
ATOM	5138	CB	PRO	D	26	66.202	68.450	16.483	1.00	71.49	6
ATOM	5139	CG	PRO	D	26	67.608	68.884	16.165	1.00	72.18	6
ATOM	5140	C	PRO	D	26	64.115	68.738	15.095	1.00	67.33	6
ATOM	5141	O	PRO	D	26	63.834	69.874	14.713	1.00	65.48	8
ATOM	5142	N	VAL	D	27	63.198	67.870	15.510	1.00	63.87	7
ATOM	5143	CA	VAL	D	27	61.806	68.258	15.596	1.00	58.65	6
ATOM	5144	CB	VAL	D	27	60.849	67.036	15.494	1.00	57.16	6
ATOM	5145	CG1	VAL	D	27	59.462	67.401	15.998	1.00	54.11	6
ATOM	5146	CG2	VAL	D	27	60.755	66.579	14.052	1.00	56.19	6
ATOM	5147	C	VAL	D	27	61.705	68.896	16.968	1.00	56.92	6
ATOM	5148	O	VAL	D	27	62.164	68.337	17.961	1.00	55.97	8
ATOM	5149	N	ALA	D	28	61.136	70.088	17.019	1.00	56.42	7
ATOM	5150	CA	ALA	D	28	60.999	70.767	18.287	1.00	55.56	6
ATOM	5151	CB	ALA	D	28	61.057	72.269	18.095	1.00	55.33	6
ATOM	5152	C	ALA	D	28	59.688	70.371	18.923	1.00	54.28	6
ATOM	5153	O	ALA	D	28	58.617	70.741	18.440	1.00	54.43	8
ATOM	5154	N	VAL	D	29	59.800	69.603	20.006	1.00	52.62	7
ATOM	5155	CA	VAL	D	29	58.657	69.127	20.775	1.00	50.60	6
ATOM	5156	CB	VAL	D	29	58.715	67.599	21.016	1.00	48.93	6
ATOM	5157	CG1	VAL	D	29	57.543	67.162	21.871	1.00	46.20	6
ATOM	5158	CG2	VAL	D	29	58.718	66.868	19.692	1.00	47.60	6
ATOM	5159	C	VAL	D	29	58.652	69.805	22.131	1.00	50.77	6
ATOM	5160	O	VAL	D	29	59.657	69.806	22.852	1.00	51.59	8
ATOM	5161	N	SER	D	30	57.517	70.395	22.471	1.00	50.31	7
ATOM	5162	CA	SER	D	30	57.373	71.049	23.754	1.00	52.56	6
ATOM	5163	CB	SER	D	30	56.794	72.449	23.575	1.00	53.44	6
ATOM	5164	OG	SER	D	30	55.514	72.393	22.966	1.00	56.80	8
ATOM	5165	C	SER	D	30	56.442	70.188	24.598	1.00	53.29	6
ATOM	5166	O	SER	D	30	55.397	69.746	24.126	1.00	55.20	8
ATOM	5167	N	VAL	D	31	56.845	69.947	25.841	1.00	54.04	7
ATOM	5168	CA	VAL	D	31	56.089	69.130	26.780	1.00	56.25	6
ATOM	5169	CB	VAL	D	31	56.911	67.898	27.241	1.00	58.16	6
ATOM	5170	CG1	VAL	D	31	56.015	66.914	27.986	1.00	56.17	6
ATOM	5171	CG2	VAL	D	31	57.573	67.234	26.043	1.00	58.28	6
ATOM	5172	C	VAL	D	31	55.753	69.947	28.015	1.00	57.41	6
ATOM	5173	O	VAL	D	31	56.607	70.632	28.570	1.00	58.01	8
ATOM	5174	N	SER	D	32	54.508	69.850	28.458	1.00	59.19	7

ATOM	5175	CA	SER	D	32	54.062	70.594	29.628	1.00	59.47	6
ATOM	5176	CB	SER	D	32	53.467	71.934	29.175	1.00	60.04	6
ATOM	5177	OG	SER	D	32	52.892	72.641	30.256	1.00	62.30	8
ATOM	5178	C	SER	D	32	53.023	69.799	30.433	1.00	58.78	6
ATOM	5179	O	SER	D	32	51.906	69.572	29.966	1.00	59.54	8
ATOM	5180	N	LEU	D	33	53.390	69.379	31.638	1.00	56.81	7
ATOM	5181	CA	LEU	D	33	52.468	68.629	32.472	1.00	56.85	6
ATOM	5182	CB	LEU	D	33	53.217	67.702	33.426	1.00	54.23	6
ATOM	5183	CG	LEU	D	33	54.192	66.726	32.775	1.00	55.08	6
ATOM	5184	CD1	LEU	D	33	54.665	65.709	33.818	1.00	53.15	6
ATOM	5185	CD2	LEU	D	33	53.513	66.034	31.614	1.00	54.80	6
ATOM	5186	C	LEU	D	33	51.623	69.572	33.291	1.00	56.91	6
ATOM	5187	O	LEU	D	33	52.136	70.542	33.829	1.00	59.29	8
ATOM	5188	N	LYS	D	34	50.327	69.294	33.366	1.00	56.10	7
ATOM	5189	CA	LYS	D	34	49.422	70.089	34.171	1.00	55.13	6
ATOM	5190	CB	LYS	D	34	48.311	70.694	33.320	1.00	58.38	6
ATOM	5191	CG	LYS	D	34	48.802	71.519	32.146	1.00	65.52	6
ATOM	5192	CD	LYS	D	34	49.581	72.764	32.581	1.00	69.06	6
ATOM	5193	CE	LYS	D	34	50.100	73.559	31.364	1.00	72.37	6
ATOM	5194	NZ	LYS	D	34	50.855	74.801	31.747	1.00	72.05	7
ATOM	5195	C	LYS	D	34	48.838	69.065	35.118	1.00	53.80	6
ATOM	5196	O	LYS	D	34	48.123	68.167	34.685	1.00	55.04	8
ATOM	5197	N	PHE	D	35	49.144	69.173	36.405	1.00	51.60	7
ATOM	5198	CA	PHE	D	35	48.616	68.200	37.346	1.00	49.19	6
ATOM	5199	CB	PHE	D	35	49.441	68.199	38.616	1.00	46.49	6
ATOM	5200	CG	PHE	D	35	50.838	67.733	38.393	1.00	48.31	6
ATOM	5201	CD1	PHE	D	35	51.823	68.617	37.964	1.00	46.94	6
ATOM	5202	CD2	PHE	D	35	51.159	66.387	38.530	1.00	49.16	6
ATOM	5203	CE1	PHE	D	35	53.109	68.170	37.668	1.00	48.04	6
ATOM	5204	CE2	PHE	D	35	52.449	65.925	38.235	1.00	50.28	6
ATOM	5205	CZ	PHE	D	35	53.424	66.818	37.802	1.00	48.13	6
ATOM	5206	C	PHE	D	35	47.136	68.352	37.642	1.00	49.07	6
ATOM	5207	O	PHE	D	35	46.626	69.449	37.869	1.00	49.57	8
ATOM	5208	N	ILE	D	36	46.451	67.217	37.600	1.00	47.68	7
ATOM	5209	CA	ILE	D	36	45.030	67.156	37.827	1.00	44.72	6
ATOM	5210	CB	ILE	D	36	44.352	66.334	36.731	1.00	43.48	6
ATOM	5211	CG2	ILE	D	36	42.850	66.369	36.914	1.00	41.45	6
ATOM	5212	CG1	ILE	D	36	44.752	66.877	35.360	1.00	43.86	6
ATOM	5213	CD1	ILE	D	36	44.398	68.324	35.152	1.00	46.64	6
ATOM	5214	C	ILE	D	36	44.719	66.525	39.164	1.00	44.81	6
ATOM	5215	O	ILE	D	36	43.677	66.798	39.743	1.00	46.51	8
ATOM	5216	N	ASN	D	37	45.612	65.678	39.661	1.00	42.08	7
ATOM	5217	CA	ASN	D	37	45.363	65.030	40.939	1.00	42.31	6
ATOM	5218	CB	ASN	D	37	44.117	64.140	40.834	1.00	41.66	6
ATOM	5219	CG	ASN	D	37	43.392	63.990	42.159	1.00	43.88	6
ATOM	5220	OD1	ASN	D	37	44.015	63.785	43.200	1.00	43.62	8
ATOM	5221	ND2	ASN	D	37	42.068	64.085	42.124	1.00	38.41	7
ATOM	5222	C	ASN	D	37	46.539	64.186	41.426	1.00	43.81	6
ATOM	5223	O	ASN	D	37	47.380	63.752	40.640	1.00	40.93	8
ATOM	5224	N	ILE	D	38	46.588	63.977	42.740	1.00	43.93	7
ATOM	5225	CA	ILE	D	38	47.612	63.163	43.372	1.00	44.58	6
ATOM	5226	CB	ILE	D	38	48.496	64.013	44.246	1.00	42.93	6
ATOM	5227	CG2	ILE	D	38	49.473	63.140	44.989	1.00	39.88	6
ATOM	5228	CG1	ILE	D	38	49.220	65.028	43.359	1.00	43.19	6
ATOM	5229	CD1	ILE	D	38	49.944	66.110	44.084	1.00	44.94	6
ATOM	5230	C	ILE	D	38	46.795	62.183	44.190	1.00	47.97	6
ATOM	5231	O	ILE	D	38	46.169	62.565	45.162	1.00	50.60	8
ATOM	5232	N	LEU	D	39	46.802	60.916	43.777	1.00	50.68	7
ATOM	5233	CA	LEU	D	39	45.979	59.874	44.388	1.00	51.24	6
ATOM	5234	CB	LEU	D	39	45.489	58.944	43.287	1.00	51.95	6
ATOM	5235	CG	LEU	D	39	44.834	59.723	42.141	1.00	54.64	6

ATOM	5236	CD1	LEU	D	39	44.356	58.777	41.068	1.00	53.53	6
ATOM	5237	CD2	LEU	D	39	43.666	60.542	42.696	1.00	53.70	6
ATOM	5238	C	LEU	D	39	46.520	59.041	45.529	1.00	53.82	6
ATOM	5239	O	LEU	D	39	45.793	58.750	46.479	1.00	54.77	8
ATOM	5240	N	GLU	D	40	47.771	58.620	45.437	1.00	54.21	7
ATOM	5241	CA	GLU	D	40	48.349	57.825	46.507	1.00	56.24	6
ATOM	5242	CB	GLU	D	40	48.278	56.339	46.204	1.00	58.19	6
ATOM	5243	CG	GLU	D	40	46.873	55.801	46.103	1.00	65.00	6
ATOM	5244	CD	GLU	D	40	46.844	54.291	45.938	1.00	68.23	6
ATOM	5245	OE1	GLU	D	40	47.443	53.791	44.955	1.00	70.63	8
ATOM	5246	OE2	GLU	D	40	46.226	53.611	46.789	1.00	68.96	8
ATOM	5247	C	GLU	D	40	49.785	58.198	46.702	1.00	56.38	6
ATOM	5248	O	GLU	D	40	50.541	58.355	45.746	1.00	59.25	8
ATOM	5249	N	VAL	D	41	50.162	58.343	47.955	1.00	55.49	7
ATOM	5250	CA	VAL	D	41	51.517	58.695	48.273	1.00	54.71	6
ATOM	5251	CB	VAL	D	41	51.590	60.145	48.811	1.00	55.08	6
ATOM	5252	CG1	VAL	D	41	52.954	60.431	49.361	1.00	55.65	6
ATOM	5253	CG2	VAL	D	41	51.273	61.125	47.696	1.00	55.07	6
ATOM	5254	C	VAL	D	41	52.003	57.713	49.309	1.00	54.17	6
ATOM	5255	O	VAL	D	41	51.232	57.239	50.136	1.00	53.51	8
ATOM	5256	N	ASN	D	42	53.280	57.381	49.233	1.00	54.90	7
ATOM	5257	CA	ASN	D	42	53.880	56.473	50.182	1.00	56.47	6
ATOM	5258	CB	ASN	D	42	53.944	55.056	49.612	1.00	55.97	6
ATOM	5259	CG	ASN	D	42	54.306	54.025	50.661	1.00	56.38	6
ATOM	5260	OD1	ASN	D	42	55.272	54.191	51.408	1.00	55.15	8
ATOM	5261	ND2	ASN	D	42	53.536	52.947	50.717	1.00	56.12	7
ATOM	5262	C	ASN	D	42	55.278	57.022	50.420	1.00	58.56	6
ATOM	5263	O	ASN	D	42	56.154	56.912	49.567	1.00	58.83	8
ATOM	5264	N	GLU	D	43	55.474	57.639	51.579	1.00	59.69	7
ATOM	5265	CA	GLU	D	43	56.771	58.208	51.905	1.00	60.97	6
ATOM	5266	CB	GLU	D	43	56.640	59.192	53.065	1.00	63.50	6
ATOM	5267	CG	GLU	D	43	57.921	59.959	53.341	1.00	67.19	6
ATOM	5268	CD	GLU	D	43	57.725	61.121	54.303	1.00	68.84	6
ATOM	5269	OE1	GLU	D	43	58.743	61.734	54.682	1.00	70.83	8
ATOM	5270	OE2	GLU	D	43	56.568	61.427	54.670	1.00	67.80	8
ATOM	5271	C	GLU	D	43	57.792	57.134	52.246	1.00	59.80	6
ATOM	5272	O	GLU	D	43	58.993	57.356	52.138	1.00	59.85	8
ATOM	5273	N	ILE	D	44	57.301	55.969	52.653	1.00	59.27	7
ATOM	5274	CA	ILE	D	44	58.164	54.858	53.006	1.00	59.05	6
ATOM	5275	CB	ILE	D	44	57.373	53.723	53.681	1.00	59.62	6
ATOM	5276	CG2	ILE	D	44	58.300	52.527	53.945	1.00	59.50	6
ATOM	5277	CG1	ILE	D	44	56.752	54.217	54.982	1.00	58.87	6
ATOM	5278	CD1	ILE	D	44	57.768	54.484	56.073	1.00	60.45	6
ATOM	5279	C	ILE	D	44	58.801	54.286	51.751	1.00	59.04	6
ATOM	5280	O	ILE	D	44	60.001	54.029	51.723	1.00	60.06	8
ATOM	5281	N	THR	D	45	57.986	54.080	50.719	1.00	57.12	7
ATOM	5282	CA	THR	D	45	58.461	53.513	49.464	1.00	54.05	6
ATOM	5283	CB	THR	D	45	57.410	52.576	48.857	1.00	52.43	6
ATOM	5284	OG1	THR	D	45	56.204	53.304	48.628	1.00	49.39	8
ATOM	5285	CG2	THR	D	45	57.128	51.426	49.788	1.00	49.70	6
ATOM	5286	C	THR	D	45	58.833	54.551	48.417	1.00	53.32	6
ATOM	5287	O	THR	D	45	59.427	54.215	47.397	1.00	56.15	8
ATOM	5288	N	ASN	D	46	58.493	55.809	48.666	1.00	51.82	7
ATOM	5289	CA	ASN	D	46	58.796	56.874	47.723	1.00	51.33	6
ATOM	5290	CB	ASN	D	46	60.305	57.022	47.567	1.00	51.66	6
ATOM	5291	CG	ASN	D	46	60.874	58.117	48.434	1.00	52.73	6
ATOM	5292	OD1	ASN	D	46	62.057	58.105	48.765	1.00	52.55	8
ATOM	5293	ND2	ASN	D	46	60.041	59.078	48.793	1.00	50.90	7
ATOM	5294	C	ASN	D	46	58.156	56.618	46.360	1.00	50.97	6
ATOM	5295	O	ASN	D	46	58.820	56.668	45.325	1.00	53.17	8
ATOM	5296	N	GLU	D	47	56.858	56.348	46.371	1.00	48.99	7

ATOM	5297	CA	GLU	D	47	56.118	56.091	45.155	1.00	48.91	6
ATOM	5298	CB	GLU	D	47	55.717	54.627	45.105	1.00	46.66	6
ATOM	5299	CG	GLU	D	47	56.888	53.678	45.006	1.00	47.02	6
ATOM	5300	CD	GLU	D	47	56.458	52.227	45.018	1.00	49.64	6
ATOM	5301	OE1	GLU	D	47	55.302	51.956	44.644	1.00	48.30	8
ATOM	5302	OE2	GLU	D	47	57.276	51.357	45.391	1.00	51.88	8
ATOM	5303	C	GLU	D	47	54.888	56.992	45.111	1.00	50.12	6
ATOM	5304	O	GLU	D	47	54.222	57.202	46.125	1.00	50.30	8
ATOM	5305	N	VAL	D	48	54.591	57.531	43.936	1.00	50.20	7
ATOM	5306	CA	VAL	D	48	53.455	58.423	43.793	1.00	52.05	6
ATOM	5307	CB	VAL	D	48	53.925	59.861	43.502	1.00	53.36	6
ATOM	5308	CG1	VAL	D	48	52.727	60.778	43.352	1.00	56.39	6
ATOM	5309	CG2	VAL	D	48	54.801	60.352	44.620	1.00	54.18	6
ATOM	5310	C	VAL	D	48	52.522	57.995	42.673	1.00	51.50	6
ATOM	5311	O	VAL	D	48	52.962	57.552	41.617	1.00	53.49	8
ATOM	5312	N	ASP	D	49	51.231	58.137	42.910	1.00	49.46	7
ATOM	5313	CA	ASP	D	49	50.241	57.777	41.920	1.00	49.81	6
ATOM	5314	CB	ASP	D	49	49.241	56.813	42.535	1.00	52.06	6
ATOM	5315	CG	ASP	D	49	48.447	56.086	41.508	1.00	53.16	6
ATOM	5316	OD1	ASP	D	49	48.086	56.719	40.499	1.00	53.36	8
ATOM	5317	OD2	ASP	D	49	48.176	54.887	41.717	1.00	57.15	8
ATOM	5318	C	ASP	D	49	49.583	59.105	41.580	1.00	49.01	6
ATOM	5319	O	ASP	D	49	48.818	59.646	42.373	1.00	48.57	8
ATOM	5320	N	VAL	D	50	49.882	59.624	40.394	1.00	48.09	7
ATOM	5321	CA	VAL	D	50	49.380	60.928	39.986	1.00	47.49	6
ATOM	5322	CB	VAL	D	50	50.561	61.946	39.980	1.00	49.68	6
ATOM	5323	CG1	VAL	D	50	51.428	61.732	38.761	1.00	49.68	6
ATOM	5324	CG2	VAL	D	50	50.048	63.356	40.017	1.00	54.48	6
ATOM	5325	C	VAL	D	50	48.671	60.966	38.630	1.00	44.84	6
ATOM	5326	O	VAL	D	50	48.885	60.107	37.791	1.00	46.99	8
ATOM	5327	N	VAL	D	51	47.816	61.971	38.443	1.00	41.91	7
ATOM	5328	CA	VAL	D	51	47.067	62.186	37.204	1.00	40.48	6
ATOM	5329	CB	VAL	D	51	45.560	62.225	37.460	1.00	37.45	6
ATOM	5330	CG1	VAL	D	51	44.837	62.697	36.213	1.00	39.17	6
ATOM	5331	CG2	VAL	D	51	45.070	60.860	37.859	1.00	36.64	6
ATOM	5332	C	VAL	D	51	47.479	63.538	36.628	1.00	42.16	6
ATOM	5333	O	VAL	D	51	47.560	64.508	37.359	1.00	46.47	8
ATOM	5334	N	PHE	D	52	47.726	63.617	35.328	1.00	40.72	7
ATOM	5335	CA	PHE	D	52	48.144	64.877	34.738	1.00	42.11	6
ATOM	5336	CB	PHE	D	52	49.635	65.072	34.984	1.00	41.64	6
ATOM	5337	CG	PHE	D	52	50.491	64.007	34.362	1.00	42.87	6
ATOM	5338	CD1	PHE	D	52	50.887	64.099	33.038	1.00	44.21	6
ATOM	5339	CD2	PHE	D	52	50.868	62.891	35.088	1.00	42.70	6
ATOM	5340	CE1	PHE	D	52	51.642	63.100	32.447	1.00	42.06	6
ATOM	5341	CE2	PHE	D	52	51.624	61.886	34.506	1.00	42.93	6
ATOM	5342	CZ	PHE	D	52	52.010	61.990	33.185	1.00	41.42	6
ATOM	5343	C	PHE	D	52	47.870	64.940	33.241	1.00	44.00	6
ATOM	5344	O	PHE	D	52	47.606	63.931	32.610	1.00	46.55	8
ATOM	5345	N	TRP	D	53	47.934	66.133	32.673	1.00	43.89	7
ATOM	5346	CA	TRP	D	53	47.726	66.294	31.253	1.00	44.08	6
ATOM	5347	CB	TRP	D	53	46.919	67.538	30.948	1.00	45.09	6
ATOM	5348	CG	TRP	D	53	45.537	67.474	31.396	1.00	46.86	6
ATOM	5349	CD2	TRP	D	53	44.596	68.542	31.383	1.00	49.97	6
ATOM	5350	CE2	TRP	D	53	43.372	68.024	31.855	1.00	50.77	6
ATOM	5351	CE3	TRP	D	53	44.666	69.891	31.017	1.00	52.22	6
ATOM	5352	CD1	TRP	D	53	44.877	66.383	31.863	1.00	47.58	6
ATOM	5353	NE1	TRP	D	53	43.571	66.700	32.141	1.00	48.69	7
ATOM	5354	CZ2	TRP	D	53	42.222	68.808	31.973	1.00	52.23	6
ATOM	5355	CZ3	TRP	D	53	43.521	70.672	31.135	1.00	54.33	6
ATOM	5356	CH2	TRP	D	53	42.313	70.126	31.610	1.00	53.10	6
ATOM	5357	C	TRP	D	53	49.085	66.452	30.640	1.00	46.17	6

ATOM	5358	O	TRP	D	53	49.803	67.384	30.960	1.00	46.13	8
ATOM	5359	N	GLN	D	54	49.444	65.532	29.760	1.00	49.02	7
ATOM	5360	CA	GLN	D	54	50.741	65.592	29.112	1.00	48.49	6
ATOM	5361	CB	GLN	D	54	51.248	64.184	28.809	1.00	48.38	6
ATOM	5362	CG	GLN	D	54	52.677	64.135	28.317	1.00	50.78	6
ATOM	5363	CD	GLN	D	54	53.339	62.792	28.583	1.00	52.08	6
ATOM	5364	OE1	GLN	D	54	53.409	62.336	29.721	1.00	52.24	8
ATOM	5365	NE2	GLN	D	54	53.832	62.158	27.532	1.00	53.79	7
ATOM	5366	C	GLN	D	54	50.560	66.408	27.849	1.00	49.01	6
ATOM	5367	O	GLN	D	54	50.504	65.892	26.735	1.00	48.80	8
ATOM	5368	N	GLN	D	55	50.441	67.708	28.058	1.00	51.39	7
ATOM	5369	CA	GLN	D	55	50.256	68.665	26.985	1.00	53.26	6
ATOM	5370	CB	GLN	D	55	49.964	70.022	27.609	1.00	56.68	6
ATOM	5371	CG	GLN	D	55	49.913	71.176	26.652	1.00	66.24	6
ATOM	5372	CD	GLN	D	55	49.355	72.406	27.326	1.00	70.72	6
ATOM	5373	OE1	GLN	D	55	49.611	72.637	28.525	1.00	72.96	8
ATOM	5374	NE2	GLN	D	55	48.584	73.210	26.573	1.00	70.76	7
ATOM	5375	C	GLN	D	55	51.494	68.697	26.092	1.00	51.66	6
ATOM	5376	O	GLN	D	55	52.533	69.249	26.457	1.00	52.73	8
ATOM	5377	N	THR	D	56	51.373	68.091	24.920	1.00	48.75	7
ATOM	5378	CA	THR	D	56	52.485	68.005	23.988	1.00	48.81	6
ATOM	5379	CB	THR	D	56	52.769	66.534	23.617	1.00	48.35	6
ATOM	5380	OG1	THR	D	56	52.793	65.733	24.801	1.00	50.12	8
ATOM	5381	CG2	THR	D	56	54.101	66.408	22.925	1.00	47.54	6
ATOM	5382	C	THR	D	56	52.198	68.771	22.709	1.00	48.92	6
ATOM	5383	O	THR	D	56	51.051	68.862	22.275	1.00	50.82	8
ATOM	5384	N	THR	D	57	53.243	69.320	22.101	1.00	48.36	7
ATOM	5385	CA	THR	D	57	53.080	70.069	20.860	1.00	47.70	6
ATOM	5386	CB	THR	D	57	52.766	71.563	21.126	1.00	47.89	6
ATOM	5387	OG1	THR	D	57	51.521	71.679	21.834	1.00	48.44	8
ATOM	5388	CG2	THR	D	57	52.642	72.317	19.826	1.00	47.29	6
ATOM	5389	C	THR	D	57	54.322	69.988	19.995	1.00	47.52	6
ATOM	5390	O	THR	D	57	55.446	69.954	20.496	1.00	48.40	8
ATOM	5391	N	TRP	D	58	54.113	69.928	18.686	1.00	46.65	7
ATOM	5392	CA	TRP	D	58	55.221	69.883	17.749	1.00	45.92	6
ATOM	5393	CB	TRP	D	58	55.890	68.501	17.750	1.00	46.07	6
ATOM	5394	CG	TRP	D	58	55.055	67.379	17.192	1.00	46.21	6
ATOM	5395	CD2	TRP	D	58	54.099	66.585	17.904	1.00	45.21	6
ATOM	5396	CE2	TRP	D	58	53.517	65.702	16.976	1.00	45.14	6
ATOM	5397	CE3	TRP	D	58	53.675	66.537	19.240	1.00	44.92	6
ATOM	5398	CD1	TRP	D	58	55.018	66.952	15.902	1.00	44.73	6
ATOM	5399	NE1	TRP	D	58	54.097	65.945	15.761	1.00	46.01	7
ATOM	5400	CZ2	TRP	D	58	52.533	64.783	17.336	1.00	46.24	6
ATOM	5401	CZ3	TRP	D	58	52.696	65.618	19.596	1.00	45.62	6
ATOM	5402	CH2	TRP	D	58	52.138	64.755	18.646	1.00	45.70	6
ATOM	5403	C	TRP	D	58	54.679	70.236	16.386	1.00	47.55	6
ATOM	5404	O	TRP	D	58	53.494	70.509	16.237	1.00	46.55	8
ATOM	5405	N	SER	D	59	55.537	70.226	15.381	1.00	51.25	7
ATOM	5406	CA	SER	D	59	55.097	70.602	14.051	1.00	54.98	6
ATOM	5407	CB	SER	D	59	55.688	71.974	13.705	1.00	56.59	6
ATOM	5408	OG	SER	D	59	54.969	72.610	12.659	1.00	61.93	8
ATOM	5409	C	SER	D	59	55.457	69.592	12.967	1.00	55.53	6
ATOM	5410	O	SER	D	59	56.587	69.119	12.889	1.00	54.93	8
ATOM	5411	N	ASP	D	60	54.479	69.279	12.126	1.00	57.49	7
ATOM	5412	CA	ASP	D	60	54.660	68.338	11.028	1.00	59.17	6
ATOM	5413	CB	ASP	D	60	53.898	67.046	11.316	1.00	61.53	6
ATOM	5414	CG	ASP	D	60	54.141	65.967	10.275	1.00	63.57	6
ATOM	5415	OD1	ASP	D	60	54.465	66.300	9.120	1.00	64.52	8
ATOM	5416	OD2	ASP	D	60	53.988	64.773	10.611	1.00	64.89	8
ATOM	5417	C	ASP	D	60	54.067	69.020	9.811	1.00	60.52	6
ATOM	5418	O	ASP	D	60	52.847	69.016	9.615	1.00	59.95	8

ATOM	5419	N	ARG	D	61	54.937	69.609	8.995	1.00	62.50	7
ATOM	5420	CA	ARG	D	61	54.503	70.334	7.800	1.00	64.61	6
ATOM	5421	CB	ARG	D	61	55.672	71.137	7.205	1.00	67.57	6
ATOM	5422	CG	ARG	D	61	56.000	72.468	7.909	1.00	73.40	6
ATOM	5423	CD	ARG	D	61	56.968	73.283	7.037	1.00	81.08	6
ATOM	5424	NE	ARG	D	61	57.268	74.635	7.537	1.00	86.56	7
ATOM	5425	CZ	ARG	D	61	58.057	75.522	6.910	1.00	87.41	6
ATOM	5426	NH1	ARG	D	61	58.642	75.210	5.749	1.00	87.01	7
ATOM	5427	NH2	ARG	D	61	58.246	76.731	7.433	1.00	87.16	7
ATOM	5428	C	ARG	D	61	53.867	69.476	6.703	1.00	64.15	6
ATOM	5429	O	ARG	D	61	53.145	69.998	5.844	1.00	63.51	8
ATOM	5430	N	THR	D	62	54.121	68.170	6.722	1.00	62.13	7
ATOM	5431	CA	THR	D	62	53.542	67.303	5.704	1.00	61.28	6
ATOM	5432	CB	THR	D	62	54.171	65.886	5.716	1.00	62.74	6
ATOM	5433	OG1	THR	D	62	53.809	65.201	6.924	1.00	65.20	8
ATOM	5434	CG2	THR	D	62	55.692	65.974	5.624	1.00	63.05	6
ATOM	5435	C	THR	D	62	52.030	67.184	5.911	1.00	60.41	6
ATOM	5436	O	THR	D	62	51.313	66.619	5.073	1.00	60.16	8
ATOM	5437	N	LEU	D	63	51.551	67.731	7.025	1.00	59.01	7
ATOM	5438	CA	LEU	D	63	50.124	67.705	7.356	1.00	57.25	6
ATOM	5439	CB	LEU	D	63	49.932	67.483	8.860	1.00	55.13	6
ATOM	5440	CG	LEU	D	63	50.567	66.242	9.489	1.00	54.37	6
ATOM	5441	CD1	LEU	D	63	50.396	66.277	10.997	1.00	51.58	6
ATOM	5442	CD2	LEU	D	63	49.917	65.002	8.903	1.00	55.32	6
ATOM	5443	C	LEU	D	63	49.446	69.017	6.973	1.00	56.83	6
ATOM	5444	O	LEU	D	63	48.228	69.091	6.904	1.00	55.62	8
ATOM	5445	N	ALA	D	64	50.241	70.052	6.730	1.00	56.52	7
ATOM	5446	CA	ALA	D	64	49.702	71.362	6.388	1.00	56.94	6
ATOM	5447	CB	ALA	D	64	50.843	72.351	6.196	1.00	56.75	6
ATOM	5448	C	ALA	D	64	48.825	71.336	5.147	1.00	57.08	6
ATOM	5449	O	ALA	D	64	49.091	70.571	4.222	1.00	59.16	8
ATOM	5450	N	TRP	D	65	47.785	72.174	5.138	1.00	56.39	7
ATOM	5451	CA	TRP	D	65	46.853	72.286	4.008	1.00	57.81	6
ATOM	5452	CB	TRP	D	65	45.718	71.279	4.183	1.00	52.06	6
ATOM	5453	CG	TRP	D	65	44.662	71.708	5.139	1.00	49.69	6
ATOM	5454	CD2	TRP	D	65	44.574	71.383	6.532	1.00	48.62	6
ATOM	5455	CE2	TRP	D	65	43.386	71.974	7.027	1.00	50.58	6
ATOM	5456	CE3	TRP	D	65	45.379	70.649	7.409	1.00	45.78	6
ATOM	5457	CD1	TRP	D	65	43.563	72.466	4.855	1.00	51.37	6
ATOM	5458	NE1	TRP	D	65	42.787	72.631	5.985	1.00	51.62	7
ATOM	5459	CZ2	TRP	D	65	42.987	71.849	8.358	1.00	48.81	6
ATOM	5460	CZ3	TRP	D	65	44.983	70.525	8.731	1.00	45.33	6
ATOM	5461	CH2	TRP	D	65	43.797	71.122	9.193	1.00	48.88	6
ATOM	5462	C	TRP	D	65	46.281	73.723	3.873	1.00	60.73	6
ATOM	5463	O	TRP	D	65	46.309	74.493	4.839	1.00	61.78	8
ATOM	5464	N	ASN	D	66	45.757	74.081	2.692	1.00	63.62	7
ATOM	5465	CA	ASN	D	66	45.198	75.423	2.474	1.00	66.29	6
ATOM	5466	CB	ASN	D	66	44.996	75.702	0.975	1.00	67.13	6
ATOM	5467	CG	ASN	D	66	44.462	77.129	0.700	1.00	70.42	6
ATOM	5468	OD1	ASN	D	66	44.317	77.560	-0.465	1.00	68.84	8
ATOM	5469	ND2	ASN	D	66	44.167	77.866	1.780	1.00	71.49	7
ATOM	5470	C	ASN	D	66	43.886	75.676	3.221	1.00	67.74	6
ATOM	5471	O	ASN	D	66	42.823	75.208	2.820	1.00	67.77	8
ATOM	5472	N	SER	D	67	43.982	76.466	4.289	1.00	70.41	7
ATOM	5473	CA	SER	D	67	42.852	76.810	5.156	1.00	72.51	6
ATOM	5474	CB	SER	D	67	43.363	77.028	6.586	1.00	71.50	6
ATOM	5475	OG	SER	D	67	42.519	77.911	7.324	1.00	70.60	8
ATOM	5476	C	SER	D	67	42.021	78.025	4.763	1.00	74.90	6
ATOM	5477	O	SER	D	67	41.148	78.434	5.530	1.00	75.98	8
ATOM	5478	N	SER	D	68	42.272	78.603	3.589	1.00	77.57	7
ATOM	5479	CA	SER	D	68	41.538	79.805	3.157	1.00	79.08	6

ATOM	5480	CB	SER	D	68	41.991	80.243	1.761	1.00	78.86	6
ATOM	5481	OG	SER	D	68	41.612	79.297	0.776	1.00	79.93	8
ATOM	5482	C	SER	D	68	40.012	79.707	3.157	1.00	80.32	6
ATOM	5483	O	SER	D	68	39.328	80.655	3.552	1.00	81.34	8
ATOM	5484	N	HIS	D	69	39.471	78.578	2.711	1.00	80.85	7
ATOM	5485	CA	HIS	D	69	38.027	78.421	2.663	1.00	81.81	6
ATOM	5486	CB	HIS	D	69	37.562	78.625	1.239	1.00	84.77	6
ATOM	5487	CG	HIS	D	69	37.857	79.994	0.729	1.00	88.72	6
ATOM	5488	CD2	HIS	D	69	38.776	80.436	-0.166	1.00	89.11	6
ATOM	5489	ND1	HIS	D	69	37.226	81.117	1.227	1.00	88.96	7
ATOM	5490	CE1	HIS	D	69	37.748	82.193	0.660	1.00	90.17	6
ATOM	5491	NE2	HIS	D	69	38.691	81.809	-0.188	1.00	89.66	7
ATOM	5492	C	HIS	D	69	37.607	77.066	3.176	1.00	81.57	6
ATOM	5493	O	HIS	D	69	36.624	76.459	2.713	1.00	80.65	8
ATOM	5494	N	SER	D	70	38.362	76.606	4.162	1.00	80.66	7
ATOM	5495	CA	SER	D	70	38.110	75.319	4.770	1.00	79.33	6
ATOM	5496	CB	SER	D	70	38.813	74.240	3.941	1.00	79.59	6
ATOM	5497	OG	SER	D	70	40.110	74.675	3.550	1.00	79.40	8
ATOM	5498	C	SER	D	70	38.624	75.348	6.211	1.00	77.66	6
ATOM	5499	O	SER	D	70	39.520	76.135	6.545	1.00	76.61	8
ATOM	5500	N	PRO	D	71	38.037	74.514	7.088	1.00	76.20	7
ATOM	5501	CD	PRO	D	71	36.862	73.660	6.801	1.00	76.18	6
ATOM	5502	CA	PRO	D	71	38.420	74.425	8.502	1.00	74.80	6
ATOM	5503	CB	PRO	D	71	37.788	73.101	8.935	1.00	75.09	6
ATOM	5504	CG	PRO	D	71	36.454	73.145	8.196	1.00	75.33	6
ATOM	5505	C	PRO	D	71	39.933	74.465	8.704	1.00	73.25	6
ATOM	5506	O	PRO	D	71	40.685	73.855	7.939	1.00	73.92	8
ATOM	5507	N	ASP	D	72	40.369	75.180	9.738	1.00	71.15	7
ATOM	5508	CA	ASP	D	72	41.794	75.329	10.033	1.00	69.88	6
ATOM	5509	CB	ASP	D	72	42.077	76.680	10.721	1.00	74.59	6
ATOM	5510	CG	ASP	D	72	40.874	77.647	10.691	1.00	79.11	6
ATOM	5511	OD1	ASP	D	72	41.131	78.882	10.737	1.00	79.05	8
ATOM	5512	OD2	ASP	D	72	39.692	77.190	10.635	1.00	80.55	8
ATOM	5513	C	ASP	D	72	42.330	74.212	10.923	1.00	67.26	6
ATOM	5514	O	ASP	D	72	43.540	73.973	10.975	1.00	66.51	8
ATOM	5515	N	GLN	D	73	41.421	73.556	11.637	1.00	63.43	7
ATOM	5516	CA	GLN	D	73	41.756	72.462	12.539	1.00	60.99	6
ATOM	5517	CB	GLN	D	73	41.653	72.909	13.981	1.00	63.13	6
ATOM	5518	CG	GLN	D	73	42.774	73.723	14.533	1.00	65.58	6
ATOM	5519	CD	GLN	D	73	42.460	74.099	15.957	1.00	67.92	6
ATOM	5520	OE1	GLN	D	73	41.413	74.692	16.216	1.00	70.47	8
ATOM	5521	NE2	GLN	D	73	43.338	73.737	16.895	1.00	69.20	7
ATOM	5522	C	GLN	D	73	40.810	71.287	12.397	1.00	58.94	6
ATOM	5523	O	GLN	D	73	39.639	71.445	12.029	1.00	59.19	8
ATOM	5524	N	VAL	D	74	41.317	70.108	12.737	1.00	56.36	7
ATOM	5525	CA	VAL	D	74	40.531	68.883	12.698	1.00	52.71	6
ATOM	5526	CB	VAL	D	74	40.635	68.177	11.329	1.00	51.38	6
ATOM	5527	CG1	VAL	D	74	39.944	68.998	10.260	1.00	48.73	6
ATOM	5528	CG2	VAL	D	74	42.087	67.951	10.973	1.00	48.36	6
ATOM	5529	C	VAL	D	74	41.089	67.959	13.760	1.00	50.70	6
ATOM	5530	O	VAL	D	74	42.240	68.108	14.173	1.00	49.32	8
ATOM	5531	N	SER	D	75	40.264	67.023	14.215	1.00	48.60	7
ATOM	5532	CA	SER	D	75	40.696	66.051	15.206	1.00	46.92	6
ATOM	5533	CB	SER	D	75	39.555	65.729	16.166	1.00	48.45	6
ATOM	5534	OG	SER	D	75	39.444	66.718	17.168	1.00	48.28	8
ATOM	5535	C	SER	D	75	41.159	64.789	14.487	1.00	44.70	6
ATOM	5536	O	SER	D	75	40.397	64.143	13.781	1.00	43.70	8
ATOM	5537	N	VAL	D	76	42.424	64.449	14.675	1.00	44.00	7
ATOM	5538	CA	VAL	D	76	43.024	63.281	14.039	1.00	43.43	6
ATOM	5539	CB	VAL	D	76	44.283	63.687	13.264	1.00	44.79	6
ATOM	5540	CG1	VAL	D	76	44.891	62.486	12.604	1.00	43.63	6

ATOM	5541	CG2	VAL	D	76	43.943	64.746	12.241	1.00	42.10	6
ATOM	5542	C	VAL	D	76	43.419	62.193	15.034	1.00	43.50	6
ATOM	5543	O	VAL	D	76	44.004	62.472	16.078	1.00	45.44	8
ATOM	5544	N	PRO	D	77	43.102	60.929	14.721	1.00	42.76	7
ATOM	5545	CD	PRO	D	77	42.235	60.402	13.656	1.00	41.52	6
ATOM	5546	CA	PRO	D	77	43.472	59.865	15.650	1.00	41.41	6
ATOM	5547	CB	PRO	D	77	42.856	58.628	15.009	1.00	42.36	6
ATOM	5548	CG	PRO	D	77	41.674	59.168	14.296	1.00	40.67	6
ATOM	5549	C	PRO	D	77	44.985	59.774	15.749	1.00	40.15	6
ATOM	5550	O	PRO	D	77	45.687	59.922	14.762	1.00	39.02	8
ATOM	5551	N	ILE	D	78	45.474	59.537	16.954	1.00	41.66	7
ATOM	5552	CA	ILE	D	78	46.899	59.421	17.217	1.00	42.23	6
ATOM	5553	CB	ILE	D	78	47.113	59.019	18.687	1.00	43.04	6
ATOM	5554	CG2	ILE	D	78	48.495	58.518	18.924	1.00	45.01	6
ATOM	5555	CG1	ILE	D	78	46.872	60.236	19.555	1.00	47.88	6
ATOM	5556	CD1	ILE	D	78	47.618	61.461	19.057	1.00	48.43	6
ATOM	5557	C	ILE	D	78	47.591	58.432	16.299	1.00	42.53	6
ATOM	5558	O	ILE	D	78	48.717	58.643	15.880	1.00	44.25	8
ATOM	5559	N	SER	D	79	46.891	57.358	15.979	1.00	43.93	7
ATOM	5560	CA	SER	D	79	47.410	56.302	15.127	1.00	43.22	6
ATOM	5561	CB	SER	D	79	46.457	55.110	15.185	1.00	42.69	6
ATOM	5562	OG	SER	D	79	45.130	55.523	14.910	1.00	43.59	8
ATOM	5563	C	SER	D	79	47.661	56.692	13.668	1.00	42.26	6
ATOM	5564	O	SER	D	79	48.319	55.953	12.937	1.00	41.56	8
ATOM	5565	N	SER	D	80	47.138	57.835	13.243	1.00	39.86	7
ATOM	5566	CA	SER	D	80	47.326	58.282	11.871	1.00	40.25	6
ATOM	5567	CB	SER	D	80	46.026	58.840	11.307	1.00	40.77	6
ATOM	5568	OG	SER	D	80	45.025	57.845	11.259	1.00	48.70	8
ATOM	5569	C	SER	D	80	48.413	59.342	11.742	1.00	41.01	6
ATOM	5570	O	SER	D	80	48.658	59.842	10.655	1.00	41.05	8
ATOM	5571	N	LEU	D	81	49.067	59.671	12.847	1.00	39.67	7
ATOM	5572	CA	LEU	D	81	50.112	60.678	12.844	1.00	39.96	6
ATOM	5573	CB	LEU	D	81	49.703	61.886	13.684	1.00	40.31	6
ATOM	5574	CG	LEU	D	81	48.371	62.571	13.448	1.00	42.96	6
ATOM	5575	CD1	LEU	D	81	48.019	63.429	14.638	1.00	41.75	6
ATOM	5576	CD2	LEU	D	81	48.454	63.382	12.191	1.00	44.21	6
ATOM	5577	C	LEU	D	81	51.357	60.109	13.472	1.00	38.80	6
ATOM	5578	O	LEU	D	81	51.303	59.077	14.119	1.00	39.28	8
ATOM	5579	N	TRP	D	82	52.478	60.795	13.276	1.00	37.55	7
ATOM	5580	CA	TRP	D	82	53.726	60.398	13.891	1.00	36.02	6
ATOM	5581	CB	TRP	D	82	54.927	60.981	13.158	1.00	39.06	6
ATOM	5582	CG	TRP	D	82	56.206	60.891	13.958	1.00	40.02	6
ATOM	5583	CD2	TRP	D	82	56.715	61.864	14.887	1.00	39.10	6
ATOM	5584	CE2	TRP	D	82	57.878	61.318	15.463	1.00	38.66	6
ATOM	5585	CE3	TRP	D	82	56.294	63.140	15.292	1.00	38.90	6
ATOM	5586	CD1	TRP	D	82	57.060	59.840	14.007	1.00	40.23	6
ATOM	5587	NE1	TRP	D	82	58.065	60.082	14.908	1.00	40.21	7
ATOM	5588	CZ2	TRP	D	82	58.630	61.997	16.422	1.00	36.80	6
ATOM	5589	CZ3	TRP	D	82	57.038	63.812	16.247	1.00	40.18	6
ATOM	5590	CH2	TRP	D	82	58.195	63.238	16.801	1.00	38.54	6
ATOM	5591	C	TRP	D	82	53.606	61.068	15.236	1.00	35.47	6
ATOM	5592	O	TRP	D	82	53.085	62.172	15.339	1.00	36.72	8
ATOM	5593	N	VAL	D	83	54.078	60.408	16.272	1.00	34.62	7
ATOM	5594	CA	VAL	D	83	53.996	60.989	17.592	1.00	36.17	6
ATOM	5595	CB	VAL	D	83	52.827	60.341	18.381	1.00	35.89	6
ATOM	5596	CG1	VAL	D	83	52.906	60.676	19.835	1.00	38.30	6
ATOM	5597	CG2	VAL	D	83	51.507	60.840	17.832	1.00	35.92	6
ATOM	5598	C	VAL	D	83	55.335	60.810	18.312	1.00	37.27	6
ATOM	5599	O	VAL	D	83	56.035	59.821	18.113	1.00	36.95	8
ATOM	5600	N	PRO	D	84	55.727	61.796	19.125	1.00	35.49	7
ATOM	5601	CD	PRO	D	84	55.073	63.095	19.324	1.00	37.20	6

ATOM	5602	CA	PRO	D	84	56.979	61.740	19.873	1.00	36.59	6
ATOM	5603	CB	PRO	D	84	56.933	63.024	20.694	1.00	37.18	6
ATOM	5604	CG	PRO	D	84	56.196	63.930	19.835	1.00	36.05	6
ATOM	5605	C	PRO	D	84	57.034	60.502	20.759	1.00	35.92	6
ATOM	5606	O	PRO	D	84	56.070	60.197	21.449	1.00	34.78	8
ATOM	5607	N	ASP	D	85	58.161	59.798	20.749	1.00	33.98	7
ATOM	5608	CA	ASP	D	85	58.283	58.609	21.565	1.00	34.25	6
ATOM	5609	CB	ASP	D	85	59.244	57.622	20.925	1.00	35.35	6
ATOM	5610	CG	ASP	D	85	60.600	58.201	20.700	1.00	38.15	6
ATOM	5611	OD1	ASP	D	85	60.645	59.379	20.327	1.00	40.37	8
ATOM	5612	OD2	ASP	D	85	61.612	57.486	20.870	1.00	36.29	8
ATOM	5613	C	ASP	D	85	58.740	58.962	22.964	1.00	37.26	6
ATOM	5614	O	ASP	D	85	59.737	58.449	23.453	1.00	38.45	8
ATOM	5615	N	LEU	D	86	57.981	59.840	23.609	1.00	35.72	7
ATOM	5616	CA	LEU	D	86	58.290	60.294	24.956	1.00	37.34	6
ATOM	5617	CB	LEU	D	86	57.397	61.471	25.325	1.00	35.58	6
ATOM	5618	CG	LEU	D	86	57.576	62.690	24.434	1.00	36.77	6
ATOM	5619	CD1	LEU	D	86	56.652	63.799	24.877	1.00	32.58	6
ATOM	5620	CD2	LEU	D	86	59.026	63.127	24.496	1.00	36.92	6
ATOM	5621	C	LEU	D	86	58.112	59.205	25.989	1.00	38.80	6
ATOM	5622	O	LEU	D	86	57.250	58.337	25.853	1.00	43.05	8
ATOM	5623	N	ALA	D	87	58.925	59.263	27.033	1.00	38.29	7
ATOM	5624	CA	ALA	D	87	58.852	58.291	28.103	1.00	38.34	6
ATOM	5625	CB	ALA	D	87	59.808	57.174	27.827	1.00	37.03	6
ATOM	5626	C	ALA	D	87	59.202	58.966	29.414	1.00	39.60	6
ATOM	5627	O	ALA	D	87	60.087	59.793	29.436	1.00	43.32	8
ATOM	5628	N	ALA	D	88	58.495	58.644	30.492	1.00	39.86	7
ATOM	5629	CA	ALA	D	88	58.804	59.234	31.786	1.00	39.70	6
ATOM	5630	CB	ALA	D	88	57.572	59.294	32.654	1.00	38.81	6
ATOM	5631	C	ALA	D	88	59.861	58.347	32.418	1.00	41.02	6
ATOM	5632	O	ALA	D	88	59.575	57.259	32.894	1.00	42.74	8
ATOM	5633	N	TYR	D	89	61.095	58.826	32.400	1.00	42.88	7
ATOM	5634	CA	TYR	D	89	62.241	58.101	32.931	1.00	44.50	6
ATOM	5635	CB	TYR	D	89	63.443	59.050	33.031	1.00	46.85	6
ATOM	5636	CG	TYR	D	89	63.940	59.583	31.709	1.00	50.97	6
ATOM	5637	CD1	TYR	D	89	64.910	60.571	31.663	1.00	55.21	6
ATOM	5638	CE1	TYR	D	89	65.384	61.063	30.441	1.00	57.34	6
ATOM	5639	CD2	TYR	D	89	63.452	59.090	30.502	1.00	52.68	6
ATOM	5640	CE2	TYR	D	89	63.916	59.569	29.288	1.00	55.92	6
ATOM	5641	CZ	TYR	D	89	64.881	60.557	29.260	1.00	57.40	6
ATOM	5642	OH	TYR	D	89	65.341	61.041	28.048	1.00	61.62	8
ATOM	5643	C	TYR	D	89	62.044	57.403	34.274	1.00	43.55	6
ATOM	5644	O	TYR	D	89	62.618	56.340	34.503	1.00	43.31	8
ATOM	5645	N	ASN	D	90	61.261	57.992	35.171	1.00	40.99	7
ATOM	5646	CA	ASN	D	90	61.059	57.368	36.470	1.00	40.89	6
ATOM	5647	CB	ASN	D	90	61.459	58.323	37.605	1.00	38.07	6
ATOM	5648	CG	ASN	D	90	60.717	59.639	37.561	1.00	38.20	6
ATOM	5649	OD1	ASN	D	90	60.602	60.270	36.515	1.00	43.00	8
ATOM	5650	ND2	ASN	D	90	60.229	60.071	38.707	1.00	36.31	7
ATOM	5651	C	ASN	D	90	59.646	56.851	36.669	1.00	41.76	6
ATOM	5652	O	ASN	D	90	59.170	56.706	37.795	1.00	42.39	8
ATOM	5653	N	ALA	D	91	58.974	56.568	35.562	1.00	42.04	7
ATOM	5654	CA	ALA	D	91	57.631	56.023	35.630	1.00	42.57	6
ATOM	5655	CB	ALA	D	91	56.985	56.010	34.260	1.00	42.26	6
ATOM	5656	C	ALA	D	91	57.820	54.603	36.150	1.00	42.84	6
ATOM	5657	O	ALA	D	91	58.716	53.882	35.717	1.00	41.70	8
ATOM	5658	N	ILE	D	92	56.963	54.222	37.084	1.00	44.08	7
ATOM	5659	CA	ILE	D	92	57.012	52.930	37.733	1.00	44.15	6
ATOM	5660	CB	ILE	D	92	56.838	53.166	39.239	1.00	48.04	6
ATOM	5661	CG2	ILE	D	92	55.423	52.860	39.672	1.00	49.55	6
ATOM	5662	CG1	ILE	D	92	57.827	52.337	40.032	1.00	51.37	6

ATOM	5663	CD1	ILE	D	92	57.559	52.447	41.544	1.00	57.95	6
ATOM	5664	C	ILE	D	92	55.921	51.998	37.180	1.00	43.63	6
ATOM	5665	O	ILE	D	92	55.867	50.816	37.502	1.00	43.77	8
ATOM	5666	N	SER	D	93	55.051	52.546	36.343	1.00	41.02	7
ATOM	5667	CA	SER	D	93	53.968	51.788	35.733	1.00	39.43	6
ATOM	5668	CB	SER	D	93	52.673	51.994	36.498	1.00	40.39	6
ATOM	5669	OG	SER	D	93	52.200	53.324	36.320	1.00	40.98	8
ATOM	5670	C	SER	D	93	53.802	52.387	34.366	1.00	39.82	6
ATOM	5671	O	SER	D	93	54.349	53.452	34.103	1.00	38.78	8
ATOM	5672	N	LYS	D	94	53.063	51.727	33.484	1.00	40.02	7
ATOM	5673	CA	LYS	D	94	52.883	52.322	32.173	1.00	42.68	6
ATOM	5674	CB	LYS	D	94	52.695	51.260	31.081	1.00	42.12	6
ATOM	5675	CG	LYS	D	94	51.789	50.113	31.405	1.00	45.31	6
ATOM	5676	CD	LYS	D	94	51.980	48.999	30.378	1.00	48.12	6
ATOM	5677	CE	LYS	D	94	51.973	49.545	28.957	1.00	49.66	6
ATOM	5678	NZ	LYS	D	94	52.092	48.466	27.938	1.00	53.06	7
ATOM	5679	C	LYS	D	94	51.738	53.319	32.205	1.00	42.30	6
ATOM	5680	O	LYS	D	94	50.899	53.299	33.104	1.00	42.15	8
ATOM	5681	N	PRO	D	95	51.707	54.230	31.234	1.00	41.20	7
ATOM	5682	CD	PRO	D	95	52.637	54.379	30.108	1.00	37.85	6
ATOM	5683	CA	PRO	D	95	50.655	55.243	31.178	1.00	40.86	6
ATOM	5684	CB	PRO	D	95	51.064	56.117	29.990	1.00	41.55	6
ATOM	5685	CG	PRO	D	95	52.512	55.834	29.821	1.00	42.69	6
ATOM	5686	C	PRO	D	95	49.263	54.691	30.981	1.00	39.96	6
ATOM	5687	O	PRO	D	95	49.030	53.893	30.080	1.00	39.70	8
ATOM	5688	N	GLU	D	96	48.344	55.113	31.835	1.00	40.14	7
ATOM	5689	CA	GLU	D	96	46.961	54.718	31.689	1.00	38.41	6
ATOM	5690	CB	GLU	D	96	46.321	54.399	33.041	1.00	40.63	6
ATOM	5691	CG	GLU	D	96	44.880	53.856	32.923	1.00	48.74	6
ATOM	5692	CD	GLU	D	96	44.232	53.503	34.273	1.00	51.27	6
ATOM	5693	OE1	GLU	D	96	44.983	53.350	35.261	1.00	50.19	8
ATOM	5694	OE2	GLU	D	96	42.979	53.360	34.345	1.00	50.07	8
ATOM	5695	C	GLU	D	96	46.324	55.963	31.084	1.00	37.34	6
ATOM	5696	O	GLU	D	96	45.998	56.900	31.799	1.00	36.63	8
ATOM	5697	N	VAL	D	97	46.199	55.988	29.760	1.00	34.71	7
ATOM	5698	CA	VAL	D	97	45.599	57.120	29.079	1.00	32.69	6
ATOM	5699	CB	VAL	D	97	45.881	57.066	27.582	1.00	30.58	6
ATOM	5700	CG1	VAL	D	97	45.289	58.260	26.896	1.00	30.36	6
ATOM	5701	CG2	VAL	D	97	47.361	57.037	27.354	1.00	28.89	6
ATOM	5702	C	VAL	D	97	44.104	57.067	29.345	1.00	34.47	6
ATOM	5703	O	VAL	D	97	43.431	56.124	28.962	1.00	35.88	8
ATOM	5704	N	LEU	D	98	43.597	58.091	30.019	1.00	35.68	7
ATOM	5705	CA	LEU	D	98	42.190	58.174	30.401	1.00	36.36	6
ATOM	5706	CB	LEU	D	98	42.071	58.943	31.713	1.00	35.92	6
ATOM	5707	CG	LEU	D	98	42.941	58.547	32.894	1.00	36.85	6
ATOM	5708	CD1	LEU	D	98	42.906	59.639	33.914	1.00	35.58	6
ATOM	5709	CD2	LEU	D	98	42.456	57.261	33.487	1.00	39.84	6
ATOM	5710	C	LEU	D	98	41.276	58.845	29.386	1.00	38.24	6
ATOM	5711	O	LEU	D	98	40.055	58.850	29.549	1.00	37.04	8
ATOM	5712	N	THR	D	99	41.862	59.409	28.338	1.00	37.00	7
ATOM	5713	CA	THR	D	99	41.082	60.130	27.344	1.00	36.28	6
ATOM	5714	CB	THR	D	99	41.449	61.644	27.378	1.00	36.19	6
ATOM	5715	OG1	THR	D	99	42.863	61.803	27.177	1.00	38.29	8
ATOM	5716	CG2	THR	D	99	41.075	62.248	28.706	1.00	31.31	6
ATOM	5717	C	THR	D	99	41.224	59.629	25.910	1.00	35.89	6
ATOM	5718	O	THR	D	99	42.148	58.883	25.588	1.00	35.45	8
ATOM	5719	N	PRO	D	100	40.281	60.026	25.034	1.00	34.88	7
ATOM	5720	CD	PRO	D	100	39.043	60.761	25.337	1.00	35.25	6
ATOM	5721	CA	PRO	D	100	40.303	59.630	23.631	1.00	33.36	6
ATOM	5722	CB	PRO	D	100	39.217	60.492	23.024	1.00	32.41	6
ATOM	5723	CG	PRO	D	100	38.223	60.527	24.093	1.00	33.73	6

ATOM	5724	C	PRO	D	100	41.666	59.955	23.077	1.00 35.04	6
ATOM	5725	O	PRO	D	100	42.188	61.028	23.310	1.00 36.02	8
ATOM	5726	N	GLN	D	101	42.256	59.026	22.350	1.00 38.56	7
ATOM	5727	CA	GLN	D	101	43.574	59.280	21.817	1.00 39.66	6
ATOM	5728	CB	GLN	D	101	44.356	57.980	21.749	1.00 38.98	6
ATOM	5729	CG	GLN	D	101	44.890	57.613	23.109	1.00 41.80	6
ATOM	5730	CD	GLN	D	101	45.318	56.175	23.201	1.00 46.38	6
ATOM	5731	OE1	GLN	D	101	46.158	55.714	22.439	1.00 50.42	8
ATOM	5732	NE2	GLN	D	101	44.735	55.447	24.143	1.00 49.13	7
ATOM	5733	C	GLN	D	101	43.543	59.994	20.486	1.00 39.27	6
ATOM	5734	O	GLN	D	101	43.965	59.463	19.463	1.00 38.19	8
ATOM	5735	N	LEU	D	102	43.037	61.224	20.540	1.00 40.46	7
ATOM	5736	CA	LEU	D	102	42.910	62.103	19.381	1.00 40.51	6
ATOM	5737	CB	LEU	D	102	41.467	62.590	19.231	1.00 37.39	6
ATOM	5738	CG	LEU	D	102	40.382	61.515	19.121	1.00 38.97	6
ATOM	5739	CD1	LEU	D	102	39.030	62.182	18.988	1.00 36.48	6
ATOM	5740	CD2	LEU	D	102	40.657	60.628	17.925	1.00 36.34	6
ATOM	5741	C	LEU	D	102	43.804	63.308	19.554	1.00 41.42	6
ATOM	5742	O	LEU	D	102	43.990	63.794	20.665	1.00 43.09	8
ATOM	5743	N	ALA	D	103	44.375	63.777	18.455	1.00 40.44	7
ATOM	5744	CA	ALA	D	103	45.221	64.953	18.489	1.00 40.53	6
ATOM	5745	CB	ALA	D	103	46.549	64.673	17.847	1.00 43.43	6
ATOM	5746	C	ALA	D	103	44.500	66.050	17.731	1.00 41.82	6
ATOM	5747	O	ALA	D	103	43.503	65.803	17.058	1.00 41.33	8
ATOM	5748	N	ARG	D	104	44.998	67.271	17.849	1.00 42.58	7
ATOM	5749	CA	ARG	D	104	44.369	68.381	17.165	1.00 43.20	6
ATOM	5750	CB	ARG	D	104	43.995	69.450	18.183	1.00 43.57	6
ATOM	5751	CG	ARG	D	104	43.032	70.480	17.678	1.00 40.98	6
ATOM	5752	CD	ARG	D	104	41.674	69.900	17.425	1.00 39.96	6
ATOM	5753	NE	ARG	D	104	40.803	70.951	16.909	1.00 41.32	7
ATOM	5754	CZ	ARG	D	104	39.517	70.802	16.635	1.00 39.52	6
ATOM	5755	NH1	ARG	D	104	38.927	69.633	16.824	1.00 40.96	7
ATOM	5756	NH2	ARG	D	104	38.826	71.832	16.175	1.00 38.44	7
ATOM	5757	C	ARG	D	104	45.380	68.896	16.162	1.00 43.89	6
ATOM	5758	O	ARG	D	104	46.508	69.192	16.526	1.00 44.97	8
ATOM	5759	N	VAL	D	105	44.989	68.966	14.894	1.00 44.88	7
ATOM	5760	CA	VAL	D	105	45.910	69.427	13.863	1.00 46.87	6
ATOM	5761	CB	VAL	D	105	46.094	68.380	12.751	1.00 44.91	6
ATOM	5762	CG1	VAL	D	105	47.165	68.838	11.787	1.00 42.60	6
ATOM	5763	CG2	VAL	D	105	46.469	67.050	13.346	1.00 43.58	6
ATOM	5764	C	VAL	D	105	45.467	70.729	13.223	1.00 48.29	6
ATOM	5765	O	VAL	D	105	44.335	70.845	12.731	1.00 47.85	8
ATOM	5766	N	VAL	D	106	46.375	71.702	13.238	1.00 48.47	7
ATOM	5767	CA	VAL	D	106	46.129	73.018	12.663	1.00 50.73	6
ATOM	5768	CB	VAL	D	106	46.855	74.106	13.472	1.00 50.55	6
ATOM	5769	CG1	VAL	D	106	46.392	75.477	13.026	1.00 51.23	6
ATOM	5770	CG2	VAL	D	106	46.601	73.903	14.951	1.00 48.01	6
ATOM	5771	C	VAL	D	106	46.636	73.025	11.216	1.00 51.91	6
ATOM	5772	O	VAL	D	106	47.664	72.420	10.918	1.00 52.36	8
ATOM	5773	N	SER	D	107	45.920	73.712	10.329	1.00 52.06	7
ATOM	5774	CA	SER	D	107	46.281	73.761	8.915	1.00 51.56	6
ATOM	5775	CB	SER	D	107	45.391	74.756	8.185	1.00 52.91	6
ATOM	5776	OG	SER	D	107	45.259	75.941	8.943	1.00 59.44	8
ATOM	5777	C	SER	D	107	47.726	74.058	8.591	1.00 50.83	6
ATOM	5778	O	SER	D	107	48.188	73.739	7.511	1.00 50.82	8
ATOM	5779	N	ASP	D	108	48.451	74.657	9.519	1.00 53.72	7
ATOM	5780	CA	ASP	D	108	49.853	74.978	9.262	1.00 57.12	6
ATOM	5781	CB	ASP	D	108	50.239	76.289	9.965	1.00 58.24	6
ATOM	5782	CG	ASP	D	108	50.271	76.163	11.475	1.00 61.04	6
ATOM	5783	OD1	ASP	D	108	49.396	75.459	12.042	1.00 63.89	8
ATOM	5784	OD2	ASP	D	108	51.162	76.782	12.095	1.00 60.97	8

ATOM	5785	C	ASP	D	108	50.827	73.870	9.665	1.00 58.88	6
ATOM	5786	O	ASP	D	108	52.043	74.071	9.635	1.00 61.62	8
ATOM	5787	N	GLY	D	109	50.293	72.711	10.051	1.00 58.94	7
ATOM	5788	CA	GLY	D	109	51.134	71.589	10.437	1.00 58.18	6
ATOM	5789	C	GLY	D	109	51.424	71.483	11.918	1.00 57.62	6
ATOM	5790	O	GLY	D	109	52.186	70.612	12.343	1.00 56.21	8
ATOM	5791	N	GLU	D	110	50.831	72.370	12.707	1.00 58.61	7
ATOM	5792	CA	GLU	D	110	51.042	72.345	14.152	1.00 59.21	6
ATOM	5793	CB	GLU	D	110	50.664	73.700	14.776	1.00 62.41	6
ATOM	5794	CG	GLU	D	110	51.327	74.002	16.134	1.00 66.58	6
ATOM	5795	CD	GLU	D	110	52.852	74.104	16.041	1.00 69.79	6
ATOM	5796	OE1	GLU	D	110	53.375	74.340	14.921	1.00 70.58	8
ATOM	5797	OE2	GLU	D	110	53.527	73.963	17.089	1.00 70.10	8
ATOM	5798	C	GLU	D	110	50.158	71.232	14.712	1.00 56.76	6
ATOM	5799	O	GLU	D	110	49.001	71.079	14.320	1.00 54.86	8
ATOM	5800	N	VAL	D	111	50.723	70.451	15.625	1.00 55.23	7
ATOM	5801	CA	VAL	D	111	50.013	69.333	16.236	1.00 53.43	6
ATOM	5802	CB	VAL	D	111	50.704	67.976	15.889	1.00 53.47	6
ATOM	5803	CG1	VAL	D	111	49.934	66.821	16.500	1.00 51.83	6
ATOM	5804	CG2	VAL	D	111	50.798	67.803	14.382	1.00 52.57	6
ATOM	5805	C	VAL	D	111	49.962	69.470	17.754	1.00 53.05	6
ATOM	5806	O	VAL	D	111	50.972	69.747	18.400	1.00 52.81	8
ATOM	5807	N	LEU	D	112	48.783	69.269	18.323	1.00 51.91	7
ATOM	5808	CA	LEU	D	112	48.631	69.354	19.766	1.00 51.71	6
ATOM	5809	CB	LEU	D	112	47.776	70.566	20.155	1.00 55.12	6
ATOM	5810	CG	LEU	D	112	47.832	71.901	19.392	1.00 55.82	6
ATOM	5811	CD1	LEU	D	112	49.269	72.287	19.035	1.00 56.65	6
ATOM	5812	CD2	LEU	D	112	46.985	71.777	18.155	1.00 55.54	6
ATOM	5813	C	LEU	D	112	47.959	68.089	20.292	1.00 51.46	6
ATOM	5814	O	LEU	D	112	46.833	67.769	19.900	1.00 51.33	8
ATOM	5815	N	TYR	D	113	48.659	67.365	21.162	1.00 48.43	7
ATOM	5816	CA	TYR	D	113	48.128	66.149	21.762	1.00 45.71	6
ATOM	5817	CB	TYR	D	113	48.941	64.928	21.318	1.00 43.52	6
ATOM	5818	CG	TYR	D	113	48.490	63.601	21.918	1.00 41.37	6
ATOM	5819	CD1	TYR	D	113	47.142	63.255	21.975	1.00 39.60	6
ATOM	5820	CE1	TYR	D	113	46.735	62.028	22.492	1.00 38.43	6
ATOM	5821	CD2	TYR	D	113	49.423	62.679	22.397	1.00 40.11	6
ATOM	5822	CE2	TYR	D	113	49.028	61.458	22.911	1.00 39.17	6
ATOM	5823	CZ	TYR	D	113	47.682	61.134	22.958	1.00 40.31	6
ATOM	5824	OH	TYR	D	113	47.283	59.921	23.470	1.00 40.08	8
ATOM	5825	C	TYR	D	113	48.218	66.325	23.262	1.00 45.22	6
ATOM	5826	O	TYR	D	113	49.302	66.442	23.812	1.00 44.34	8
ATOM	5827	N	MET	D	114	47.073	66.352	23.924	1.00 47.16	7
ATOM	5828	CA	MET	D	114	47.044	66.541	25.368	1.00 48.56	6
ATOM	5829	CB	MET	D	114	46.457	67.906	25.681	1.00 53.17	6
ATOM	5830	CG	MET	D	114	46.536	68.281	27.130	1.00 58.47	6
ATOM	5831	SD	MET	D	114	45.470	69.687	27.429	1.00 64.86	16
ATOM	5832	CE	MET	D	114	46.527	70.991	26.840	1.00 63.87	6
ATOM	5833	C	MET	D	114	46.214	65.472	26.062	1.00 47.72	6
ATOM	5834	O	MET	D	114	45.060	65.705	26.424	1.00 47.31	8
ATOM	5835	N	PRO	D	115	46.790	64.279	26.251	1.00 45.85	7
ATOM	5836	CD	PRO	D	115	48.108	63.831	25.761	1.00 45.44	6
ATOM	5837	CA	PRO	D	115	46.080	63.184	26.903	1.00 44.65	6
ATOM	5838	CB	PRO	D	115	46.818	61.967	26.385	1.00 46.29	6
ATOM	5839	CG	PRO	D	115	48.231	62.454	26.372	1.00 45.12	6
ATOM	5840	C	PRO	D	115	46.159	63.283	28.416	1.00 44.40	6
ATOM	5841	O	PRO	D	115	47.145	63.787	28.954	1.00 43.35	8
ATOM	5842	N	SER	D	116	45.124	62.811	29.102	1.00 42.71	7
ATOM	5843	CA	SER	D	116	45.142	62.828	30.551	1.00 40.50	6
ATOM	5844	CB	SER	D	116	43.752	62.976	31.110	1.00 37.94	6
ATOM	5845	OG	SER	D	116	43.829	63.015	32.516	1.00 44.37	8

ATOM	5846	C	SER	D	116	45.712	61.484	30.957	1.00	42.16	6
ATOM	5847	O	SER	D	116	45.190	60.448	30.569	1.00	45.67	8
ATOM	5848	N	ILE	D	117	46.781	61.493	31.739	1.00	39.79	7
ATOM	5849	CA	ILE	D	117	47.409	60.252	32.135	1.00	38.51	6
ATOM	5850	CB	ILE	D	117	48.842	60.179	31.565	1.00	38.14	6
ATOM	5851	CG2	ILE	D	117	49.545	58.932	32.041	1.00	38.72	6
ATOM	5852	CG1	ILE	D	117	48.802	60.188	30.045	1.00	37.23	6
ATOM	5853	CD1	ILE	D	117	50.137	60.454	29.422	1.00	31.06	6
ATOM	5854	C	ILE	D	117	47.506	60.000	33.635	1.00	40.56	6
ATOM	5855	O	ILE	D	117	47.838	60.894	34.407	1.00	41.12	8
ATOM	5856	N	ARG	D	118	47.196	58.773	34.042	1.00	40.57	7
ATOM	5857	CA	ARG	D	118	47.356	58.386	35.429	1.00	39.48	6
ATOM	5858	CB	ARG	D	118	46.151	57.623	35.966	1.00	37.31	6
ATOM	5859	CG	ARG	D	118	46.420	57.119	37.377	1.00	36.74	6
ATOM	5860	CD	ARG	D	118	45.196	56.638	38.101	1.00	36.75	6
ATOM	5861	NE	ARG	D	118	45.554	56.131	39.414	1.00	36.89	7
ATOM	5862	CZ	ARG	D	118	44.687	55.838	40.367	1.00	36.15	6
ATOM	5863	NH1	ARG	D	118	43.396	56.001	40.163	1.00	38.10	7
ATOM	5864	NH2	ARG	D	118	45.118	55.381	41.523	1.00	35.81	7
ATOM	5865	C	ARG	D	118	48.581	57.469	35.376	1.00	39.50	6
ATOM	5866	O	ARG	D	118	48.661	56.579	34.541	1.00	39.41	8
ATOM	5867	N	GLN	D	119	49.541	57.678	36.260	1.00	39.25	7
ATOM	5868	CA	GLN	D	119	50.739	56.865	36.222	1.00	40.77	6
ATOM	5869	CB	GLN	D	119	51.588	57.357	35.059	1.00	39.61	6
ATOM	5870	CG	GLN	D	119	52.879	56.638	34.807	1.00	39.00	6
ATOM	5871	CD	GLN	D	119	53.483	57.037	33.476	1.00	37.41	6
ATOM	5872	OE1	GLN	D	119	53.349	58.169	33.043	1.00	42.14	8
ATOM	5873	NE2	GLN	D	119	54.154	56.112	32.831	1.00	38.80	7
ATOM	5874	C	GLN	D	119	51.491	56.961	37.534	1.00	42.32	6
ATOM	5875	O	GLN	D	119	51.421	57.965	38.213	1.00	43.53	8
ATOM	5876	N	ARG	D	120	52.197	55.908	37.906	1.00	43.85	7
ATOM	5877	CA	ARG	D	120	52.950	55.944	39.149	1.00	47.43	6
ATOM	5878	CB	ARG	D	120	52.819	54.632	39.900	1.00	50.39	6
ATOM	5879	CG	ARG	D	120	51.389	54.278	40.235	1.00	58.64	6
ATOM	5880	CD	ARG	D	120	51.352	53.441	41.493	1.00	64.21	6
ATOM	5881	NE	ARG	D	120	51.387	54.244	42.725	1.00	67.25	7
ATOM	5882	CZ	ARG	D	120	52.129	53.942	43.790	1.00	65.70	6
ATOM	5883	NH1	ARG	D	120	52.911	52.870	43.763	1.00	64.48	7
ATOM	5884	NH2	ARG	D	120	52.049	54.678	44.895	1.00	62.69	7
ATOM	5885	C	ARG	D	120	54.411	56.231	38.913	1.00	46.83	6
ATOM	5886	O	ARG	D	120	54.969	55.848	37.885	1.00	46.53	8
ATOM	5887	N	PHE	D	121	55.032	56.912	39.869	1.00	45.77	7
ATOM	5888	CA	PHE	D	121	56.443	57.249	39.743	1.00	45.26	6
ATOM	5889	CB	PHE	D	121	56.627	58.737	39.416	1.00	42.47	6
ATOM	5890	CG	PHE	D	121	55.893	59.186	38.199	1.00	41.19	6
ATOM	5891	CD1	PHE	D	121	54.546	59.483	38.266	1.00	39.80	6
ATOM	5892	CD2	PHE	D	121	56.544	59.284	36.979	1.00	39.10	6
ATOM	5893	CE1	PHE	D	121	53.855	59.872	37.141	1.00	39.49	6
ATOM	5894	CE2	PHE	D	121	55.862	59.670	35.858	1.00	37.48	6
ATOM	5895	CZ	PHE	D	121	54.512	59.965	35.937	1.00	38.89	6
ATOM	5896	C	PHE	D	121	57.256	56.947	40.980	1.00	46.08	6
ATOM	5897	O	PHE	D	121	56.729	56.783	42.077	1.00	43.10	8
ATOM	5898	N	SER	D	122	58.560	56.881	40.769	1.00	48.75	7
ATOM	5899	CA	SER	D	122	59.520	56.672	41.837	1.00	51.22	6
ATOM	5900	CB	SER	D	122	60.535	55.604	41.442	1.00	51.58	6
ATOM	5901	OG	SER	D	122	61.510	55.455	42.453	1.00	51.33	8
ATOM	5902	C	SER	D	122	60.224	58.027	42.004	1.00	51.78	6
ATOM	5903	O	SER	D	122	60.968	58.460	41.123	1.00	50.44	8
ATOM	5904	N	CYS	D	123	59.965	58.699	43.120	1.00	52.36	7
ATOM	5905	CA	CYS	D	123	60.564	59.999	43.370	1.00	55.03	6
ATOM	5906	C	CYS	D	123	60.584	60.314	44.860	1.00	57.50	6

ATOM	5907	O	CYS	D	123	60.131	59.513	45.676	1.00	58.47	8
ATOM	5908	CB	CYS	D	123	59.784	61.083	42.631	1.00	54.89	6
ATOM	5909	SG	CYS	D	123	58.043	61.147	43.136	1.00	52.88	16
ATOM	5910	N	ASP	D	124	61.104	61.487	45.218	1.00	58.85	7
ATOM	5911	CA	ASP	D	124	61.196	61.865	46.619	1.00	59.59	6
ATOM	5912	CB	ASP	D	124	62.205	62.994	46.816	1.00	60.38	6
ATOM	5913	CG	ASP	D	124	62.876	62.937	48.182	1.00	61.57	6
ATOM	5914	OD1	ASP	D	124	62.207	62.519	49.151	1.00	60.87	8
ATOM	5915	OD2	ASP	D	124	64.067	63.306	48.289	1.00	61.86	8
ATOM	5916	C	ASP	D	124	59.864	62.294	47.198	1.00	59.72	6
ATOM	5917	O	ASP	D	124	59.310	63.329	46.822	1.00	59.12	8
ATOM	5918	N	VAL	D	125	59.366	61.492	48.131	1.00	60.02	7
ATOM	5919	CA	VAL	D	125	58.096	61.758	48.795	1.00	61.00	6
ATOM	5920	CB	VAL	D	125	57.274	60.469	48.906	1.00	57.98	6
ATOM	5921	CG1	VAL	D	125	56.007	60.721	49.664	1.00	56.31	6
ATOM	5922	CG2	VAL	D	125	56.973	59.946	47.526	1.00	58.88	6
ATOM	5923	C	VAL	D	125	58.305	62.346	50.199	1.00	63.48	6
ATOM	5924	O	VAL	D	125	57.391	62.956	50.781	1.00	64.81	8
ATOM	5925	N	SER	D	126	59.511	62.177	50.738	1.00	64.05	7
ATOM	5926	CA	SER	D	126	59.824	62.684	52.072	1.00	64.03	6
ATOM	5927	CB	SER	D	126	61.317	62.517	52.362	1.00	63.15	6
ATOM	5928	OG	SER	D	126	62.088	63.277	51.455	1.00	61.24	8
ATOM	5929	C	SER	D	126	59.426	64.146	52.233	1.00	63.55	6
ATOM	5930	O	SER	D	126	59.745	64.989	51.396	1.00	62.30	8
ATOM	5931	N	GLY	D	127	58.716	64.434	53.315	1.00	64.29	7
ATOM	5932	CA	GLY	D	127	58.285	65.794	53.564	1.00	67.20	6
ATOM	5933	C	GLY	D	127	56.868	66.085	53.115	1.00	68.64	6
ATOM	5934	O	GLY	D	127	56.368	67.190	53.321	1.00	69.55	8
ATOM	5935	N	VAL	D	128	56.207	65.103	52.510	1.00	70.10	7
ATOM	5936	CA	VAL	D	128	54.845	65.323	52.038	1.00	71.31	6
ATOM	5937	CB	VAL	D	128	54.252	64.077	51.378	1.00	69.98	6
ATOM	5938	CG1	VAL	D	128	54.873	63.859	50.035	1.00	72.53	6
ATOM	5939	CG2	VAL	D	128	54.476	62.877	52.271	1.00	70.16	6
ATOM	5940	C	VAL	D	128	53.883	65.707	53.136	1.00	71.70	6
ATOM	5941	O	VAL	D	128	53.089	66.634	52.978	1.00	69.47	8
ATOM	5942	N	ASP	D	129	53.960	64.993	54.251	1.00	73.53	7
ATOM	5943	CA	ASP	D	129	53.022	65.233	55.320	1.00	77.21	6
ATOM	5944	CB	ASP	D	129	53.171	64.197	56.428	1.00	78.32	6
ATOM	5945	CG	ASP	D	129	51.860	63.985	57.204	1.00	80.24	6
ATOM	5946	OD1	ASP	D	129	51.521	62.805	57.509	1.00	81.78	8
ATOM	5947	OD2	ASP	D	129	51.172	64.996	57.504	1.00	78.07	8
ATOM	5948	C	ASP	D	129	53.027	66.618	55.915	1.00	79.33	6
ATOM	5949	O	ASP	D	129	52.082	66.963	56.644	1.00	80.54	8
ATOM	5950	N	THR	D	130	54.041	67.433	55.604	1.00	80.13	7
ATOM	5951	CA	THR	D	130	54.048	68.779	56.171	1.00	80.39	6
ATOM	5952	CB	THR	D	130	54.064	68.702	57.716	1.00	83.74	6
ATOM	5953	OG1	THR	D	130	54.418	67.359	58.114	1.00	84.65	8
ATOM	5954	CG2	THR	D	130	52.670	69.136	58.320	1.00	81.78	6
ATOM	5955	C	THR	D	130	55.110	69.794	55.795	1.00	78.83	6
ATOM	5956	O	THR	D	130	56.241	69.440	55.449	1.00	77.71	8
ATOM	5957	N	GLU	D	131	54.701	71.065	55.921	1.00	78.93	7
ATOM	5958	CA	GLU	D	131	55.520	72.272	55.705	1.00	78.30	6
ATOM	5959	CB	GLU	D	131	56.825	72.165	56.518	1.00	81.28	6
ATOM	5960	CG	GLU	D	131	56.641	72.410	58.024	1.00	83.84	6
ATOM	5961	CD	GLU	D	131	57.696	71.715	58.856	1.00	84.29	6
ATOM	5962	OE1	GLU	D	131	58.893	71.821	58.485	1.00	85.14	8
ATOM	5963	OE2	GLU	D	131	57.321	71.068	59.870	1.00	82.70	8
ATOM	5964	C	GLU	D	131	55.869	72.672	54.295	1.00	75.98	6
ATOM	5965	O	GLU	D	131	55.047	73.205	53.552	1.00	74.51	8
ATOM	5966	N	SER	D	132	57.136	72.452	53.973	1.00	75.06	7
ATOM	5967	CA	SER	D	132	57.689	72.733	52.665	1.00	74.59	6

ATOM	5968	CB	SER	D	132	59.215	72.882	52.788	1.00	75.96	6
ATOM	5969	OG	SER	D	132	59.812	71.733	53.401	1.00	76.36	8
ATOM	5970	C	SER	D	132	57.316	71.551	51.753	1.00	72.89	6
ATOM	5971	O	SER	D	132	57.636	71.530	50.563	1.00	73.06	8
ATOM	5972	N	GLY	D	133	56.630	70.575	52.337	1.00	70.56	7
ATOM	5973	CA	GLY	D	133	56.203	69.406	51.599	1.00	67.95	6
ATOM	5974	C	GLY	D	133	57.326	68.647	50.917	1.00	66.74	6
ATOM	5975	O	GLY	D	133	58.504	68.784	51.257	1.00	65.57	8
ATOM	5976	N	ALA	D	134	56.950	67.830	49.942	1.00	65.62	7
ATOM	5977	CA	ALA	D	134	57.922	67.052	49.194	1.00	63.00	6
ATOM	5978	CB	ALA	D	134	57.506	65.586	49.145	1.00	62.05	6
ATOM	5979	C	ALA	D	134	58.060	67.597	47.785	1.00	60.69	6
ATOM	5980	O	ALA	D	134	57.215	68.357	47.298	1.00	57.71	8
ATOM	5981	N	THR	D	135	59.149	67.206	47.139	1.00	60.08	7
ATOM	5982	CA	THR	D	135	59.417	67.619	45.777	1.00	59.14	6
ATOM	5983	CB	THR	D	135	60.585	68.590	45.703	1.00	59.67	6
ATOM	5984	OG1	THR	D	135	60.291	69.735	46.516	1.00	62.19	8
ATOM	5985	CG2	THR	D	135	60.811	69.031	44.263	1.00	57.77	6
ATOM	5986	C	THR	D	135	59.726	66.387	44.963	1.00	57.95	6
ATOM	5987	O	THR	D	135	60.801	65.804	45.065	1.00	56.51	8
ATOM	5988	N	CYS	D	136	58.740	65.995	44.170	1.00	56.67	7
ATOM	5989	CA	CYS	D	136	58.825	64.836	43.314	1.00	55.02	6
ATOM	5990	C	CYS	D	136	59.172	65.310	41.906	1.00	55.53	6
ATOM	5991	O	CYS	D	136	58.413	66.060	41.282	1.00	53.64	8
ATOM	5992	CB	CYS	D	136	57.475	64.115	43.347	1.00	55.35	6
ATOM	5993	SG	CYS	D	136	57.280	62.756	42.175	1.00	52.04	16
ATOM	5994	N	ARG	D	137	60.331	64.889	41.414	1.00	55.15	7
ATOM	5995	CA	ARG	D	137	60.752	65.291	40.084	1.00	56.13	6
ATOM	5996	CB	ARG	D	137	62.233	65.664	40.080	1.00	59.85	6
ATOM	5997	CG	ARG	D	137	62.587	66.818	40.993	1.00	64.22	6
ATOM	5998	CD	ARG	D	137	64.042	66.718	41.445	1.00	67.87	6
ATOM	5999	NE	ARG	D	137	64.261	67.425	42.706	1.00	72.81	7
ATOM	6000	CZ	ARG	D	137	64.221	68.753	42.848	1.00	76.15	6
ATOM	6001	NH1	ARG	D	137	63.975	69.545	41.798	1.00	76.59	7
ATOM	6002	NH2	ARG	D	137	64.408	69.295	44.051	1.00	75.96	7
ATOM	6003	C	ARG	D	137	60.511	64.156	39.112	1.00	54.79	6
ATOM	6004	O	ARG	D	137	60.844	63.011	39.394	1.00	55.64	8
ATOM	6005	N	ILE	D	138	59.935	64.498	37.966	1.00	52.46	7
ATOM	6006	CA	ILE	D	138	59.618	63.551	36.923	1.00	49.86	6
ATOM	6007	CB	ILE	D	138	58.092	63.516	36.686	1.00	47.60	6
ATOM	6008	CG2	ILE	D	138	57.769	62.562	35.565	1.00	46.55	6
ATOM	6009	CG1	ILE	D	138	57.368	63.120	37.975	1.00	44.38	6
ATOM	6010	CD1	ILE	D	138	55.873	63.274	37.903	1.00	39.29	6
ATOM	6011	C	ILE	D	138	60.307	64.004	35.645	1.00	50.53	6
ATOM	6012	O	ILE	D	138	60.056	65.103	35.163	1.00	47.86	8
ATOM	6013	N	LYS	D	139	61.171	63.158	35.093	1.00	52.17	7
ATOM	6014	CA	LYS	D	139	61.881	63.497	33.857	1.00	53.46	6
ATOM	6015	CB	LYS	D	139	63.381	63.195	33.988	1.00	54.96	6
ATOM	6016	CG	LYS	D	139	64.040	63.838	35.187	1.00	59.06	6
ATOM	6017	CD	LYS	D	139	65.558	63.761	35.119	1.00	60.55	6
ATOM	6018	CE	LYS	D	139	66.116	64.685	34.044	1.00	62.84	6
ATOM	6019	NZ	LYS	D	139	67.604	64.584	33.930	1.00	64.96	7
ATOM	6020	C	LYS	D	139	61.335	62.715	32.667	1.00	52.45	6
ATOM	6021	O	LYS	D	139	61.269	61.493	32.708	1.00	52.48	8
ATOM	6022	N	ILE	D	140	60.953	63.411	31.604	1.00	51.17	7
ATOM	6023	CA	ILE	D	140	60.453	62.723	30.426	1.00	51.40	6
ATOM	6024	CB	ILE	D	140	58.886	62.781	30.369	1.00	52.71	6
ATOM	6025	CG2	ILE	D	140	58.303	62.478	31.748	1.00	53.74	6
ATOM	6026	CG1	ILE	D	140	58.387	64.171	30.003	1.00	52.18	6
ATOM	6027	CD1	ILE	D	140	56.892	64.354	30.322	1.00	51.22	6
ATOM	6028	C	ILE	D	140	61.078	63.251	29.123	1.00	50.75	6

ATOM	6029	O	ILE	D	140	61.189	64.451	28.918	1.00	50.51	8
ATOM	6030	N	GLY	D	141	61.511	62.340	28.258	1.00	48.91	7
ATOM	6031	CA	GLY	D	141	62.112	62.735	26.997	1.00	48.03	6
ATOM	6032	C	GLY	D	141	62.036	61.611	25.983	1.00	47.81	6
ATOM	6033	O	GLY	D	141	61.636	60.511	26.340	1.00	50.42	8
ATOM	6034	N	SER	D	142	62.405	61.865	24.729	1.00	45.08	7
ATOM	6035	CA	SER	D	142	62.364	60.824	23.713	1.00	42.21	6
ATOM	6036	CB	SER	D	142	62.872	61.334	22.376	1.00	43.40	6
ATOM	6037	OG	SER	D	142	63.079	60.255	21.482	1.00	43.21	8
ATOM	6038	C	SER	D	142	63.194	59.630	24.126	1.00	44.37	6
ATOM	6039	O	SER	D	142	64.284	59.758	24.688	1.00	45.99	8
ATOM	6040	N	TRP	D	143	62.673	58.452	23.825	1.00	46.12	7
ATOM	6041	CA	TRP	D	143	63.338	57.222	24.196	1.00	45.24	6
ATOM	6042	CB	TRP	D	143	62.300	56.121	24.425	1.00	42.93	6
ATOM	6043	CG	TRP	D	143	62.872	54.893	25.051	1.00	39.90	6
ATOM	6044	CD2	TRP	D	143	63.244	54.737	26.418	1.00	37.42	6
ATOM	6045	CE2	TRP	D	143	63.740	53.425	26.567	1.00	37.64	6
ATOM	6046	CE3	TRP	D	143	63.204	55.581	27.536	1.00	35.75	6
ATOM	6047	CD1	TRP	D	143	63.154	53.702	24.436	1.00	40.17	6
ATOM	6048	NE1	TRP	D	143	63.676	52.817	25.341	1.00	38.55	7
ATOM	6049	CZ2	TRP	D	143	64.187	52.935	27.788	1.00	38.02	6
ATOM	6050	CZ3	TRP	D	143	63.647	55.100	28.741	1.00	36.62	6
ATOM	6051	CH2	TRP	D	143	64.133	53.784	28.863	1.00	39.07	6
ATOM	6052	C	TRP	D	143	64.348	56.758	23.170	1.00	46.24	6
ATOM	6053	O	TRP	D	143	65.328	56.109	23.509	1.00	48.11	8
ATOM	6054	N	THR	D	144	64.124	57.080	21.910	1.00	45.62	7
ATOM	6055	CA	THR	D	144	65.047	56.616	20.894	1.00	44.68	6
ATOM	6056	CB	THR	D	144	64.336	55.633	19.955	1.00	44.87	6
ATOM	6057	OG1	THR	D	144	63.155	56.242	19.421	1.00	41.93	8
ATOM	6058	CG2	THR	D	144	63.931	54.394	20.720	1.00	44.03	6
ATOM	6059	C	THR	D	144	65.703	57.710	20.075	1.00	46.21	6
ATOM	6060	O	THR	D	144	66.662	57.452	19.366	1.00	47.29	8
ATOM	6061	N	HIS	D	145	65.198	58.931	20.173	1.00	47.13	7
ATOM	6062	CA	HIS	D	145	65.772	60.021	19.403	1.00	50.18	6
ATOM	6063	CB	HIS	D	145	64.672	60.793	18.679	1.00	50.55	6
ATOM	6064	CG	HIS	D	145	63.961	59.997	17.630	1.00	52.45	6
ATOM	6065	CD2	HIS	D	145	64.369	59.558	16.416	1.00	51.92	6
ATOM	6066	ND1	HIS	D	145	62.652	59.589	17.765	1.00	50.59	7
ATOM	6067	CE1	HIS	D	145	62.282	58.936	16.679	1.00	51.27	6
ATOM	6068	NE2	HIS	D	145	63.305	58.902	15.844	1.00	52.81	7
ATOM	6069	C	HIS	D	145	66.611	60.990	20.241	1.00	52.96	6
ATOM	6070	O	HIS	D	145	66.147	61.554	21.236	1.00	51.74	8
ATOM	6071	N	HIS	D	146	67.856	61.179	19.828	1.00	53.81	7
ATOM	6072	CA	HIS	D	146	68.748	62.081	20.532	1.00	55.05	6
ATOM	6073	CB	HIS	D	146	70.205	61.691	20.267	1.00	53.71	6
ATOM	6074	CG	HIS	D	146	70.555	61.617	18.816	1.00	52.77	6
ATOM	6075	CD2	HIS	D	146	70.425	62.526	17.821	1.00	53.89	6
ATOM	6076	ND1	HIS	D	146	71.083	60.487	18.236	1.00	49.45	7
ATOM	6077	CE1	HIS	D	146	71.261	60.700	16.945	1.00	49.76	6
ATOM	6078	NE2	HIS	D	146	70.869	61.929	16.667	1.00	51.93	7
ATOM	6079	C	HIS	D	146	68.489	63.521	20.094	1.00	56.51	6
ATOM	6080	O	HIS	D	146	67.682	63.770	19.185	1.00	58.53	8
ATOM	6081	N	SER	D	147	69.190	64.455	20.738	1.00	57.97	7
ATOM	6082	CA	SER	D	147	69.054	65.902	20.497	1.00	58.69	6
ATOM	6083	CB	SER	D	147	70.097	66.646	21.332	1.00	58.36	6
ATOM	6084	OG	SER	D	147	71.365	66.032	21.179	1.00	58.90	8
ATOM	6085	C	SER	D	147	69.114	66.404	19.049	1.00	57.67	6
ATOM	6086	O	SER	D	147	68.570	67.470	18.727	1.00	55.79	8
ATOM	6087	N	ARG	D	148	69.768	65.647	18.180	1.00	57.54	7
ATOM	6088	CA	ARG	D	148	69.878	66.061	16.790	1.00	59.37	6
ATOM	6089	CB	ARG	D	148	71.054	65.340	16.126	1.00	64.67	6

ATOM	6090	CG	ARG	D	148	72.382	65.498	16.869	1.00	73.01	6
ATOM	6091	CD	ARG	D	148	73.494	64.621	16.270	1.00	79.78	6
ATOM	6092	NE	ARG	D	148	74.652	64.495	17.172	1.00	86.45	7
ATOM	6093	CZ	ARG	D	148	75.435	65.508	17.558	1.00	88.85	6
ATOM	6094	NH1	ARG	D	148	75.200	66.749	17.126	1.00	90.23	7
ATOM	6095	NH2	ARG	D	148	76.462	65.284	18.381	1.00	89.74	7
ATOM	6096	C	ARG	D	148	68.603	65.790	16.001	1.00	58.14	6
ATOM	6097	O	ARG	D	148	68.406	66.351	14.921	1.00	57.28	8
ATOM	6098	N	GLU	D	149	67.737	64.932	16.546	1.00	58.44	7
ATOM	6099	CA	GLU	D	149	66.488	64.555	15.881	1.00	54.51	6
ATOM	6100	CB	GLU	D	149	66.394	63.030	15.787	1.00	54.24	6
ATOM	6101	CG	GLU	D	149	67.744	62.384	15.474	1.00	56.46	6
ATOM	6102	CD	GLU	D	149	67.687	60.886	15.343	1.00	57.56	6
ATOM	6103	OE1	GLU	D	149	67.015	60.226	16.171	1.00	60.61	8
ATOM	6104	OE2	GLU	D	149	68.336	60.365	14.415	1.00	56.79	8
ATOM	6105	C	GLU	D	149	65.315	65.123	16.638	1.00	51.56	6
ATOM	6106	O	GLU	D	149	64.396	65.667	16.050	1.00	48.50	8
ATOM	6107	N	ILE	D	150	65.355	65.002	17.954	1.00	51.48	7
ATOM	6108	CA	ILE	D	150	64.284	65.533	18.783	1.00	53.11	6
ATOM	6109	CB	ILE	D	150	63.382	64.424	19.410	1.00	55.50	6
ATOM	6110	CG2	ILE	D	150	62.530	65.013	20.542	1.00	52.41	6
ATOM	6111	CG1	ILE	D	150	62.440	63.830	18.352	1.00	55.09	6
ATOM	6112	CD1	ILE	D	150	61.549	62.728	18.884	1.00	53.30	6
ATOM	6113	C	ILE	D	150	64.841	66.339	19.925	1.00	54.06	6
ATOM	6114	O	ILE	D	150	65.809	65.944	20.573	1.00	49.46	8
ATOM	6115	N	SER	D	151	64.199	67.474	20.162	1.00	55.80	7
ATOM	6116	CA	SER	D	151	64.570	68.365	21.245	1.00	57.52	6
ATOM	6117	CB	SER	D	151	65.190	69.660	20.688	1.00	59.00	6
ATOM	6118	OG	SER	D	151	64.256	70.404	19.906	1.00	62.67	8
ATOM	6119	C	SER	D	151	63.269	68.663	21.989	1.00	57.81	6
ATOM	6120	O	SER	D	151	62.241	68.932	21.373	1.00	55.28	8
ATOM	6121	N	VAL	D	152	63.315	68.592	23.312	1.00	59.48	7
ATOM	6122	CA	VAL	D	152	62.142	68.851	24.132	1.00	62.33	6
ATOM	6123	CB	VAL	D	152	61.940	67.742	25.188	1.00	63.11	6
ATOM	6124	CG1	VAL	D	152	61.945	66.373	24.511	1.00	63.08	6
ATOM	6125	CG2	VAL	D	152	63.038	67.821	26.259	1.00	61.64	6
ATOM	6126	C	VAL	D	152	62.350	70.167	24.854	1.00	63.67	6
ATOM	6127	O	VAL	D	152	63.478	70.496	25.231	1.00	63.11	8
ATOM	6128	N	ASP	D	153	61.266	70.909	25.070	1.00	65.73	7
ATOM	6129	CA	ASP	D	153	61.365	72.206	25.740	1.00	68.62	6
ATOM	6130	CB	ASP	D	153	61.524	73.296	24.680	1.00	70.73	6
ATOM	6131	CG	ASP	D	153	62.698	73.023	23.733	1.00	74.59	6
ATOM	6132	OD1	ASP	D	153	63.854	73.332	24.118	1.00	73.93	8
ATOM	6133	OD2	ASP	D	153	62.473	72.483	22.612	1.00	76.61	8
ATOM	6134	C	ASP	D	153	60.144	72.513	26.601	1.00	69.92	6
ATOM	6135	O	ASP	D	153	59.022	72.176	26.227	1.00	71.07	8
ATOM	6136	N	PRO	D	154	60.345	73.139	27.778	1.00	71.13	7
ATOM	6137	CD	PRO	D	154	61.609	73.207	28.536	1.00	70.02	6
ATOM	6138	CA	PRO	D	154	59.199	73.471	28.645	1.00	72.68	6
ATOM	6139	CB	PRO	D	154	59.863	73.882	29.955	1.00	71.74	6
ATOM	6140	CG	PRO	D	154	61.135	73.062	29.962	1.00	70.60	6
ATOM	6141	C	PRO	D	154	58.374	74.609	28.030	1.00	75.79	6
ATOM	6142	O	PRO	D	154	58.732	75.140	26.983	1.00	76.11	8
ATOM	6143	N	THR	D	155	57.286	75.001	28.686	1.00	80.37	7
ATOM	6144	CA	THR	D	155	56.419	76.060	28.148	1.00	84.32	6
ATOM	6145	CB	THR	D	155	55.208	75.436	27.393	1.00	84.09	6
ATOM	6146	OG1	THR	D	155	54.342	74.785	28.337	1.00	83.35	8
ATOM	6147	CG2	THR	D	155	55.685	74.412	26.360	1.00	83.23	6
ATOM	6148	C	THR	D	155	55.861	77.068	29.184	1.00	88.09	6
ATOM	6149	O	THR	D	155	56.510	77.366	30.211	1.00	88.59	8
ATOM	6150	N	THR	D	156	54.654	77.578	28.886	1.00	91.07	7

ATOM	6151	CA	THR	D	156	53.911	78.559	29.705	1.00 93.25	6
ATOM	6152	CB	THR	D	156	52.372	78.483	29.424	1.00 94.48	6
ATOM	6153	OG1	THR	D	156	52.115	78.686	28.019	1.00 94.94	8
ATOM	6154	CG2	THR	D	156	51.619	79.546	30.255	1.00 93.74	6
ATOM	6155	C	THR	D	156	54.104	78.445	31.220	1.00 94.44	6
ATOM	6156	O	THR	D	156	53.471	77.615	31.898	1.00 93.56	8
ATOM	6157	N	GLU	D	157	54.955	79.314	31.750	1.00 96.79	7
ATOM	6158	CA	GLU	D	157	55.252	79.320	33.183	1.00 99.37	6
ATOM	6159	CB	GLU	D	157	56.670	79.865	33.416	1.00100.34	6
ATOM	6160	CG	GLU	D	157	57.701	79.333	32.426	1.00102.84	6
ATOM	6161	CD	GLU	D	157	59.086	79.955	32.629	1.00104.89	6
ATOM	6162	OE1	GLU	D	157	59.179	81.213	32.700	1.00104.68	8
ATOM	6163	OE2	GLU	D	157	60.085	79.189	32.707	1.00105.54	8
ATOM	6164	C	GLU	D	157	54.237	80.165	33.967	1.00 99.49	6
ATOM	6165	O	GLU	D	157	54.273	80.216	35.210	1.00100.21	8
ATOM	6166	N	ASN	D	158	53.336	80.828	33.248	1.00 98.56	7
ATOM	6167	CA	ASN	D	158	52.340	81.657	33.911	1.00 98.16	6
ATOM	6168	CB	ASN	D	158	51.632	82.550	32.894	1.00100.26	6
ATOM	6169	CG	ASN	D	158	52.610	83.378	32.064	1.00102.10	6
ATOM	6170	OD1	ASN	D	158	53.425	84.153	32.607	1.00101.77	8
ATOM	6171	ND2	ASN	D	158	52.533	83.221	30.735	1.00102.21	7
ATOM	6172	C	ASN	D	158	51.313	80.786	34.613	1.00 96.52	6
ATOM	6173	O	ASN	D	158	51.475	80.452	35.797	1.00 96.76	8
ATOM	6174	N	SER	D	159	50.257	80.447	33.864	1.00 94.02	7
ATOM	6175	CA	SER	D	159	49.142	79.599	34.313	1.00 90.18	6
ATOM	6176	CB	SER	D	159	48.996	78.422	33.331	1.00 90.25	6
ATOM	6177	OG	SER	D	159	50.277	77.932	32.940	1.00 90.19	8
ATOM	6178	C	SER	D	159	49.254	79.071	35.751	1.00 87.40	6
ATOM	6179	O	SER	D	159	50.208	78.372	36.094	1.00 87.99	8
ATOM	6180	N	ASP	D	160	48.282	79.408	36.594	1.00 83.57	7
ATOM	6181	CA	ASP	D	160	48.300	78.947	37.984	1.00 79.69	6
ATOM	6182	CB	ASP	D	160	46.950	79.189	38.660	1.00 79.26	6
ATOM	6183	CG	ASP	D	160	46.902	78.632	40.079	1.00 79.02	6
ATOM	6184	OD1	ASP	D	160	45.785	78.385	40.596	1.00 78.94	8
ATOM	6185	OD2	ASP	D	160	47.987	78.446	40.679	1.00 77.43	8
ATOM	6186	C	ASP	D	160	48.579	77.453	37.995	1.00 77.55	6
ATOM	6187	O	ASP	D	160	47.797	76.670	37.429	1.00 77.70	8
ATOM	6188	N	ASP	D	161	49.676	77.062	38.646	1.00 74.02	7
ATOM	6189	CA	ASP	D	161	50.070	75.657	38.719	1.00 69.51	6
ATOM	6190	CB	ASP	D	161	51.277	75.466	39.642	1.00 68.24	6
ATOM	6191	CG	ASP	D	161	52.556	76.004	39.050	1.00 67.15	6
ATOM	6192	OD1	ASP	D	161	52.734	75.886	37.827	1.00 67.47	8
ATOM	6193	OD2	ASP	D	161	53.397	76.536	39.803	1.00 70.25	8
ATOM	6194	C	ASP	D	161	48.972	74.697	39.147	1.00 67.31	6
ATOM	6195	O	ASP	D	161	49.071	73.497	38.890	1.00 68.61	8
ATOM	6196	N	SER	D	162	47.924	75.191	39.788	1.00 64.39	7
ATOM	6197	CA	SER	D	162	46.871	74.280	40.210	1.00 63.54	6
ATOM	6198	CB	SER	D	162	46.897	74.097	41.736	1.00 63.26	6
ATOM	6199	OG	SER	D	162	46.555	75.286	42.417	1.00 65.64	8
ATOM	6200	C	SER	D	162	45.494	74.722	39.761	1.00 62.73	6
ATOM	6201	O	SER	D	162	44.490	74.439	40.425	1.00 60.67	8
ATOM	6202	N	GLU	D	163	45.435	75.400	38.620	1.00 63.28	7
ATOM	6203	CA	GLU	D	163	44.149	75.861	38.139	1.00 66.60	6
ATOM	6204	CB	GLU	D	163	44.325	76.984	37.105	1.00 69.72	6
ATOM	6205	CG	GLU	D	163	44.576	76.546	35.681	1.00 72.12	6
ATOM	6206	CD	GLU	D	163	44.506	77.720	34.698	1.00 74.42	6
ATOM	6207	OE1	GLU	D	163	45.442	78.557	34.703	1.00 75.59	8
ATOM	6208	OE2	GLU	D	163	43.510	77.808	33.932	1.00 73.89	8
ATOM	6209	C	GLU	D	163	43.310	74.712	37.572	1.00 65.25	6
ATOM	6210	O	GLU	D	163	42.126	74.885	37.264	1.00 65.73	8
ATOM	6211	N	TYR	D	164	43.926	73.539	37.448	1.00 64.10	7

ATOM	6212	CA	TYR	D	164	43.236	72.353	36.946	1.00	61.14	6
ATOM	6213	CB	TYR	D	164	43.901	71.828	35.675	1.00	62.34	6
ATOM	6214	CG	TYR	D	164	43.794	72.756	34.501	1.00	62.07	6
ATOM	6215	CD1	TYR	D	164	44.937	73.264	33.887	1.00	62.29	6
ATOM	6216	CE1	TYR	D	164	44.846	74.152	32.813	1.00	64.14	6
ATOM	6217	CD2	TYR	D	164	42.547	73.151	34.016	1.00	63.36	6
ATOM	6218	CE2	TYR	D	164	42.438	74.038	32.940	1.00	65.18	6
ATOM	6219	CZ	TYR	D	164	43.594	74.536	32.337	1.00	65.18	6
ATOM	6220	OH	TYR	D	164	43.495	75.380	31.240	1.00	65.32	8
ATOM	6221	C	TYR	D	164	43.257	71.263	38.000	1.00	59.77	6
ATOM	6222	O	TYR	D	164	42.602	70.231	37.853	1.00	59.16	8
ATOM	6223	N	PHE	D	165	44.008	71.497	39.068	1.00	57.70	7
ATOM	6224	CA	PHE	D	165	44.113	70.518	40.143	1.00	56.00	6
ATOM	6225	CB	PHE	D	165	45.105	70.988	41.202	1.00	53.27	6
ATOM	6226	CG	PHE	D	165	45.635	69.885	42.053	1.00	51.93	6
ATOM	6227	CD1	PHE	D	165	46.436	68.891	41.502	1.00	50.62	6
ATOM	6228	CD2	PHE	D	165	45.326	69.820	43.398	1.00	52.41	6
ATOM	6229	CE1	PHE	D	165	46.922	67.845	42.283	1.00	49.13	6
ATOM	6230	CE2	PHE	D	165	45.807	68.777	44.188	1.00	52.20	6
ATOM	6231	CZ	PHE	D	165	46.608	67.788	43.624	1.00	51.98	6
ATOM	6232	C	PHE	D	165	42.773	70.241	40.801	1.00	55.90	6
ATOM	6233	O	PHE	D	165	41.970	71.149	41.005	1.00	56.82	8
ATOM	6234	N	SER	D	166	42.524	68.980	41.126	1.00	55.56	7
ATOM	6235	CA	SER	D	166	41.273	68.627	41.771	1.00	55.90	6
ATOM	6236	CB	SER	D	166	41.115	67.117	41.887	1.00	55.69	6
ATOM	6237	OG	SER	D	166	39.855	66.799	42.457	1.00	55.69	8
ATOM	6238	C	SER	D	166	41.280	69.229	43.158	1.00	56.73	6
ATOM	6239	O	SER	D	166	42.315	69.229	43.839	1.00	56.74	8
ATOM	6240	N	GLN	D	167	40.121	69.729	43.578	1.00	57.58	7
ATOM	6241	CA	GLN	D	167	39.999	70.353	44.892	1.00	57.81	6
ATOM	6242	CB	GLN	D	167	38.867	71.383	44.885	1.00	59.24	6
ATOM	6243	CG	GLN	D	167	37.541	70.794	44.439	1.00	63.59	6
ATOM	6244	CD	GLN	D	167	36.485	71.854	44.107	1.00	65.57	6
ATOM	6245	OE1	GLN	D	167	36.054	72.607	44.979	1.00	65.98	8
ATOM	6246	NE2	GLN	D	167	36.067	71.909	42.831	1.00	65.54	7
ATOM	6247	C	GLN	D	167	39.752	69.328	45.977	1.00	56.65	6
ATOM	6248	O	GLN	D	167	39.990	69.598	47.151	1.00	56.95	8
ATOM	6249	N	TYR	D	168	39.293	68.145	45.586	1.00	56.16	7
ATOM	6250	CA	TYR	D	168	39.014	67.091	46.556	1.00	53.65	6
ATOM	6251	CB	TYR	D	168	37.798	66.297	46.096	1.00	54.14	6
ATOM	6252	CG	TYR	D	168	36.675	67.217	45.707	1.00	53.82	6
ATOM	6253	CD1	TYR	D	168	36.446	67.545	44.371	1.00	53.19	6
ATOM	6254	CE1	TYR	D	168	35.445	68.454	44.020	1.00	54.20	6
ATOM	6255	CD2	TYR	D	168	35.880	67.816	46.681	1.00	52.39	6
ATOM	6256	CE2	TYR	D	168	34.881	68.722	46.342	1.00	52.03	6
ATOM	6257	CZ	TYR	D	168	34.670	69.035	45.016	1.00	53.04	6
ATOM	6258	OH	TYR	D	168	33.683	69.917	44.689	1.00	53.97	8
ATOM	6259	C	TYR	D	168	40.181	66.162	46.851	1.00	52.39	6
ATOM	6260	O	TYR	D	168	40.025	65.185	47.575	1.00	53.02	8
ATOM	6261	N	SER	D	169	41.347	66.479	46.299	1.00	51.48	7
ATOM	6262	CA	SER	D	169	42.543	65.686	46.513	1.00	51.84	6
ATOM	6263	CB	SER	D	169	43.664	66.151	45.584	1.00	52.14	6
ATOM	6264	OG	SER	D	169	44.878	65.483	45.881	1.00	50.95	8
ATOM	6265	C	SER	D	169	43.001	65.828	47.953	1.00	53.72	6
ATOM	6266	O	SER	D	169	42.832	66.880	48.570	1.00	51.67	8
ATOM	6267	N	ARG	D	170	43.583	64.761	48.487	1.00	54.84	7
ATOM	6268	CA	ARG	D	170	44.079	64.778	49.850	1.00	54.97	6
ATOM	6269	CB	ARG	D	170	44.460	63.366	50.297	1.00	54.29	6
ATOM	6270	CG	ARG	D	170	43.369	62.647	51.081	1.00	57.60	6
ATOM	6271	CD	ARG	D	170	43.436	61.124	50.955	1.00	58.91	6
ATOM	6272	NE	ARG	D	170	44.726	60.543	51.323	1.00	61.45	7

ATOM	6273	CZ	ARG	D	170	45.504	59.853	50.483	1.00	64.08	6
ATOM	6274	NH1	ARG	D	170	45.140	59.656	49.220	1.00	60.98	7
ATOM	6275	NH2	ARG	D	170	46.649	59.334	50.906	1.00	64.65	7
ATOM	6276	C	ARG	D	170	45.293	65.683	49.928	1.00	56.57	6
ATOM	6277	O	ARG	D	170	45.719	66.078	51.022	1.00	59.46	8
ATOM	6278	N	PHE	D	171	45.842	66.033	48.770	1.00	55.26	7
ATOM	6279	CA	PHE	D	171	47.034	66.864	48.739	1.00	54.09	6
ATOM	6280	CB	PHE	D	171	48.172	66.094	48.070	1.00	53.61	6
ATOM	6281	CG	PHE	D	171	48.319	64.688	48.585	1.00	54.38	6
ATOM	6282	CD1	PHE	D	171	47.427	63.698	48.191	1.00	55.63	6
ATOM	6283	CD2	PHE	D	171	49.315	64.364	49.498	1.00	54.14	6
ATOM	6284	CE1	PHE	D	171	47.521	62.415	48.694	1.00	54.27	6
ATOM	6285	CE2	PHE	D	171	49.414	63.078	50.008	1.00	54.92	6
ATOM	6286	CZ	PHE	D	171	48.516	62.103	49.605	1.00	54.58	6
ATOM	6287	C	PHE	D	171	46.821	68.195	48.049	1.00	53.25	6
ATOM	6288	O	PHE	D	171	45.759	68.457	47.500	1.00	52.23	8
ATOM	6289	N	GLU	D	172	47.836	69.045	48.100	1.00	52.75	7
ATOM	6290	CA	GLU	D	172	47.741	70.347	47.479	1.00	55.31	6
ATOM	6291	CB	GLU	D	172	47.327	71.413	48.505	1.00	58.80	6
ATOM	6292	CG	GLU	D	172	48.293	71.616	49.686	1.00	62.32	6
ATOM	6293	CD	GLU	D	172	47.773	72.633	50.693	1.00	64.33	6
ATOM	6294	OE1	GLU	D	172	47.132	73.617	50.251	1.00	64.06	8
ATOM	6295	OE2	GLU	D	172	48.012	72.456	51.915	1.00	65.29	8
ATOM	6296	C	GLU	D	172	49.083	70.671	46.861	1.00	56.32	6
ATOM	6297	O	GLU	D	172	50.115	70.122	47.265	1.00	54.59	8
ATOM	6298	N	ILE	D	173	49.063	71.550	45.864	1.00	56.82	7
ATOM	6299	CA	ILE	D	173	50.286	71.928	45.171	1.00	57.96	6
ATOM	6300	CB	ILE	D	173	50.062	72.033	43.644	1.00	57.06	6
ATOM	6301	CG2	ILE	D	173	51.332	72.535	42.959	1.00	56.84	6
ATOM	6302	CG1	ILE	D	173	49.663	70.675	43.080	1.00	55.34	6
ATOM	6303	CD1	ILE	D	173	49.371	70.720	41.622	1.00	53.59	6
ATOM	6304	C	ILE	D	173	50.848	73.250	45.653	1.00	59.20	6
ATOM	6305	O	ILE	D	173	50.132	74.249	45.756	1.00	58.03	8
ATOM	6306	N	LEU	D	174	52.140	73.251	45.949	1.00	60.22	7
ATOM	6307	CA	LEU	D	174	52.784	74.473	46.394	1.00	61.88	6
ATOM	6308	CB	LEU	D	174	53.929	74.136	47.340	1.00	61.02	6
ATOM	6309	CG	LEU	D	174	53.512	73.196	48.469	1.00	61.46	6
ATOM	6310	CD1	LEU	D	174	54.722	72.881	49.330	1.00	62.06	6
ATOM	6311	CD2	LEU	D	174	52.395	73.823	49.284	1.00	59.37	6
ATOM	6312	C	LEU	D	174	53.302	75.193	45.151	1.00	63.17	6
ATOM	6313	O	LEU	D	174	52.979	76.357	44.899	1.00	63.68	8
ATOM	6314	N	ASP	D	175	54.080	74.479	44.349	1.00	64.58	7
ATOM	6315	CA	ASP	D	175	54.627	75.067	43.145	1.00	65.97	6
ATOM	6316	CB	ASP	D	175	55.789	75.993	43.538	1.00	67.34	6
ATOM	6317	CG	ASP	D	175	56.390	76.748	42.354	1.00	69.43	6
ATOM	6318	OD1	ASP	D	175	55.636	77.413	41.584	1.00	69.68	8
ATOM	6319	OD2	ASP	D	175	57.635	76.685	42.214	1.00	69.28	8
ATOM	6320	C	ASP	D	175	55.085	73.984	42.164	1.00	66.38	6
ATOM	6321	O	ASP	D	175	55.380	72.846	42.561	1.00	66.58	8
ATOM	6322	N	VAL	D	176	55.118	74.342	40.881	1.00	65.75	7
ATOM	6323	CA	VAL	D	176	55.536	73.436	39.831	1.00	65.19	6
ATOM	6324	CB	VAL	D	176	54.330	72.945	38.992	1.00	64.89	6
ATOM	6325	CG1	VAL	D	176	54.818	72.085	37.811	1.00	64.67	6
ATOM	6326	CG2	VAL	D	176	53.382	72.145	39.865	1.00	65.95	6
ATOM	6327	C	VAL	D	176	56.477	74.190	38.919	1.00	66.36	6
ATOM	6328	O	VAL	D	176	56.178	75.314	38.513	1.00	66.32	8
ATOM	6329	N	THR	D	177	57.614	73.576	38.602	1.00	68.04	7
ATOM	6330	CA	THR	D	177	58.598	74.184	37.708	1.00	69.05	6
ATOM	6331	CB	THR	D	177	59.763	74.819	38.496	1.00	67.62	6
ATOM	6332	OG1	THR	D	177	60.349	73.843	39.370	1.00	63.42	8
ATOM	6333	CG2	THR	D	177	59.258	76.013	39.305	1.00	66.11	6

ATOM	6334	C	THR	D	177	59.165	73.144	36.739	1.00	71.66	6
ATOM	6335	O	THR	D	177	59.373	71.973	37.111	1.00	73.56	8
ATOM	6336	N	GLN	D	178	59.417	73.568	35.501	1.00	71.95	7
ATOM	6337	CA	GLN	D	178	59.941	72.667	34.488	1.00	72.06	6
ATOM	6338	CB	GLN	D	178	58.932	72.511	33.347	1.00	74.14	6
ATOM	6339	CG	GLN	D	178	57.466	72.700	33.754	1.00	76.97	6
ATOM	6340	CD	GLN	D	178	56.497	72.041	32.772	1.00	78.22	6
ATOM	6341	OE1	GLN	D	178	56.603	72.230	31.551	1.00	79.44	8
ATOM	6342	NE2	GLN	D	178	55.544	71.266	33.302	1.00	76.76	7
ATOM	6343	C	GLN	D	178	61.219	73.240	33.936	1.00	71.25	6
ATOM	6344	O	GLN	D	178	61.226	74.368	33.462	1.00	71.24	8
ATOM	6345	N	LYS	D	179	62.291	72.461	33.979	1.00	71.70	7
ATOM	6346	CA	LYS	D	179	63.593	72.904	33.474	1.00	71.59	6
ATOM	6347	CB	LYS	D	179	64.553	73.170	34.642	1.00	73.63	6
ATOM	6348	CG	LYS	D	179	63.906	73.953	35.800	1.00	77.80	6
ATOM	6349	CD	LYS	D	179	64.795	74.018	37.040	1.00	78.53	6
ATOM	6350	CE	LYS	D	179	64.016	74.470	38.273	1.00	79.16	6
ATOM	6351	NZ	LYS	D	179	62.899	73.537	38.610	1.00	77.90	7
ATOM	6352	C	LYS	D	179	64.173	71.807	32.601	1.00	70.50	6
ATOM	6353	O	LYS	D	179	64.549	70.754	33.112	1.00	69.32	8
ATOM	6354	N	LYS	D	180	64.252	72.044	31.294	1.00	69.56	7
ATOM	6355	CA	LYS	D	180	64.803	71.039	30.382	1.00	69.55	6
ATOM	6356	CB	LYS	D	180	64.581	71.464	28.924	1.00	69.05	6
ATOM	6357	CG	LYS	D	180	65.462	72.584	28.419	1.00	68.35	6
ATOM	6358	CD	LYS	D	180	66.773	72.041	27.860	1.00	66.86	6
ATOM	6359	CE	LYS	D	180	66.550	71.200	26.619	1.00	63.97	6
ATOM	6360	NZ	LYS	D	180	66.096	72.020	25.476	1.00	64.54	7
ATOM	6361	C	LYS	D	180	66.293	70.795	30.642	1.00	68.87	6
ATOM	6362	O	LYS	D	180	66.869	71.406	31.536	1.00	69.83	8
ATOM	6363	N	ASN	D	181	66.905	69.879	29.897	1.00	68.37	7
ATOM	6364	CA	ASN	D	181	68.326	69.615	30.060	1.00	70.05	6
ATOM	6365	CB	ASN	D	181	68.711	69.461	31.540	1.00	70.86	6
ATOM	6366	CG	ASN	D	181	67.808	68.533	32.291	1.00	71.68	6
ATOM	6367	OD1	ASN	D	181	67.498	67.446	31.823	1.00	74.38	8
ATOM	6368	ND2	ASN	D	181	67.395	68.945	33.487	1.00	72.61	7
ATOM	6369	C	ASN	D	181	68.905	68.449	29.281	1.00	70.12	6
ATOM	6370	O	ASN	D	181	68.535	67.303	29.491	1.00	68.91	8
ATOM	6371	N	SER	D	182	69.844	68.760	28.385	1.00	71.81	7
ATOM	6372	CA	SER	D	182	70.519	67.744	27.577	1.00	71.83	6
ATOM	6373	CB	SER	D	182	71.361	68.418	26.495	1.00	70.60	6
ATOM	6374	OG	SER	D	182	71.817	67.463	25.557	1.00	71.86	8
ATOM	6375	C	SER	D	182	71.405	66.866	28.482	1.00	71.03	6
ATOM	6376	O	SER	D	182	71.794	67.281	29.572	1.00	72.13	8
ATOM	6377	N	VAL	D	183	71.715	65.653	28.037	1.00	70.45	7
ATOM	6378	CA	VAL	D	183	72.528	64.736	28.842	1.00	69.61	6
ATOM	6379	CB	VAL	D	183	71.728	64.221	30.066	1.00	69.93	6
ATOM	6380	CG1	VAL	D	183	70.268	63.988	29.671	1.00	71.71	6
ATOM	6381	CG2	VAL	D	183	72.331	62.909	30.584	1.00	68.31	6
ATOM	6382	C	VAL	D	183	73.046	63.521	28.069	1.00	69.82	6
ATOM	6383	O	VAL	D	183	72.317	62.887	27.305	1.00	69.28	8
ATOM	6384	N	THR	D	184	74.314	63.194	28.272	1.00	71.03	7
ATOM	6385	CA	THR	D	184	74.898	62.041	27.596	1.00	72.40	6
ATOM	6386	CB	THR	D	184	76.314	62.360	27.027	1.00	71.67	6
ATOM	6387	OG1	THR	D	184	76.207	63.364	26.010	1.00	69.65	8
ATOM	6388	CG2	THR	D	184	76.944	61.110	26.404	1.00	71.24	6
ATOM	6389	C	THR	D	184	74.997	60.901	28.602	1.00	73.76	6
ATOM	6390	O	THR	D	184	75.273	61.132	29.786	1.00	74.26	8
ATOM	6391	N	TYR	D	185	74.749	59.679	28.139	1.00	74.82	7
ATOM	6392	CA	TYR	D	185	74.818	58.515	29.024	1.00	76.20	6
ATOM	6393	CB	TYR	D	185	73.477	57.755	29.046	1.00	77.17	6
ATOM	6394	CG	TYR	D	185	72.286	58.637	29.324	1.00	77.03	6

ATOM	6395	CD1	TYR	D	185	71.822	59.527	28.362	1.00	77.16	6
ATOM	6396	CE1	TYR	D	185	70.781	60.416	28.640	1.00	78.65	6
ATOM	6397	CD2	TYR	D	185	71.676	58.643	30.578	1.00	78.44	6
ATOM	6398	CE2	TYR	D	185	70.629	59.532	30.873	1.00	78.76	6
ATOM	6399	CZ	TYR	D	185	70.190	60.417	29.897	1.00	78.44	6
ATOM	6400	OH	TYR	D	185	69.173	61.311	30.160	1.00	78.64	8
ATOM	6401	C	TYR	D	185	75.909	57.595	28.525	1.00	76.37	6
ATOM	6402	O	TYR	D	185	76.062	57.403	27.320	1.00	75.86	8
ATOM	6403	N	SER	D	186	76.669	57.031	29.454	1.00	78.41	7
ATOM	6404	CA	SER	D	186	77.762	56.127	29.097	1.00	80.47	6
ATOM	6405	CB	SER	D	186	78.353	55.494	30.361	1.00	80.37	6
ATOM	6406	OG	SER	D	186	77.324	55.000	31.202	1.00	80.82	8
ATOM	6407	C	SER	D	186	77.259	55.042	28.139	1.00	81.49	6
ATOM	6408	O	SER	D	186	77.977	54.637	27.205	1.00	80.86	8
ATOM	6409	N	CYS	D	187	76.018	54.601	28.370	1.00	82.03	7
ATOM	6410	CA	CYS	D	187	75.366	53.573	27.553	1.00	82.11	6
ATOM	6411	C	CYS	D	187	75.259	54.005	26.123	1.00	82.74	6
ATOM	6412	O	CYS	D	187	75.445	53.226	25.179	1.00	81.67	8
ATOM	6413	CB	CYS	D	187	73.908	53.360	27.980	1.00	82.28	6
ATOM	6414	SG	CYS	D	187	72.725	54.778	27.707	1.00	81.64	16
ATOM	6415	N	CYS	D	188	74.954	55.287	25.990	1.00	83.43	7
ATOM	6416	CA	CYS	D	188	74.614	55.827	24.701	1.00	83.03	6
ATOM	6417	C	CYS	D	188	75.379	57.070	24.204	1.00	81.94	6
ATOM	6418	O	CYS	D	188	75.401	58.127	24.860	1.00	81.77	8
ATOM	6419	CB	CYS	D	188	73.091	56.059	24.777	1.00	83.56	6
ATOM	6420	SG	CYS	D	188	72.115	54.783	25.740	1.00	85.15	16
ATOM	6421	N	PRO	D	189	76.000	56.945	23.013	1.00	80.60	7
ATOM	6422	CD	PRO	D	189	75.862	55.676	22.263	1.00	80.05	6
ATOM	6423	CA	PRO	D	189	76.809	57.921	22.254	1.00	78.99	6
ATOM	6424	CB	PRO	D	189	76.804	57.341	20.836	1.00	79.15	6
ATOM	6425	CG	PRO	D	189	76.835	55.852	21.097	1.00	80.06	6
ATOM	6426	C	PRO	D	189	76.386	59.408	22.258	1.00	76.71	6
ATOM	6427	O	PRO	D	189	77.106	60.265	22.777	1.00	76.06	8
ATOM	6428	N	GLU	D	190	75.237	59.713	21.663	1.00	73.54	7
ATOM	6429	CA	GLU	D	190	74.762	61.101	21.583	1.00	70.67	6
ATOM	6430	CB	GLU	D	190	73.735	61.233	20.462	1.00	72.95	6
ATOM	6431	CG	GLU	D	190	73.941	60.272	19.292	1.00	76.22	6
ATOM	6432	CD	GLU	D	190	74.959	60.778	18.284	1.00	77.17	6
ATOM	6433	OE1	GLU	D	190	74.920	61.987	17.949	1.00	75.78	8
ATOM	6434	OE2	GLU	D	190	75.786	59.961	17.819	1.00	78.06	8
ATOM	6435	C	GLU	D	190	74.113	61.576	22.874	1.00	67.13	6
ATOM	6436	O	GLU	D	190	74.060	60.842	23.861	1.00	66.77	8
ATOM	6437	N	ALA	D	191	73.595	62.797	22.852	1.00	63.73	7
ATOM	6438	CA	ALA	D	191	72.924	63.362	24.027	1.00	63.96	6
ATOM	6439	CB	ALA	D	191	73.293	64.833	24.188	1.00	60.91	6
ATOM	6440	C	ALA	D	191	71.398	63.226	23.935	1.00	63.09	6
ATOM	6441	O	ALA	D	191	70.824	63.324	22.848	1.00	63.27	8
ATOM	6442	N	TYR	D	192	70.737	63.015	25.073	1.00	61.86	7
ATOM	6443	CA	TYR	D	192	69.284	62.883	25.077	1.00	60.02	6
ATOM	6444	CB	TYR	D	192	68.874	61.483	25.544	1.00	58.87	6
ATOM	6445	CG	TYR	D	192	69.185	60.408	24.531	1.00	59.77	6
ATOM	6446	CD1	TYR	D	192	70.447	59.804	24.491	1.00	59.82	6
ATOM	6447	CE1	TYR	D	192	70.762	58.849	23.514	1.00	59.91	6
ATOM	6448	CD2	TYR	D	192	68.234	60.030	23.568	1.00	59.23	6
ATOM	6449	CE2	TYR	D	192	68.534	59.084	22.592	1.00	60.37	6
ATOM	6450	CZ	TYR	D	192	69.803	58.496	22.566	1.00	61.99	6
ATOM	6451	OH	TYR	D	192	70.120	57.582	21.581	1.00	61.54	8
ATOM	6452	C	TYR	D	192	68.590	63.938	25.922	1.00	59.37	6
ATOM	6453	O	TYR	D	192	68.594	63.874	27.150	1.00	61.63	8
ATOM	6454	N	GLU	D	193	67.986	64.909	25.248	1.00	59.03	7
ATOM	6455	CA	GLU	D	193	67.280	65.992	25.915	1.00	60.46	6

ATOM	6456	CB	GLU	D	193	66.832	67.054	24.898	1.00	61.02	6
ATOM	6457	CG	GLU	D	193	67.985	67.781	24.196	1.00	65.53	6
ATOM	6458	CD	GLU	D	193	67.522	68.937	23.292	1.00	66.58	6
ATOM	6459	OE1	GLU	D	193	66.678	69.760	23.739	1.00	66.15	8
ATOM	6460	OE2	GLU	D	193	68.017	69.023	22.138	1.00	66.88	8
ATOM	6461	C	GLU	D	193	66.066	65.455	26.658	1.00	61.32	6
ATOM	6462	O	GLU	D	193	65.498	64.428	26.278	1.00	61.10	8
ATOM	6463	N	ASP	D	194	65.682	66.157	27.724	1.00	62.11	7
ATOM	6464	CA	ASP	D	194	64.533	65.788	28.537	1.00	60.32	6
ATOM	6465	CB	ASP	D	194	64.855	64.571	29.416	1.00	60.68	6
ATOM	6466	CG	ASP	D	194	65.759	64.907	30.589	1.00	61.25	6
ATOM	6467	OD1	ASP	D	194	66.929	64.453	30.591	1.00	62.58	8
ATOM	6468	OD2	ASP	D	194	65.297	65.619	31.509	1.00	61.10	8
ATOM	6469	C	ASP	D	194	64.086	66.951	29.417	1.00	59.85	6
ATOM	6470	O	ASP	D	194	64.890	67.793	29.816	1.00	60.03	8
ATOM	6471	N	VAL	D	195	62.792	66.993	29.704	1.00	57.38	7
ATOM	6472	CA	VAL	D	195	62.225	68.024	30.538	1.00	55.36	6
ATOM	6473	CB	VAL	D	195	60.864	68.480	30.001	1.00	52.24	6
ATOM	6474	CG1	VAL	D	195	60.179	69.394	31.001	1.00	51.69	6
ATOM	6475	CG2	VAL	D	195	61.058	69.189	28.693	1.00	52.14	6
ATOM	6476	C	VAL	D	195	62.044	67.460	31.935	1.00	56.36	6
ATOM	6477	O	VAL	D	195	61.452	66.412	32.114	1.00	57.76	8
ATOM	6478	N	GLU	D	196	62.571	68.151	32.930	1.00	58.67	7
ATOM	6479	CA	GLU	D	196	62.425	67.712	34.303	1.00	58.26	6
ATOM	6480	CB	GLU	D	196	63.754	67.833	35.035	1.00	58.61	6
ATOM	6481	CG	GLU	D	196	63.725	67.326	36.460	1.00	61.95	6
ATOM	6482	CD	GLU	D	196	65.062	67.533	37.172	1.00	63.50	6
ATOM	6483	OE1	GLU	D	196	66.083	67.014	36.679	1.00	62.21	8
ATOM	6484	OE2	GLU	D	196	65.099	68.218	38.222	1.00	65.74	8
ATOM	6485	C	GLU	D	196	61.370	68.598	34.959	1.00	58.08	6
ATOM	6486	O	GLU	D	196	61.500	69.822	34.997	1.00	59.87	8
ATOM	6487	N	VAL	D	197	60.305	67.979	35.452	1.00	57.22	7
ATOM	6488	CA	VAL	D	197	59.242	68.721	36.104	1.00	54.36	6
ATOM	6489	CB	VAL	D	197	57.863	68.304	35.567	1.00	52.68	6
ATOM	6490	CG1	VAL	D	197	56.772	69.095	36.255	1.00	49.60	6
ATOM	6491	CG2	VAL	D	197	57.809	68.517	34.068	1.00	50.84	6
ATOM	6492	C	VAL	D	197	59.317	68.420	37.587	1.00	55.10	6
ATOM	6493	O	VAL	D	197	59.367	67.264	37.995	1.00	55.27	8
ATOM	6494	N	SER	D	198	59.351	69.467	38.399	1.00	56.68	7
ATOM	6495	CA	SER	D	198	59.413	69.284	39.839	1.00	56.39	6
ATOM	6496	CB	SER	D	198	60.487	70.188	40.448	1.00	55.89	6
ATOM	6497	OG	SER	D	198	61.789	69.767	40.066	1.00	57.83	8
ATOM	6498	C	SER	D	198	58.058	69.593	40.448	1.00	56.61	6
ATOM	6499	O	SER	D	198	57.536	70.698	40.317	1.00	56.25	8
ATOM	6500	N	LEU	D	199	57.481	68.597	41.101	1.00	56.92	7
ATOM	6501	CA	LEU	D	199	56.189	68.770	41.728	1.00	56.84	6
ATOM	6502	CB	LEU	D	199	55.303	67.561	41.468	1.00	57.08	6
ATOM	6503	CG	LEU	D	199	53.981	67.553	42.243	1.00	57.99	6
ATOM	6504	CD1	LEU	D	199	53.094	68.726	41.834	1.00	57.12	6
ATOM	6505	CD2	LEU	D	199	53.272	66.246	41.971	1.00	58.22	6
ATOM	6506	C	LEU	D	199	56.354	68.953	43.220	1.00	57.85	6
ATOM	6507	O	LEU	D	199	56.625	67.998	43.950	1.00	58.46	8
ATOM	6508	N	ASN	D	200	56.207	70.192	43.671	1.00	58.52	7
ATOM	6509	CA	ASN	D	200	56.315	70.486	45.084	1.00	57.07	6
ATOM	6510	CB	ASN	D	200	57.017	71.827	45.311	1.00	59.47	6
ATOM	6511	CG	ASN	D	200	57.126	72.184	46.781	1.00	61.26	6
ATOM	6512	OD1	ASN	D	200	57.508	71.359	47.613	1.00	60.78	8
ATOM	6513	ND2	ASN	D	200	56.792	73.423	47.108	1.00	63.13	7
ATOM	6514	C	ASN	D	200	54.886	70.533	45.593	1.00	55.28	6
ATOM	6515	O	ASN	D	200	54.108	71.422	45.242	1.00	53.93	8
ATOM	6516	N	PHE	D	201	54.549	69.554	46.419	1.00	53.26	7

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ATOM   6517  CA  PHE D 201      53.218  69.444  46.973  1.00 51.91   6
ATOM   6518  CB  PHE D 201      52.408  68.434  46.168  1.00 49.89   6
ATOM   6519  CG  PHE D 201      52.870  67.013  46.348  1.00 46.59   6
ATOM   6520  CD1 PHE D 201      52.068  66.086  47.003  1.00 45.61   6
ATOM   6521  CD2 PHE D 201      54.133  66.613  45.903  1.00 46.86   6
ATOM   6522  CE1 PHE D 201      52.519  64.779  47.218  1.00 45.68   6
ATOM   6523  CE2 PHE D 201      54.597  65.312  46.112  1.00 44.48   6
ATOM   6524  CZ  PHE D 201      53.788  64.394  46.772  1.00 44.43   6
ATOM   6525  C   PHE D 201      53.360  68.940  48.386  1.00 53.35   6
ATOM   6526  O   PHE D 201      54.456  68.570  48.818  1.00 52.18   8
ATOM   6527  N   ARG D 202      52.238  68.902  49.093  1.00 55.22   7
ATOM   6528  CA  ARG D 202      52.211  68.426  50.470  1.00 57.74   6
ATOM   6529  CB  ARG D 202      52.632  69.546  51.412  1.00 58.53   6
ATOM   6530  CG  ARG D 202      51.564  70.612  51.484  1.00 62.76   6
ATOM   6531  CD  ARG D 202      51.956  71.797  52.313  1.00 64.76   6
ATOM   6532  NE  ARG D 202      50.901  72.806  52.296  1.00 64.52   7
ATOM   6533  CZ  ARG D 202      51.046  74.035  52.779  1.00 65.00   6
ATOM   6534  NH1 ARG D 202      52.206  74.409  53.323  1.00 65.86   7
ATOM   6535  NH2 ARG D 202      50.045  74.896  52.708  1.00 62.46   7
ATOM   6536  C   ARG D 202      50.788  67.997  50.835  1.00 57.64   6
ATOM   6537  O   ARG D 202      49.822  68.392  50.186  1.00 55.63   8
ATOM   6538  N   LYS D 203      50.668  67.189  51.878  1.00 58.55   7
ATOM   6539  CA  LYS D 203      49.359  66.759  52.332  1.00 59.55   6
ATOM   6540  CB  LYS D 203      49.505  65.708  53.428  1.00 60.97   6
ATOM   6541  CG  LYS D 203      48.195  65.258  54.031  1.00 62.61   6
ATOM   6542  CD  LYS D 203      48.445  64.319  55.194  1.00 66.11   6
ATOM   6543  CE  LYS D 203      47.142  63.813  55.784  1.00 68.33   6
ATOM   6544  NZ  LYS D 203      46.380  62.985  54.804  1.00 69.98   7
ATOM   6545  C   LYS D 203      48.702  68.008  52.914  1.00 60.27   6
ATOM   6546  O   LYS D 203      49.402  68.886  53.428  1.00 60.55   8
ATOM   6547  N   LYS D 204      47.374  68.105  52.832  1.00 59.32   7
ATOM   6548  CA  LYS D 204      46.680  69.260  53.395  1.00 60.40   6
ATOM   6549  CB  LYS D 204      45.221  69.284  52.947  1.00 59.66   6
ATOM   6550  CG  LYS D 204      45.054  69.738  51.495  1.00 56.15   6
ATOM   6551  CD  LYS D 204      43.652  69.489  50.974  1.00 52.10   6
ATOM   6552  CE  LYS D 204      43.593  69.775  49.488  1.00 52.88   6
ATOM   6553  NZ  LYS D 204      42.334  69.320  48.856  1.00 54.65   7
ATOM   6554  C   LYS D 204      46.776  69.201  54.919  1.00 62.27   6
ATOM   6555  O   LYS D 204      47.031  68.129  55.479  1.00 63.85   8
ATOM   6556  N   GLY D 205      46.590  70.344  55.587  1.00 61.70   7
ATOM   6557  CA  GLY D 205      46.701  70.390  57.043  1.00 61.46   6
ATOM   6558  C   GLY D 205      45.432  70.704  57.821  1.00 60.96   6
ATOM   6559  OT1 GLY D 205      44.364  70.809  57.191  1.00 61.45   8
ATOM   6560  OT2 GLY D 205      45.495  70.835  59.067  1.00 60.53   8
ATOM   6561  CB  PHE E   1      68.481  57.493   1.362  1.00 63.85   6
ATOM   6562  CG  PHE E   1      68.496  56.384   0.357  1.00 65.93   6
ATOM   6563  CD1 PHE E   1      67.431  56.207  -0.526  1.00 67.13   6
ATOM   6564  CD2 PHE E   1      69.549  55.462   0.345  1.00 67.48   6
ATOM   6565  CE1 PHE E   1      67.410  55.116  -1.409  1.00 68.65   6
ATOM   6566  CE2 PHE E   1      69.548  54.364  -0.528  1.00 67.48   6
ATOM   6567  CZ  PHE E   1      68.481  54.185  -1.406  1.00 69.10   6
ATOM   6568  C   PHE E   1      67.191  59.419   2.218  1.00 61.93   6
ATOM   6569  O   PHE E   1      67.898  59.384   3.225  1.00 62.32   8
ATOM   6570  N   PHE E   1      68.457  59.591   0.037  1.00 62.93   7
ATOM   6571  CA  PHE E   1      67.655  58.712   0.943  1.00 62.89   6
ATOM   6572  N   ASP E   2      66.011  60.038   2.205  1.00 61.01   7
ATOM   6573  CA  ASP E   2      65.524  60.730   3.406  1.00 60.82   6
ATOM   6574  CB  ASP E   2      64.448  61.754   3.027  1.00 59.66   6
ATOM   6575  CG  ASP E   2      63.263  61.126   2.346  1.00 61.52   6
ATOM   6576  OD1 ASP E   2      62.587  60.347   3.035  1.00 62.72   8
ATOM   6577  OD2 ASP E   2      63.006  61.396   1.142  1.00 60.96   8
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ATOM	6578	C	ASP	E	2	65.012	59.731	4.459	1.00	60.89	6
ATOM	6579	O	ASP	E	2	64.990	58.525	4.216	1.00	62.95	8
ATOM	6580	N	ARG	E	3	64.624	60.214	5.635	1.00	60.20	7
ATOM	6581	CA	ARG	E	3	64.161	59.321	6.697	1.00	57.08	6
ATOM	6582	CB	ARG	E	3	63.746	60.128	7.933	1.00	56.21	6
ATOM	6583	CG	ARG	E	3	64.906	60.475	8.878	1.00	56.67	6
ATOM	6584	CD	ARG	E	3	65.314	59.266	9.702	1.00	57.53	6
ATOM	6585	NE	ARG	E	3	66.519	59.426	10.524	1.00	58.61	7
ATOM	6586	CZ	ARG	E	3	66.825	60.497	11.258	1.00	60.79	6
ATOM	6587	NH1	ARG	E	3	66.024	61.559	11.294	1.00	61.35	7
ATOM	6588	NH2	ARG	E	3	67.943	60.499	11.975	1.00	58.97	7
ATOM	6589	C	ARG	E	3	63.008	58.447	6.244	1.00	56.93	6
ATOM	6590	O	ARG	E	3	62.949	57.256	6.567	1.00	58.08	8
ATOM	6591	N	ALA	E	4	62.102	59.033	5.473	1.00	54.21	7
ATOM	6592	CA	ALA	E	4	60.937	58.311	4.993	1.00	52.85	6
ATOM	6593	CB	ALA	E	4	60.002	59.262	4.270	1.00	50.53	6
ATOM	6594	C	ALA	E	4	61.342	57.168	4.075	1.00	53.00	6
ATOM	6595	O	ALA	E	4	60.858	56.056	4.225	1.00	53.30	8
ATOM	6596	N	ASP	E	5	62.235	57.443	3.132	1.00	54.00	7
ATOM	6597	CA	ASP	E	5	62.692	56.433	2.190	1.00	54.02	6
ATOM	6598	CB	ASP	E	5	63.702	57.021	1.197	1.00	56.37	6
ATOM	6599	CG	ASP	E	5	63.153	58.223	0.435	1.00	60.25	6
ATOM	6600	OD1	ASP	E	5	62.018	58.154	-0.072	1.00	61.70	8
ATOM	6601	OD2	ASP	E	5	63.864	59.247	0.327	1.00	64.63	8
ATOM	6602	C	ASP	E	5	63.341	55.278	2.924	1.00	54.45	6
ATOM	6603	O	ASP	E	5	63.192	54.127	2.532	1.00	54.26	8
ATOM	6604	N	ILE	E	6	64.060	55.582	3.997	1.00	54.54	7
ATOM	6605	CA	ILE	E	6	64.734	54.535	4.755	1.00	55.28	6
ATOM	6606	CB	ILE	E	6	65.727	55.121	5.781	1.00	56.90	6
ATOM	6607	CG2	ILE	E	6	66.476	53.991	6.489	1.00	56.40	6
ATOM	6608	CG1	ILE	E	6	66.728	56.031	5.068	1.00	58.74	6
ATOM	6609	CD1	ILE	E	6	67.833	56.589	5.976	1.00	60.73	6
ATOM	6610	C	ILE	E	6	63.765	53.617	5.482	1.00	53.47	6
ATOM	6611	O	ILE	E	6	63.830	52.401	5.322	1.00	53.23	8
ATOM	6612	N	LEU	E	7	62.883	54.199	6.290	1.00	53.23	7
ATOM	6613	CA	LEU	E	7	61.897	53.423	7.033	1.00	52.57	6
ATOM	6614	CB	LEU	E	7	61.060	54.354	7.899	1.00	52.03	6
ATOM	6615	CG	LEU	E	7	61.862	55.020	9.017	1.00	52.39	6
ATOM	6616	CD1	LEU	E	7	61.074	56.183	9.607	1.00	53.72	6
ATOM	6617	CD2	LEU	E	7	62.185	53.989	10.070	1.00	47.50	6
ATOM	6618	C	LEU	E	7	61.003	52.660	6.065	1.00	52.40	6
ATOM	6619	O	LEU	E	7	60.665	51.503	6.302	1.00	53.43	8
ATOM	6620	N	TYR	E	8	60.644	53.311	4.967	1.00	51.20	7
ATOM	6621	CA	TYR	E	8	59.810	52.707	3.951	1.00	52.74	6
ATOM	6622	CB	TYR	E	8	59.622	53.686	2.804	1.00	54.75	6
ATOM	6623	CG	TYR	E	8	58.825	53.102	1.660	1.00	60.00	6
ATOM	6624	CD1	TYR	E	8	57.448	52.902	1.773	1.00	59.81	6
ATOM	6625	CE1	TYR	E	8	56.723	52.341	0.734	1.00	59.72	6
ATOM	6626	CD2	TYR	E	8	59.453	52.717	0.465	1.00	61.59	6
ATOM	6627	CE2	TYR	E	8	58.727	52.148	-0.580	1.00	59.67	6
ATOM	6628	CZ	TYR	E	8	57.367	51.967	-0.433	1.00	59.94	6
ATOM	6629	OH	TYR	E	8	56.646	51.411	-1.457	1.00	63.44	8
ATOM	6630	C	TYR	E	8	60.399	51.405	3.404	1.00	54.02	6
ATOM	6631	O	TYR	E	8	59.692	50.414	3.259	1.00	54.84	8
ATOM	6632	N	ASN	E	9	61.688	51.411	3.082	1.00	53.58	7
ATOM	6633	CA	ASN	E	9	62.338	50.224	2.559	1.00	52.96	6
ATOM	6634	CB	ASN	E	9	63.790	50.524	2.182	1.00	58.69	6
ATOM	6635	CG	ASN	E	9	63.907	51.445	0.966	1.00	62.10	6
ATOM	6636	OD1	ASN	E	9	62.908	51.771	0.321	1.00	64.59	8
ATOM	6637	ND2	ASN	E	9	65.137	51.861	0.645	1.00	63.43	7
ATOM	6638	C	ASN	E	9	62.297	49.112	3.584	1.00	52.17	6

ATOM	6639	O	ASN	E	9	61.870	48.003	3.287	1.00 51.04	8
ATOM	6640	N	ILE	E	10	62.746	49.410	4.794	1.00 53.05	7
ATOM	6641	CA	ILE	E	10	62.752	48.424	5.866	1.00 53.91	6
ATOM	6642	CB	ILE	E	10	63.189	49.053	7.195	1.00 53.67	6
ATOM	6643	CG2	ILE	E	10	63.060	48.027	8.316	1.00 51.86	6
ATOM	6644	CG1	ILE	E	10	64.627	49.564	7.077	1.00 51.89	6
ATOM	6645	CD1	ILE	E	10	65.085	50.379	8.251	1.00 50.06	6
ATOM	6646	C	ILE	E	10	61.358	47.835	6.054	1.00 55.10	6
ATOM	6647	O	ILE	E	10	61.186	46.631	6.216	1.00 55.00	8
ATOM	6648	N	ARG	E	11	60.364	48.708	6.032	1.00 56.28	7
ATOM	6649	CA	ARG	E	11	58.975	48.308	6.199	1.00 57.92	6
ATOM	6650	CB	ARG	E	11	58.084	49.543	6.106	1.00 61.96	6
ATOM	6651	CG	ARG	E	11	56.628	49.280	6.323	1.00 69.38	6
ATOM	6652	CD	ARG	E	11	56.359	49.040	7.797	1.00 79.46	6
ATOM	6653	NE	ARG	E	11	54.957	49.274	8.149	1.00 85.84	7
ATOM	6654	CZ	ARG	E	11	54.244	50.315	7.713	1.00 89.11	6
ATOM	6655	NH1	ARG	E	11	54.801	51.215	6.892	1.00 90.35	7
ATOM	6656	NH2	ARG	E	11	52.980	50.475	8.117	1.00 90.14	7
ATOM	6657	C	ARG	E	11	58.559	47.314	5.126	1.00 56.77	6
ATOM	6658	O	ARG	E	11	57.986	46.264	5.415	1.00 55.32	8
ATOM	6659	N	GLN	E	12	58.866	47.663	3.881	1.00 56.51	7
ATOM	6660	CA	GLN	E	12	58.511	46.850	2.730	1.00 54.24	6
ATOM	6661	CB	GLN	E	12	58.583	47.698	1.485	1.00 53.75	6
ATOM	6662	CG	GLN	E	12	57.341	47.645	0.673	1.00 58.35	6
ATOM	6663	CD	GLN	E	12	56.287	48.540	1.223	1.00 59.21	6
ATOM	6664	OE1	GLN	E	12	56.517	49.726	1.375	1.00 63.59	8
ATOM	6665	NE2	GLN	E	12	55.121	47.990	1.528	1.00 59.83	7
ATOM	6666	C	GLN	E	12	59.312	45.581	2.484	1.00 53.65	6
ATOM	6667	O	GLN	E	12	58.820	44.677	1.825	1.00 52.67	8
ATOM	6668	N	THR	E	13	60.536	45.507	2.995	1.00 54.14	7
ATOM	6669	CA	THR	E	13	61.369	44.331	2.771	1.00 55.96	6
ATOM	6670	CB	THR	E	13	62.714	44.726	2.181	1.00 55.93	6
ATOM	6671	OG1	THR	E	13	63.380	45.612	3.090	1.00 55.29	8
ATOM	6672	CG2	THR	E	13	62.526	45.400	0.822	1.00 55.33	6
ATOM	6673	C	THR	E	13	61.656	43.486	4.005	1.00 58.24	6
ATOM	6674	O	THR	E	13	62.096	42.343	3.892	1.00 58.85	8
ATOM	6675	N	SER	E	14	61.414	44.042	5.182	1.00 60.49	7
ATOM	6676	CA	SER	E	14	61.681	43.317	6.408	1.00 61.17	6
ATOM	6677	CB	SER	E	14	61.629	44.265	7.599	1.00 62.69	6
ATOM	6678	OG	SER	E	14	62.247	43.658	8.723	1.00 66.18	8
ATOM	6679	C	SER	E	14	60.727	42.151	6.644	1.00 60.36	6
ATOM	6680	O	SER	E	14	59.579	42.153	6.184	1.00 59.94	8
ATOM	6681	N	ARG	E	15	61.233	41.156	7.369	1.00 58.70	7
ATOM	6682	CA	ARG	E	15	60.487	39.949	7.703	1.00 58.01	6
ATOM	6683	CB	ARG	E	15	60.926	38.792	6.805	1.00 57.94	6
ATOM	6684	CG	ARG	E	15	60.686	39.058	5.325	1.00 59.93	6
ATOM	6685	CD	ARG	E	15	60.746	37.761	4.547	1.00 63.77	6
ATOM	6686	NE	ARG	E	15	59.755	36.818	5.060	1.00 66.81	7
ATOM	6687	CZ	ARG	E	15	59.714	35.516	4.772	1.00 66.79	6
ATOM	6688	NH1	ARG	E	15	60.622	34.982	3.964	1.00 64.79	7
ATOM	6689	NH2	ARG	E	15	58.748	34.752	5.287	1.00 67.36	7
ATOM	6690	C	ARG	E	15	60.743	39.621	9.170	1.00 55.75	6
ATOM	6691	O	ARG	E	15	61.705	38.928	9.513	1.00 55.70	8
ATOM	6692	N	PRO	E	16	59.869	40.121	10.057	1.00 54.09	7
ATOM	6693	CD	PRO	E	16	58.682	40.932	9.727	1.00 50.97	6
ATOM	6694	CA	PRO	E	16	59.961	39.919	11.503	1.00 51.94	6
ATOM	6695	CB	PRO	E	16	58.731	40.650	12.031	1.00 50.89	6
ATOM	6696	CG	PRO	E	16	58.463	41.680	10.997	1.00 51.98	6
ATOM	6697	C	PRO	E	16	59.986	38.473	11.945	1.00 50.22	6
ATOM	6698	O	PRO	E	16	60.418	38.176	13.046	1.00 49.19	8
ATOM	6699	N	ASP	E	17	59.512	37.579	11.095	1.00 50.78	7

ATOM	6700	CA	ASP	E	17	59.477	36.171	11.446	1.00	53.11	6
ATOM	6701	CB	ASP	E	17	58.244	35.492	10.832	1.00	58.78	6
ATOM	6702	CG	ASP	E	17	56.931	35.917	11.513	1.00	64.95	6
ATOM	6703	OD1	ASP	E	17	56.959	36.261	12.732	1.00	65.29	8
ATOM	6704	OD2	ASP	E	17	55.865	35.887	10.831	1.00	66.80	8
ATOM	6705	C	ASP	E	17	60.716	35.401	11.039	1.00	52.04	6
ATOM	6706	O	ASP	E	17	60.787	34.194	11.242	1.00	53.16	8
ATOM	6707	N	VAL	E	18	61.701	36.090	10.481	1.00	52.13	7
ATOM	6708	CA	VAL	E	18	62.906	35.410	10.034	1.00	51.75	6
ATOM	6709	CB	VAL	E	18	63.050	35.519	8.509	1.00	53.20	6
ATOM	6710	CG1	VAL	E	18	64.265	34.728	8.037	1.00	54.22	6
ATOM	6711	CG2	VAL	E	18	61.797	35.010	7.843	1.00	52.93	6
ATOM	6712	C	VAL	E	18	64.193	35.897	10.675	1.00	50.84	6
ATOM	6713	O	VAL	E	18	64.595	37.039	10.513	1.00	50.74	8
ATOM	6714	N	ILE	E	19	64.841	34.990	11.387	1.00	51.04	7
ATOM	6715	CA	ILE	E	19	66.092	35.270	12.077	1.00	53.80	6
ATOM	6716	CB	ILE	E	19	66.478	34.027	12.940	1.00	52.99	6
ATOM	6717	CG2	ILE	E	19	66.791	32.842	12.040	1.00	52.72	6
ATOM	6718	CG1	ILE	E	19	67.644	34.346	13.870	1.00	52.81	6
ATOM	6719	CD1	ILE	E	19	67.867	33.290	14.923	1.00	49.41	6
ATOM	6720	C	ILE	E	19	67.184	35.628	11.053	1.00	55.50	6
ATOM	6721	O	ILE	E	19	67.399	34.903	10.087	1.00	54.87	8
ATOM	6722	N	PRO	E	20	67.879	36.765	11.250	1.00	57.80	7
ATOM	6723	CD	PRO	E	20	67.710	37.684	12.385	1.00	58.20	6
ATOM	6724	CA	PRO	E	20	68.948	37.253	10.359	1.00	60.68	6
ATOM	6725	CB	PRO	E	20	69.252	38.664	10.897	1.00	58.99	6
ATOM	6726	CG	PRO	E	20	68.056	39.007	11.744	1.00	60.19	6
ATOM	6727	C	PRO	E	20	70.201	36.370	10.360	1.00	62.73	6
ATOM	6728	O	PRO	E	20	71.317	36.854	10.568	1.00	61.22	8
ATOM	6729	N	THR	E	21	70.008	35.080	10.117	1.00	65.32	7
ATOM	6730	CA	THR	E	21	71.107	34.128	10.106	1.00	69.19	6
ATOM	6731	CB	THR	E	21	70.573	32.698	10.364	1.00	68.56	6
ATOM	6732	OG1	THR	E	21	70.744	32.370	11.751	1.00	66.59	8
ATOM	6733	CG2	THR	E	21	71.300	31.677	9.502	1.00	68.21	6
ATOM	6734	C	THR	E	21	71.964	34.121	8.840	1.00	72.78	6
ATOM	6735	O	THR	E	21	71.450	34.096	7.716	1.00	72.75	8
ATOM	6736	N	GLN	E	22	73.282	34.128	9.051	1.00	77.19	7
ATOM	6737	CA	GLN	E	22	74.279	34.102	7.971	1.00	80.45	6
ATOM	6738	CB	GLN	E	22	75.303	35.209	8.192	1.00	81.20	6
ATOM	6739	CG	GLN	E	22	74.691	36.597	8.264	1.00	83.07	6
ATOM	6740	CD	GLN	E	22	75.515	37.542	9.131	1.00	85.11	6
ATOM	6741	OE1	GLN	E	22	75.640	37.329	10.355	1.00	85.67	8
ATOM	6742	NE2	GLN	E	22	76.087	38.587	8.510	1.00	84.48	7
ATOM	6743	C	GLN	E	22	74.980	32.739	8.023	1.00	81.85	6
ATOM	6744	O	GLN	E	22	75.783	32.480	8.929	1.00	81.74	8
ATOM	6745	N	ARG	E	23	74.676	31.880	7.050	1.00	84.04	7
ATOM	6746	CA	ARG	E	23	75.235	30.521	7.001	1.00	84.92	6
ATOM	6747	CB	ARG	E	23	76.767	30.550	6.931	1.00	84.82	6
ATOM	6748	CG	ARG	E	23	77.314	30.929	5.558	1.00	87.29	6
ATOM	6749	CD	ARG	E	23	77.788	32.397	5.462	1.00	90.43	6
ATOM	6750	NE	ARG	E	23	78.140	32.777	4.081	1.00	92.74	7
ATOM	6751	CZ	ARG	E	23	78.982	32.103	3.287	1.00	93.28	6
ATOM	6752	NH1	ARG	E	23	79.592	30.993	3.712	1.00	92.22	7
ATOM	6753	NH2	ARG	E	23	79.204	32.535	2.047	1.00	92.78	7
ATOM	6754	C	ARG	E	23	74.790	29.736	8.237	1.00	85.32	6
ATOM	6755	O	ARG	E	23	73.673	29.929	8.747	1.00	85.55	8
ATOM	6756	N	ASP	E	24	75.648	28.842	8.718	1.00	85.95	7
ATOM	6757	CA	ASP	E	24	75.304	28.062	9.907	1.00	86.37	6
ATOM	6758	CB	ASP	E	24	76.103	26.752	9.985	1.00	90.45	6
ATOM	6759	CG	ASP	E	24	76.671	26.317	8.636	1.00	93.77	6
ATOM	6760	OD1	ASP	E	24	75.856	26.082	7.698	1.00	95.19	8

ATOM	6761	OD2	ASP	E	24	77.930	26.212	8.533	1.00	94.96	8
ATOM	6762	C	ASP	E	24	75.657	28.917	11.116	1.00	84.76	6
ATOM	6763	O	ASP	E	24	75.551	28.466	12.259	1.00	84.92	8
ATOM	6764	N	ARG	E	25	76.097	30.146	10.857	1.00	82.51	7
ATOM	6765	CA	ARG	E	25	76.465	31.063	11.930	1.00	80.45	6
ATOM	6766	CB	ARG	E	25	77.208	32.289	11.382	1.00	83.04	6
ATOM	6767	CG	ARG	E	25	78.635	32.032	10.918	1.00	87.73	6
ATOM	6768	CD	ARG	E	25	79.370	33.358	10.688	1.00	91.97	6
ATOM	6769	NE	ARG	E	25	80.781	33.171	10.340	1.00	95.94	7
ATOM	6770	CZ	ARG	E	25	81.667	34.164	10.199	1.00	97.73	6
ATOM	6771	NH1	ARG	E	25	81.285	35.435	10.379	1.00	98.12	7
ATOM	6772	NH2	ARG	E	25	82.938	33.892	9.880	1.00	97.12	7
ATOM	6773	C	ARG	E	25	75.256	31.557	12.708	1.00	76.54	6
ATOM	6774	O	ARG	E	25	74.265	31.999	12.122	1.00	76.16	8
ATOM	6775	N	PRO	E	26	75.322	31.483	14.045	1.00	73.86	7
ATOM	6776	CD	PRO	E	26	76.343	30.778	14.834	1.00	73.05	6
ATOM	6777	CA	PRO	E	26	74.231	31.936	14.916	1.00	70.73	6
ATOM	6778	CB	PRO	E	26	74.647	31.425	16.295	1.00	70.99	6
ATOM	6779	CG	PRO	E	26	75.529	30.257	15.984	1.00	72.42	6
ATOM	6780	C	PRO	E	26	74.199	33.466	14.891	1.00	67.63	6
ATOM	6781	O	PRO	E	26	75.173	34.110	14.493	1.00	66.91	8
ATOM	6782	N	VAL	E	27	73.076	34.046	15.288	1.00	63.36	7
ATOM	6783	CA	VAL	E	27	72.980	35.487	15.346	1.00	57.94	6
ATOM	6784	CB	VAL	E	27	71.537	35.949	15.266	1.00	55.79	6
ATOM	6785	CG1	VAL	E	27	71.403	37.366	15.780	1.00	54.61	6
ATOM	6786	CG2	VAL	E	27	71.082	35.870	13.839	1.00	57.04	6
ATOM	6787	C	VAL	E	27	73.554	35.821	16.706	1.00	57.83	6
ATOM	6788	O	VAL	E	27	73.180	35.207	17.711	1.00	58.05	8
ATOM	6789	N	ALA	E	28	74.490	36.760	16.744	1.00	55.79	7
ATOM	6790	CA	ALA	E	28	75.087	37.130	18.014	1.00	55.59	6
ATOM	6791	CB	ALA	E	28	76.508	37.588	17.810	1.00	54.25	6
ATOM	6792	C	ALA	E	28	74.270	38.224	18.677	1.00	54.76	6
ATOM	6793	O	ALA	E	28	74.244	39.370	18.216	1.00	54.28	8
ATOM	6794	N	VAL	E	29	73.596	37.850	19.759	1.00	53.10	7
ATOM	6795	CA	VAL	E	29	72.769	38.783	20.514	1.00	53.62	6
ATOM	6796	CB	VAL	E	29	71.338	38.222	20.767	1.00	52.63	6
ATOM	6797	CG1	VAL	E	29	70.531	39.210	21.591	1.00	47.51	6
ATOM	6798	CG2	VAL	E	29	70.641	37.940	19.446	1.00	52.51	6
ATOM	6799	C	VAL	E	29	73.412	39.051	21.865	1.00	53.21	6
ATOM	6800	O	VAL	E	29	73.760	38.119	22.599	1.00	53.58	8
ATOM	6801	N	SER	E	30	73.583	40.325	22.184	1.00	51.51	7
ATOM	6802	CA	SER	E	30	74.154	40.681	23.459	1.00	54.05	6
ATOM	6803	CB	SER	E	30	75.288	41.690	23.276	1.00	52.43	6
ATOM	6804	OG	SER	E	30	74.821	42.854	22.632	1.00	55.74	8
ATOM	6805	C	SER	E	30	73.024	41.277	24.301	1.00	56.57	6
ATOM	6806	O	SER	E	30	72.236	42.110	23.825	1.00	54.93	8
ATOM	6807	N	VAL	E	31	72.946	40.824	25.550	1.00	58.33	7
ATOM	6808	CA	VAL	E	31	71.934	41.280	26.493	1.00	60.16	6
ATOM	6809	CB	VAL	E	31	71.058	40.118	26.966	1.00	59.85	6
ATOM	6810	CG1	VAL	E	31	69.842	40.662	27.700	1.00	60.72	6
ATOM	6811	CG2	VAL	E	31	70.653	39.264	25.783	1.00	60.11	6
ATOM	6812	C	VAL	E	31	72.599	41.891	27.724	1.00	61.00	6
ATOM	6813	O	VAL	E	31	73.542	41.327	28.279	1.00	62.05	8
ATOM	6814	N	SER	E	32	72.092	43.037	28.160	1.00	61.21	7
ATOM	6815	CA	SER	E	32	72.648	43.717	29.318	1.00	60.47	6
ATOM	6816	CB	SER	E	32	73.688	44.743	28.851	1.00	61.09	6
ATOM	6817	OG	SER	E	32	74.162	45.553	29.919	1.00	63.13	8
ATOM	6818	C	SER	E	32	71.552	44.422	30.111	1.00	60.62	6
ATOM	6819	O	SER	E	32	70.941	45.375	29.621	1.00	62.55	8
ATOM	6820	N	LEU	E	33	71.300	43.962	31.332	1.00	58.26	7
ATOM	6821	CA	LEU	E	33	70.282	44.591	32.165	1.00	56.62	6

ATOM	6822	CB	LEU	E	33	69.658	43.578	33.122	1.00	54.43	6
ATOM	6823	CG	LEU	E	33	69.031	42.344	32.487	1.00	55.79	6
ATOM	6824	CD1	LEU	E	33	68.247	41.561	33.532	1.00	53.82	6
ATOM	6825	CD2	LEU	E	33	68.132	42.781	31.348	1.00	56.32	6
ATOM	6826	C	LEU	E	33	70.880	45.717	32.985	1.00	56.68	6
ATOM	6827	O	LEU	E	33	71.954	45.572	33.556	1.00	58.07	8
ATOM	6828	N	LYS	E	34	70.186	46.843	33.029	1.00	55.71	7
ATOM	6829	CA	LYS	E	34	70.616	47.978	33.822	1.00	54.48	6
ATOM	6830	CB	LYS	E	34	70.799	49.207	32.948	1.00	57.11	6
ATOM	6831	CG	LYS	E	34	71.726	48.985	31.774	1.00	66.06	6
ATOM	6832	CD	LYS	E	34	73.179	48.679	32.205	1.00	71.51	6
ATOM	6833	CE	LYS	E	34	74.103	48.409	30.973	1.00	73.37	6
ATOM	6834	NZ	LYS	E	34	75.541	48.135	31.351	1.00	72.80	7
ATOM	6835	C	LYS	E	34	69.459	48.201	34.776	1.00	53.15	6
ATOM	6836	O	LYS	E	34	68.373	48.590	34.356	1.00	52.81	8
ATOM	6837	N	PHE	E	35	69.668	47.947	36.059	1.00	51.67	7
ATOM	6838	CA	PHE	E	35	68.584	48.120	37.011	1.00	49.05	6
ATOM	6839	CB	PHE	E	35	68.890	47.364	38.292	1.00	46.62	6
ATOM	6840	CG	PHE	E	35	68.921	45.883	38.095	1.00	47.20	6
ATOM	6841	CD1	PHE	E	35	70.071	45.254	37.651	1.00	46.38	6
ATOM	6842	CD2	PHE	E	35	67.766	45.125	38.253	1.00	49.08	6
ATOM	6843	CE1	PHE	E	35	70.074	43.897	37.363	1.00	47.59	6
ATOM	6844	CE2	PHE	E	35	67.755	43.760	37.964	1.00	48.98	6
ATOM	6845	CZ	PHE	E	35	68.913	43.145	37.517	1.00	48.13	6
ATOM	6846	C	PHE	E	35	68.225	49.560	37.285	1.00	48.83	6
ATOM	6847	O	PHE	E	35	69.086	50.401	37.492	1.00	50.99	8
ATOM	6848	N	ILE	E	36	66.927	49.831	37.259	1.00	47.58	7
ATOM	6849	CA	ILE	E	36	66.403	51.166	37.465	1.00	44.93	6
ATOM	6850	CB	ILE	E	36	65.398	51.532	36.370	1.00	44.37	6
ATOM	6851	CG2	ILE	E	36	64.927	52.956	36.547	1.00	39.93	6
ATOM	6852	CG1	ILE	E	36	66.034	51.328	34.994	1.00	45.24	6
ATOM	6853	CD1	ILE	E	36	67.290	52.114	34.776	1.00	46.74	6
ATOM	6854	C	ILE	E	36	65.698	51.266	38.792	1.00	46.03	6
ATOM	6855	O	ILE	E	36	65.588	52.350	39.347	1.00	46.58	8
ATOM	6856	N	ASN	E	37	65.201	50.142	39.299	1.00	45.38	7
ATOM	6857	CA	ASN	E	37	64.510	50.163	40.580	1.00	44.10	6
ATOM	6858	CB	ASN	E	37	63.256	51.022	40.471	1.00	42.99	6
ATOM	6859	CG	ASN	E	37	62.870	51.660	41.784	1.00	46.14	6
ATOM	6860	OD1	ASN	E	37	62.892	51.018	42.832	1.00	45.55	8
ATOM	6861	ND2	ASN	E	37	62.497	52.931	41.731	1.00	45.29	7
ATOM	6862	C	ASN	E	37	64.125	48.777	41.087	1.00	45.25	6
ATOM	6863	O	ASN	E	37	64.009	47.825	40.317	1.00	42.90	8
ATOM	6864	N	ILE	E	38	63.951	48.680	42.401	1.00	46.26	7
ATOM	6865	CA	ILE	E	38	63.537	47.453	43.057	1.00	47.22	6
ATOM	6866	CB	ILE	E	38	64.646	46.913	43.940	1.00	46.57	6
ATOM	6867	CG2	ILE	E	38	64.152	45.692	44.685	1.00	46.43	6
ATOM	6868	CG1	ILE	E	38	65.848	46.561	43.058	1.00	47.22	6
ATOM	6869	CD1	ILE	E	38	67.109	46.207	43.784	1.00	46.51	6
ATOM	6870	C	ILE	E	38	62.346	47.902	43.879	1.00	48.14	6
ATOM	6871	O	ILE	E	38	62.504	48.619	44.855	1.00	49.04	8
ATOM	6872	N	LEU	E	39	61.157	47.476	43.466	1.00	49.65	7
ATOM	6873	CA	LEU	E	39	59.908	47.897	44.092	1.00	51.44	6
ATOM	6874	CB	LEU	E	39	58.856	48.052	43.004	1.00	53.02	6
ATOM	6875	CG	LEU	E	39	59.359	48.916	41.847	1.00	54.99	6
ATOM	6876	CD1	LEU	E	39	58.314	49.019	40.767	1.00	54.07	6
ATOM	6877	CD2	LEU	E	39	59.717	50.289	42.377	1.00	53.65	6
ATOM	6878	C	LEU	E	39	59.312	47.104	45.241	1.00	52.90	6
ATOM	6879	O	LEU	E	39	58.795	47.690	46.184	1.00	53.53	8
ATOM	6880	N	GLU	E	40	59.332	45.781	45.163	1.00	54.20	7
ATOM	6881	CA	GLU	E	40	58.781	44.988	46.249	1.00	56.14	6
ATOM	6882	CB	GLU	E	40	57.357	44.549	45.960	1.00	58.59	6

ATOM	6883	CG	GLU	E	40	56.377	45.678	45.865	1.00	64.95	6
ATOM	6884	CD	GLU	E	40	54.960	45.178	45.718	1.00	68.54	6
ATOM	6885	OE1	GLU	E	40	54.697	44.405	44.757	1.00	70.88	8
ATOM	6886	OE2	GLU	E	40	54.119	45.561	46.564	1.00	69.89	8
ATOM	6887	C	GLU	E	40	59.620	43.773	46.449	1.00	55.88	6
ATOM	6888	O	GLU	E	40	60.029	43.134	45.498	1.00	58.42	8
ATOM	6889	N	VAL	E	41	59.876	43.454	47.700	1.00	55.75	7
ATOM	6890	CA	VAL	E	41	60.675	42.300	48.021	1.00	55.46	6
ATOM	6891	CB	VAL	E	41	62.067	42.732	48.550	1.00	56.94	6
ATOM	6892	CG1	VAL	E	41	62.802	41.547	49.107	1.00	58.11	6
ATOM	6893	CG2	VAL	E	41	62.878	43.361	47.433	1.00	55.88	6
ATOM	6894	C	VAL	E	41	59.925	41.520	49.078	1.00	55.20	6
ATOM	6895	O	VAL	E	41	59.230	42.094	49.908	1.00	55.44	8
ATOM	6896	N	ASN	E	42	60.042	40.204	49.025	1.00	55.58	7
ATOM	6897	CA	ASN	E	42	59.381	39.350	49.995	1.00	56.97	6
ATOM	6898	CB	ASN	E	42	58.077	38.794	49.430	1.00	55.95	6
ATOM	6899	CG	ASN	E	42	57.220	38.135	50.490	1.00	55.31	6
ATOM	6900	OD1	ASN	E	42	57.696	37.306	51.267	1.00	56.29	8
ATOM	6901	ND2	ASN	E	42	55.948	38.499	50.526	1.00	53.42	7
ATOM	6902	C	ASN	E	42	60.360	38.222	50.241	1.00	59.68	6
ATOM	6903	O	ASN	E	42	60.527	37.337	49.393	1.00	60.84	8
ATOM	6904	N	GLU	E	43	61.014	38.255	51.398	1.00	61.29	7
ATOM	6905	CA	GLU	E	43	62.005	37.242	51.717	1.00	62.43	6
ATOM	6906	CB	GLU	E	43	62.898	37.721	52.857	1.00	65.13	6
ATOM	6907	CG	GLU	E	43	64.066	36.787	53.120	1.00	70.44	6
ATOM	6908	CD	GLU	E	43	65.091	37.358	54.094	1.00	73.76	6
ATOM	6909	OE1	GLU	E	43	66.010	36.601	54.486	1.00	74.81	8
ATOM	6910	OE2	GLU	E	43	64.982	38.557	54.460	1.00	74.43	8
ATOM	6911	C	GLU	E	43	61.355	35.920	52.070	1.00	61.19	6
ATOM	6912	O	GLU	E	43	61.977	34.861	51.958	1.00	58.53	8
ATOM	6913	N	ILE	E	44	60.094	35.994	52.484	1.00	61.32	7
ATOM	6914	CA	ILE	E	44	59.330	34.809	52.852	1.00	61.37	6
ATOM	6915	CB	ILE	E	44	57.999	35.178	53.536	1.00	62.70	6
ATOM	6916	CG2	ILE	E	44	57.197	33.897	53.812	1.00	63.01	6
ATOM	6917	CG1	ILE	E	44	58.258	35.946	54.836	1.00	62.78	6
ATOM	6918	CD1	ILE	E	44	58.852	35.088	55.947	1.00	63.28	6
ATOM	6919	C	ILE	E	44	58.983	34.000	51.608	1.00	60.40	6
ATOM	6920	O	ILE	E	44	59.114	32.774	51.592	1.00	61.80	8
ATOM	6921	N	THR	E	45	58.532	34.692	50.569	1.00	58.56	7
ATOM	6922	CA	THR	E	45	58.149	34.033	49.326	1.00	57.28	6
ATOM	6923	CB	THR	E	45	56.906	34.696	48.710	1.00	56.47	6
ATOM	6924	OG1	THR	E	45	57.189	36.074	48.443	1.00	55.94	8
ATOM	6925	CG2	THR	E	45	55.724	34.588	49.658	1.00	52.56	6
ATOM	6926	C	THR	E	45	59.245	34.029	48.275	1.00	55.65	6
ATOM	6927	O	THR	E	45	59.120	33.357	47.262	1.00	55.71	8
ATOM	6928	N	ASN	E	46	60.313	34.782	48.514	1.00	55.17	7
ATOM	6929	CA	ASN	E	46	61.420	34.850	47.564	1.00	54.46	6
ATOM	6930	CB	ASN	E	46	62.057	33.472	47.435	1.00	54.61	6
ATOM	6931	CG	ASN	E	46	63.288	33.322	48.290	1.00	56.45	6
ATOM	6932	OD1	ASN	E	46	63.674	32.213	48.638	1.00	57.64	8
ATOM	6933	ND2	ASN	E	46	63.922	34.436	48.621	1.00	53.06	7
ATOM	6934	C	ASN	E	46	60.972	35.362	46.187	1.00	54.17	6
ATOM	6935	O	ASN	E	46	61.259	34.764	45.149	1.00	54.29	8
ATOM	6936	N	GLU	E	47	60.267	36.482	46.191	1.00	52.96	7
ATOM	6937	CA	GLU	E	47	59.769	37.074	44.970	1.00	51.83	6
ATOM	6938	CB	GLU	E	47	58.247	36.956	44.926	1.00	50.20	6
ATOM	6939	CG	GLU	E	47	57.750	35.530	44.856	1.00	50.29	6
ATOM	6940	CD	GLU	E	47	56.236	35.438	44.877	1.00	52.98	6
ATOM	6941	OE1	GLU	E	47	55.589	36.442	44.516	1.00	50.88	8
ATOM	6942	OE2	GLU	E	47	55.692	34.358	45.237	1.00	56.10	8
ATOM	6943	C	GLU	E	47	60.186	38.534	44.919	1.00	51.43	6

ATOM	6944	O	GLU	E	47	60.134	39.243	45.919	1.00	51.14	8
ATOM	6945	N	VAL	E	48	60.597	38.980	43.742	1.00	51.27	7
ATOM	6946	CA	VAL	E	48	61.037	40.352	43.574	1.00	51.20	6
ATOM	6947	CB	VAL	E	48	62.554	40.402	43.276	1.00	52.39	6
ATOM	6948	CG1	VAL	E	48	63.000	41.822	43.081	1.00	54.32	6
ATOM	6949	CG2	VAL	E	48	63.319	39.778	44.411	1.00	53.03	6
ATOM	6950	C	VAL	E	48	60.290	41.062	42.452	1.00	49.53	6
ATOM	6951	O	VAL	E	48	59.974	40.474	41.425	1.00	47.97	8
ATOM	6952	N	ASP	E	49	60.005	42.334	42.669	1.00	47.94	7
ATOM	6953	CA	ASP	E	49	59.335	43.146	41.680	1.00	48.29	6
ATOM	6954	CB	ASP	E	49	58.107	43.795	42.290	1.00	49.64	6
ATOM	6955	CG	ASP	E	49	57.146	44.300	41.249	1.00	50.04	6
ATOM	6956	OD1	ASP	E	49	57.596	44.853	40.228	1.00	47.78	8
ATOM	6957	OD2	ASP	E	49	55.931	44.151	41.459	1.00	53.33	8
ATOM	6958	C	ASP	E	49	60.373	44.200	41.330	1.00	48.39	6
ATOM	6959	O	ASP	E	49	60.644	45.101	42.118	1.00	48.55	8
ATOM	6960	N	VAL	E	50	60.950	44.085	40.140	1.00	48.88	7
ATOM	6961	CA	VAL	E	50	62.011	44.988	39.718	1.00	48.55	6
ATOM	6962	CB	VAL	E	50	63.353	44.220	39.707	1.00	50.40	6
ATOM	6963	CG1	VAL	E	50	63.428	43.303	38.492	1.00	49.66	6
ATOM	6964	CG2	VAL	E	50	64.511	45.188	39.721	1.00	55.70	6
ATOM	6965	C	VAL	E	50	61.801	45.642	38.354	1.00	47.28	6
ATOM	6966	O	VAL	E	50	61.057	45.134	37.523	1.00	48.34	8
ATOM	6967	N	VAL	E	51	62.467	46.777	38.144	1.00	45.37	7
ATOM	6968	CA	VAL	E	51	62.407	47.540	36.896	1.00	43.25	6
ATOM	6969	CB	VAL	E	51	61.930	48.993	37.131	1.00	41.43	6
ATOM	6970	CG1	VAL	E	51	62.118	49.820	35.865	1.00	39.28	6
ATOM	6971	CG2	VAL	E	51	60.478	49.000	37.546	1.00	39.33	6
ATOM	6972	C	VAL	E	51	63.821	47.597	36.333	1.00	44.33	6
ATOM	6973	O	VAL	E	51	64.764	47.841	37.078	1.00	46.78	8
ATOM	6974	N	PHE	E	52	63.978	47.383	35.029	1.00	43.60	7
ATOM	6975	CA	PHE	E	52	65.304	47.416	34.430	1.00	41.93	6
ATOM	6976	CB	PHE	E	52	65.997	46.085	34.678	1.00	41.48	6
ATOM	6977	CG	PHE	E	52	65.275	44.917	34.070	1.00	42.18	6
ATOM	6978	CD1	PHE	E	52	65.486	44.566	32.745	1.00	41.86	6
ATOM	6979	CD2	PHE	E	52	64.347	44.200	34.809	1.00	43.51	6
ATOM	6980	CE1	PHE	E	52	64.784	43.527	32.167	1.00	42.36	6
ATOM	6981	CE2	PHE	E	52	63.638	43.153	34.236	1.00	45.87	6
ATOM	6982	CZ	PHE	E	52	63.859	42.818	32.911	1.00	43.76	6
ATOM	6983	C	PHE	E	52	65.239	47.675	32.933	1.00	44.18	6
ATOM	6984	O	PHE	E	52	64.183	47.574	32.314	1.00	43.22	8
ATOM	6985	N	TRP	E	53	66.384	48.014	32.354	1.00	46.10	7
ATOM	6986	CA	TRP	E	53	66.466	48.252	30.927	1.00	47.08	6
ATOM	6987	CB	TRP	E	53	67.367	49.431	30.614	1.00	46.54	6
ATOM	6988	CG	TRP	E	53	66.822	50.726	31.015	1.00	49.25	6
ATOM	6989	CD2	TRP	E	53	67.510	51.972	30.991	1.00	51.55	6
ATOM	6990	CE2	TRP	E	53	66.616	52.951	31.471	1.00	52.89	6
ATOM	6991	CE3	TRP	E	53	68.804	52.358	30.614	1.00	53.33	6
ATOM	6992	CD1	TRP	E	53	65.577	50.980	31.486	1.00	50.42	6
ATOM	6993	NE1	TRP	E	53	65.440	52.318	31.765	1.00	52.93	7
ATOM	6994	CZ2	TRP	E	53	66.969	54.299	31.589	1.00	54.65	6
ATOM	6995	CZ3	TRP	E	53	69.162	53.706	30.730	1.00	55.02	6
ATOM	6996	CH2	TRP	E	53	68.245	54.658	31.215	1.00	56.13	6
ATOM	6997	C	TRP	E	53	67.070	47.018	30.316	1.00	48.44	6
ATOM	6998	O	TRP	E	53	68.201	46.680	30.616	1.00	50.00	8
ATOM	6999	N	GLN	E	54	66.313	46.342	29.465	1.00	49.02	7
ATOM	7000	CA	GLN	E	54	66.805	45.143	28.818	1.00	49.56	6
ATOM	7001	CB	GLN	E	54	65.648	44.193	28.517	1.00	50.24	6
ATOM	7002	CG	GLN	E	54	66.076	42.837	28.017	1.00	52.86	6
ATOM	7003	CD	GLN	E	54	65.043	41.768	28.313	1.00	57.64	6
ATOM	7004	OE1	GLN	E	54	64.668	41.564	29.465	1.00	59.29	8

ATOM	7005	NE2	GLN	E	54	64.576	41.078	27.275	1.00	58.15	7
ATOM	7006	C	GLN	E	54	67.500	45.583	27.547	1.00	50.68	6
ATOM	7007	O	GLN	E	54	66.972	45.458	26.446	1.00	50.31	8
ATOM	7008	N	GLN	E	55	68.692	46.132	27.735	1.00	53.08	7
ATOM	7009	CA	GLN	E	55	69.534	46.620	26.647	1.00	55.55	6
ATOM	7010	CB	GLN	E	55	70.723	47.342	27.257	1.00	57.75	6
ATOM	7011	CG	GLN	E	55	71.798	47.759	26.296	1.00	65.99	6
ATOM	7012	CD	GLN	E	55	72.759	48.745	26.952	1.00	70.80	6
ATOM	7013	OE1	GLN	E	55	73.057	48.637	28.158	1.00	74.02	8
ATOM	7014	NE2	GLN	E	55	73.245	49.710	26.175	1.00	70.33	7
ATOM	7015	C	GLN	E	55	69.978	45.446	25.768	1.00	54.06	6
ATOM	7016	O	GLN	E	55	70.834	44.648	26.147	1.00	55.16	8
ATOM	7017	N	THR	E	56	69.370	45.350	24.592	1.00	51.47	7
ATOM	7018	CA	THR	E	56	69.638	44.266	23.664	1.00	49.57	6
ATOM	7019	CB	THR	E	56	68.340	43.527	23.323	1.00	48.99	6
ATOM	7020	OG1	THR	E	56	67.621	43.259	24.530	1.00	51.03	8
ATOM	7021	CG2	THR	E	56	68.638	42.228	22.613	1.00	48.81	6
ATOM	7022	C	THR	E	56	70.245	44.780	22.374	1.00	48.56	6
ATOM	7023	O	THR	E	56	69.919	45.870	21.916	1.00	47.42	8
ATOM	7024	N	THR	E	57	71.131	43.984	21.789	1.00	48.33	7
ATOM	7025	CA	THR	E	57	71.778	44.370	20.545	1.00	48.63	6
ATOM	7026	CB	THR	E	57	73.079	45.153	20.803	1.00	48.38	6
ATOM	7027	OG1	THR	E	57	72.786	46.369	21.504	1.00	49.73	8
ATOM	7028	CG2	THR	E	57	73.737	45.498	19.488	1.00	53.54	6
ATOM	7029	C	THR	E	57	72.115	43.162	19.688	1.00	47.10	6
ATOM	7030	O	THR	E	57	72.462	42.094	20.196	1.00	47.16	8
ATOM	7031	N	TRP	E	58	71.996	43.337	18.382	1.00	44.64	7
ATOM	7032	CA	TRP	E	58	72.302	42.272	17.443	1.00	45.43	6
ATOM	7033	CB	TRP	E	58	71.217	41.185	17.463	1.00	44.32	6
ATOM	7034	CG	TRP	E	58	69.901	41.590	16.907	1.00	41.75	6
ATOM	7035	CD2	TRP	E	58	68.834	42.225	17.617	1.00	41.25	6
ATOM	7036	CE2	TRP	E	58	67.800	42.458	16.689	1.00	43.06	6
ATOM	7037	CE3	TRP	E	58	68.653	42.622	18.948	1.00	42.08	6
ATOM	7038	CD1	TRP	E	58	69.485	41.463	15.622	1.00	39.77	6
ATOM	7039	NE1	TRP	E	58	68.229	41.982	15.477	1.00	43.20	7
ATOM	7040	CZ2	TRP	E	58	66.598	43.072	17.043	1.00	42.98	6
ATOM	7041	CZ3	TRP	E	58	67.462	43.232	19.301	1.00	45.88	6
ATOM	7042	CH2	TRP	E	58	66.447	43.451	18.347	1.00	46.11	6
ATOM	7043	C	TRP	E	58	72.450	42.872	16.060	1.00	46.92	6
ATOM	7044	O	TRP	E	58	72.312	44.079	15.874	1.00	46.99	8
ATOM	7045	N	SER	E	59	72.737	42.039	15.076	1.00	49.39	7
ATOM	7046	CA	SER	E	59	72.933	42.571	13.738	1.00	52.86	6
ATOM	7047	CB	SER	E	59	74.423	42.477	13.382	1.00	55.16	6
ATOM	7048	OG	SER	E	59	74.777	43.368	12.335	1.00	59.85	8
ATOM	7049	C	SER	E	59	72.093	41.873	12.673	1.00	53.08	6
ATOM	7050	O	SER	E	59	72.023	40.640	12.621	1.00	50.22	8
ATOM	7051	N	ASP	E	60	71.461	42.685	11.833	1.00	55.39	7
ATOM	7052	CA	ASP	E	60	70.616	42.206	10.743	1.00	58.98	6
ATOM	7053	CB	ASP	E	60	69.144	42.502	11.027	1.00	59.87	6
ATOM	7054	CG	ASP	E	60	68.214	41.871	10.006	1.00	61.83	6
ATOM	7055	OD1	ASP	E	60	68.625	41.701	8.835	1.00	62.51	8
ATOM	7056	OD2	ASP	E	60	67.060	41.556	10.374	1.00	62.82	8
ATOM	7057	C	ASP	E	60	71.041	42.975	9.508	1.00	61.07	6
ATOM	7058	O	ASP	E	60	70.599	44.106	9.293	1.00	60.13	8
ATOM	7059	N	ARG	E	61	71.896	42.351	8.701	1.00	63.73	7
ATOM	7060	CA	ARG	E	61	72.428	42.989	7.501	1.00	66.18	6
ATOM	7061	CB	ARG	E	61	73.580	42.155	6.908	1.00	70.24	6
ATOM	7062	CG	ARG	E	61	74.957	42.308	7.596	1.00	74.18	6
ATOM	7063	CD	ARG	E	61	76.042	41.679	6.722	1.00	80.58	6
ATOM	7064	NE	ARG	E	61	77.411	41.855	7.223	1.00	86.19	7
ATOM	7065	CZ	ARG	E	61	78.505	41.397	6.598	1.00	88.23	6

ATOM	7066	NH1	ARG	E	61	78.383	40.734	5.447	1.00	88.94	7
ATOM	7067	NH2	ARG	E	61	79.724	41.603	7.111	1.00	88.58	7
ATOM	7068	C	ARG	E	61	71.404	43.289	6.414	1.00	65.48	6
ATOM	7069	O	ARG	E	61	71.655	44.145	5.561	1.00	65.84	8
ATOM	7070	N	THR	E	62	70.255	42.610	6.439	1.00	64.00	7
ATOM	7071	CA	THR	E	62	69.232	42.842	5.410	1.00	61.93	6
ATOM	7072	CB	THR	E	62	68.113	41.764	5.439	1.00	62.28	6
ATOM	7073	OG1	THR	E	62	67.367	41.879	6.652	1.00	65.24	8
ATOM	7074	CG2	THR	E	62	68.707	40.361	5.372	1.00	61.73	6
ATOM	7075	C	THR	E	62	68.602	44.218	5.595	1.00	59.03	6
ATOM	7076	O	THR	E	62	67.827	44.676	4.761	1.00	57.27	8
ATOM	7077	N	LEU	E	63	68.962	44.868	6.697	1.00	57.62	7
ATOM	7078	CA	LEU	E	63	68.461	46.200	7.029	1.00	57.37	6
ATOM	7079	CB	LEU	E	63	68.214	46.316	8.543	1.00	55.66	6
ATOM	7080	CG	LEU	E	63	67.253	45.322	9.196	1.00	55.07	6
ATOM	7081	CD1	LEU	E	63	67.231	45.508	10.692	1.00	52.03	6
ATOM	7082	CD2	LEU	E	63	65.875	45.519	8.612	1.00	55.09	6
ATOM	7083	C	LEU	E	63	69.471	47.277	6.625	1.00	57.97	6
ATOM	7084	O	LEU	E	63	69.135	48.460	6.549	1.00	56.59	8
ATOM	7085	N	ALA	E	64	70.715	46.862	6.389	1.00	58.86	7
ATOM	7086	CA	ALA	E	64	71.770	47.798	6.018	1.00	60.30	6
ATOM	7087	CB	ALA	E	64	73.077	47.055	5.844	1.00	58.52	6
ATOM	7088	C	ALA	E	64	71.440	48.571	4.745	1.00	61.25	6
ATOM	7089	O	ALA	E	64	70.814	48.041	3.830	1.00	59.01	8
ATOM	7090	N	TRP	E	65	71.845	49.832	4.702	1.00	63.42	7
ATOM	7091	CA	TRP	E	65	71.619	50.631	3.514	1.00	67.05	6
ATOM	7092	CB	TRP	E	65	70.406	51.537	3.704	1.00	66.45	6
ATOM	7093	CG	TRP	E	65	70.513	52.506	4.835	1.00	66.84	6
ATOM	7094	CD2	TRP	E	65	70.173	52.266	6.209	1.00	67.35	6
ATOM	7095	CE2	TRP	E	65	70.352	53.488	6.904	1.00	67.71	6
ATOM	7096	CE3	TRP	E	65	69.730	51.141	6.920	1.00	65.56	6
ATOM	7097	CD1	TRP	E	65	70.882	53.816	4.756	1.00	66.32	6
ATOM	7098	NE1	TRP	E	65	70.785	54.415	5.993	1.00	67.91	7
ATOM	7099	CZ2	TRP	E	65	70.101	53.615	8.270	1.00	65.59	6
ATOM	7100	CZ3	TRP	E	65	69.483	51.267	8.272	1.00	64.14	6
ATOM	7101	CH2	TRP	E	65	69.668	52.497	8.935	1.00	65.02	6
ATOM	7102	C	TRP	E	65	72.874	51.449	3.253	1.00	69.81	6
ATOM	7103	O	TRP	E	65	73.908	51.237	3.902	1.00	70.35	8
ATOM	7104	N	ASN	E	66	72.801	52.370	2.297	1.00	71.64	7
ATOM	7105	CA	ASN	E	66	73.956	53.203	1.999	1.00	72.49	6
ATOM	7106	CB	ASN	E	66	74.174	53.318	0.486	1.00	73.41	6
ATOM	7107	CG	ASN	E	66	75.497	53.990	0.131	1.00	75.13	6
ATOM	7108	OD1	ASN	E	66	75.513	55.081	-0.456	1.00	76.49	8
ATOM	7109	ND2	ASN	E	66	76.614	53.347	0.487	1.00	73.59	7
ATOM	7110	C	ASN	E	66	73.707	54.561	2.602	1.00	72.73	6
ATOM	7111	O	ASN	E	66	72.930	55.361	2.068	1.00	72.23	8
ATOM	7112	N	SER	E	67	74.367	54.810	3.726	1.00	74.00	7
ATOM	7113	CA	SER	E	67	74.231	56.076	4.441	1.00	76.61	6
ATOM	7114	CB	SER	E	67	74.159	55.805	5.942	1.00	76.40	6
ATOM	7115	OG	SER	E	67	75.161	54.878	6.307	1.00	75.84	8
ATOM	7116	C	SER	E	67	75.378	57.041	4.150	1.00	78.08	6
ATOM	7117	O	SER	E	67	75.512	58.093	4.807	1.00	77.79	8
ATOM	7118	N	SER	E	68	76.199	56.678	3.162	1.00	79.24	7
ATOM	7119	CA	SER	E	68	77.353	57.486	2.769	1.00	79.93	6
ATOM	7120	CB	SER	E	68	78.217	56.734	1.730	1.00	80.16	6
ATOM	7121	OG	SER	E	68	77.535	56.523	0.495	1.00	81.02	8
ATOM	7122	C	SER	E	68	76.896	58.835	2.219	1.00	79.10	6
ATOM	7123	O	SER	E	68	77.586	59.471	1.411	1.00	79.89	8
ATOM	7124	N	HIS	E	69	75.722	59.261	2.664	1.00	77.21	7
ATOM	7125	CA	HIS	E	69	75.176	60.529	2.247	1.00	76.33	6
ATOM	7126	CB	HIS	E	69	75.229	60.665	0.732	1.00	76.74	6

ATOM	7127	CG	HIS	E	69	75.366	62.083	0.283	1.00	77.46	6
ATOM	7128	CD2	HIS	E	69	74.568	62.857	-0.491	1.00	76.01	6
ATOM	7129	ND1	HIS	E	69	76.390	62.898	0.720	1.00	75.50	7
ATOM	7130	CE1	HIS	E	69	76.212	64.114	0.239	1.00	74.91	6
ATOM	7131	NE2	HIS	E	69	75.115	64.117	-0.497	1.00	77.04	7
ATOM	7132	C	HIS	E	69	73.748	60.641	2.716	1.00	75.96	6
ATOM	7133	O	HIS	E	69	72.954	61.408	2.170	1.00	75.96	8
ATOM	7134	N	SER	E	70	73.431	59.880	3.754	1.00	75.27	7
ATOM	7135	CA	SER	E	70	72.086	59.867	4.308	1.00	72.77	6
ATOM	7136	CB	SER	E	70	71.307	58.758	3.639	1.00	71.14	6
ATOM	7137	OG	SER	E	70	72.085	57.578	3.703	1.00	68.45	8
ATOM	7138	C	SER	E	70	72.177	59.585	5.806	1.00	72.84	6
ATOM	7139	O	SER	E	70	73.254	59.212	6.304	1.00	73.59	8
ATOM	7140	N	PRO	E	71	71.065	59.789	6.550	1.00	71.65	7
ATOM	7141	CD	PRO	E	71	69.793	60.434	6.160	1.00	70.63	6
ATOM	7142	CA	PRO	E	71	71.091	59.521	7.989	1.00	69.54	6
ATOM	7143	CB	PRO	E	71	69.627	59.649	8.376	1.00	69.50	6
ATOM	7144	CG	PRO	E	71	69.172	60.783	7.505	1.00	69.75	6
ATOM	7145	C	PRO	E	71	71.611	58.104	8.128	1.00	67.45	6
ATOM	7146	O	PRO	E	71	71.371	57.288	7.249	1.00	67.47	8
ATOM	7147	N	ASP	E	72	72.332	57.813	9.202	1.00	65.90	7
ATOM	7148	CA	ASP	E	72	72.888	56.480	9.401	1.00	65.38	6
ATOM	7149	CB	ASP	E	72	74.336	56.595	9.864	1.00	66.99	6
ATOM	7150	CG	ASP	E	72	74.623	57.933	10.513	1.00	69.68	6
ATOM	7151	OD1	ASP	E	72	75.809	58.349	10.511	1.00	72.85	8
ATOM	7152	OD2	ASP	E	72	73.659	58.564	11.022	1.00	69.14	8
ATOM	7153	C	ASP	E	72	72.078	55.656	10.387	1.00	64.69	6
ATOM	7154	O	ASP	E	72	72.273	54.438	10.492	1.00	62.72	8
ATOM	7155	N	GLN	E	73	71.194	56.334	11.122	1.00	63.38	7
ATOM	7156	CA	GLN	E	73	70.291	55.692	12.073	1.00	62.59	6
ATOM	7157	CB	GLN	E	73	70.703	55.968	13.502	1.00	63.56	6
ATOM	7158	CG	GLN	E	73	71.812	55.147	14.064	1.00	66.36	6
ATOM	7159	CD	GLN	E	73	72.073	55.601	15.478	1.00	69.74	6
ATOM	7160	OE1	GLN	E	73	72.311	56.794	15.711	1.00	71.52	8
ATOM	7161	NE2	GLN	E	73	72.005	54.676	16.437	1.00	70.16	7
ATOM	7162	C	GLN	E	73	68.850	56.189	11.932	1.00	60.94	6
ATOM	7163	O	GLN	E	73	68.599	57.336	11.548	1.00	60.74	8
ATOM	7164	N	VAL	E	74	67.910	55.318	12.281	1.00	57.54	7
ATOM	7165	CA	VAL	E	74	66.495	55.652	12.254	1.00	54.00	6
ATOM	7166	CB	VAL	E	74	65.857	55.296	10.901	1.00	52.88	6
ATOM	7167	CG1	VAL	E	74	66.391	56.201	9.814	1.00	52.07	6
ATOM	7168	CG2	VAL	E	74	66.151	53.846	10.564	1.00	53.11	6
ATOM	7169	C	VAL	E	74	65.816	54.844	13.349	1.00	51.46	6
ATOM	7170	O	VAL	E	74	66.355	53.838	13.804	1.00	51.44	8
ATOM	7171	N	SER	E	75	64.649	55.299	13.789	1.00	48.05	7
ATOM	7172	CA	SER	E	75	63.893	54.592	14.812	1.00	45.32	6
ATOM	7173	CB	SER	E	75	63.222	55.583	15.761	1.00	44.86	6
ATOM	7174	OG	SER	E	75	64.122	56.022	16.763	1.00	42.99	8
ATOM	7175	C	SER	E	75	62.846	53.727	14.123	1.00	45.51	6
ATOM	7176	O	SER	E	75	61.959	54.228	13.431	1.00	45.94	8
ATOM	7177	N	VAL	E	76	62.953	52.420	14.325	1.00	44.89	7
ATOM	7178	CA	VAL	E	76	62.052	51.463	13.706	1.00	43.76	6
ATOM	7179	CB	VAL	E	76	62.857	50.400	12.943	1.00	44.31	6
ATOM	7180	CG1	VAL	E	76	61.930	49.411	12.296	1.00	45.29	6
ATOM	7181	CG2	VAL	E	76	63.734	51.060	11.907	1.00	45.23	6
ATOM	7182	C	VAL	E	76	61.169	50.751	14.718	1.00	43.81	6
ATOM	7183	O	VAL	E	76	61.641	50.331	15.772	1.00	46.08	8
ATOM	7184	N	PRO	E	77	59.868	50.612	14.418	1.00	41.91	7
ATOM	7185	CD	PRO	E	77	59.085	51.238	13.344	1.00	41.05	6
ATOM	7186	CA	PRO	E	77	58.987	49.923	15.360	1.00	39.46	6
ATOM	7187	CB	PRO	E	77	57.619	50.076	14.719	1.00	39.68	6

ATOM	7188	CG	PRO	E	77	57.736	51.362	13.981	1.00	41.25	6
ATOM	7189	C	PRO	E	77	59.407	48.464	15.456	1.00	39.33	6
ATOM	7190	O	PRO	E	77	59.766	47.848	14.457	1.00	39.91	8
ATOM	7191	N	ILE	E	78	59.368	47.929	16.665	1.00	39.53	7
ATOM	7192	CA	ILE	E	78	59.729	46.550	16.938	1.00	39.36	6
ATOM	7193	CB	ILE	E	78	59.440	46.235	18.408	1.00	41.90	6
ATOM	7194	CG2	ILE	E	78	59.421	44.753	18.667	1.00	44.69	6
ATOM	7195	CG1	ILE	E	78	60.512	46.887	19.259	1.00	45.61	6
ATOM	7196	CD1	ILE	E	78	61.904	46.569	18.783	1.00	45.82	6
ATOM	7197	C	ILE	E	78	59.002	45.562	16.048	1.00	39.58	6
ATOM	7198	O	ILE	E	78	59.556	44.550	15.645	1.00	39.79	8
ATOM	7199	N	SER	E	79	57.755	45.870	15.729	1.00	41.50	7
ATOM	7200	CA	SER	E	79	56.932	45.011	14.891	1.00	41.99	6
ATOM	7201	CB	SER	E	79	55.497	45.502	14.931	1.00	40.86	6
ATOM	7202	OG	SER	E	79	55.441	46.876	14.633	1.00	44.60	8
ATOM	7203	C	SER	E	79	57.370	44.887	13.441	1.00	43.24	6
ATOM	7204	O	SER	E	79	56.883	44.020	12.730	1.00	43.62	8
ATOM	7205	N	SER	E	80	58.278	45.750	12.996	1.00	44.61	7
ATOM	7206	CA	SER	E	80	58.751	45.713	11.619	1.00	44.15	6
ATOM	7207	CB	SER	E	80	58.841	47.133	11.062	1.00	43.26	6
ATOM	7208	OG	SER	E	80	57.568	47.744	11.017	1.00	47.92	8
ATOM	7209	C	SER	E	80	60.110	45.033	11.482	1.00	45.19	6
ATOM	7210	O	SER	E	80	60.661	44.963	10.387	1.00	46.20	8
ATOM	7211	N	LEU	E	81	60.645	44.533	12.589	1.00	42.25	7
ATOM	7212	CA	LEU	E	81	61.949	43.891	12.577	1.00	42.76	6
ATOM	7213	CB	LEU	E	81	62.950	44.702	13.400	1.00	41.44	6
ATOM	7214	CG	LEU	E	81	63.144	46.190	13.150	1.00	39.51	6
ATOM	7215	CD1	LEU	E	81	63.861	46.826	14.314	1.00	38.48	6
ATOM	7216	CD2	LEU	E	81	63.908	46.367	11.891	1.00	43.00	6
ATOM	7217	C	LEU	E	81	61.846	42.530	13.216	1.00	42.93	6
ATOM	7218	O	LEU	E	81	60.845	42.221	13.865	1.00	47.16	8
ATOM	7219	N	TRP	E	82	62.880	41.715	13.028	1.00	39.63	7
ATOM	7220	CA	TRP	E	82	62.925	40.412	13.657	1.00	38.60	6
ATOM	7221	CB	TRP	E	82	63.872	39.465	12.941	1.00	37.23	6
ATOM	7222	CG	TRP	E	82	64.186	38.241	13.753	1.00	39.34	6
ATOM	7223	CD2	TRP	E	82	65.272	38.087	14.678	1.00	41.49	6
ATOM	7224	CE2	TRP	E	82	65.142	36.811	15.266	1.00	40.40	6
ATOM	7225	CE3	TRP	E	82	66.344	38.909	15.071	1.00	41.39	6
ATOM	7226	CD1	TRP	E	82	63.469	37.086	13.814	1.00	37.83	6
ATOM	7227	NE1	TRP	E	82	64.032	36.222	14.719	1.00	40.75	7
ATOM	7228	CZ2	TRP	E	82	66.044	36.335	16.228	1.00	39.91	6
ATOM	7229	CZ3	TRP	E	82	67.237	38.436	16.025	1.00	38.98	6
ATOM	7230	CH2	TRP	E	82	67.080	37.161	16.591	1.00	40.84	6
ATOM	7231	C	TRP	E	82	63.513	40.766	14.999	1.00	38.10	6
ATOM	7232	O	TRP	E	82	64.356	41.636	15.086	1.00	39.18	8
ATOM	7233	N	VAL	E	83	63.068	40.104	16.049	1.00	39.36	7
ATOM	7234	CA	VAL	E	83	63.578	40.395	17.367	1.00	38.27	6
ATOM	7235	CB	VAL	E	83	62.562	41.277	18.141	1.00	39.12	6
ATOM	7236	CG1	VAL	E	83	62.919	41.352	19.596	1.00	43.60	6
ATOM	7237	CG2	VAL	E	83	62.557	42.678	17.565	1.00	38.09	6
ATOM	7238	C	VAL	E	83	63.853	39.081	18.089	1.00	37.11	6
ATOM	7239	O	VAL	E	83	63.154	38.098	17.896	1.00	39.80	8
ATOM	7240	N	PRO	E	84	64.909	39.039	18.899	1.00	35.89	7
ATOM	7241	CD	PRO	E	84	65.921	40.088	19.075	1.00	38.94	6
ATOM	7242	CA	PRO	E	84	65.276	37.842	19.651	1.00	35.46	6
ATOM	7243	CB	PRO	E	84	66.485	38.306	20.456	1.00	36.52	6
ATOM	7244	CG	PRO	E	84	67.087	39.306	19.600	1.00	37.91	6
ATOM	7245	C	PRO	E	84	64.134	37.398	20.555	1.00	36.04	6
ATOM	7246	O	PRO	E	84	63.541	38.220	21.246	1.00	34.75	8
ATOM	7247	N	ASP	E	85	63.839	36.103	20.565	1.00	33.87	7
ATOM	7248	CA	ASP	E	85	62.771	35.595	21.400	1.00	35.26	6

ATOM	7249	CB	ASP	E	85	62.150	34.350	20.779	1.00	37.18	6
ATOM	7250	CG	ASP	E	85	63.150	33.259	20.556	1.00	40.21	6
ATOM	7251	OD1	ASP	E	85	64.268	33.583	20.129	1.00	41.52	8
ATOM	7252	OD2	ASP	E	85	62.828	32.079	20.789	1.00	38.39	8
ATOM	7253	C	ASP	E	85	63.277	35.290	22.794	1.00	36.88	6
ATOM	7254	O	ASP	E	85	63.139	34.174	23.287	1.00	37.96	8
ATOM	7255	N	LEU	E	86	63.848	36.307	23.427	1.00	34.95	7
ATOM	7256	CA	LEU	E	86	64.387	36.185	24.769	1.00	36.75	6
ATOM	7257	CB	LEU	E	86	65.211	37.414	25.116	1.00	36.06	6
ATOM	7258	CG	LEU	E	86	66.410	37.646	24.221	1.00	34.31	6
ATOM	7259	CD1	LEU	E	86	67.131	38.893	24.653	1.00	32.72	6
ATOM	7260	CD2	LEU	E	86	67.300	36.446	24.287	1.00	35.49	6
ATOM	7261	C	LEU	E	86	63.317	36.021	25.816	1.00	37.61	6
ATOM	7262	O	LEU	E	86	62.226	36.557	25.694	1.00	41.91	8
ATOM	7263	N	ALA	E	87	63.652	35.293	26.865	1.00	38.39	7
ATOM	7264	CA	ALA	E	87	62.727	35.060	27.949	1.00	39.76	6
ATOM	7265	CB	ALA	E	87	61.950	33.766	27.692	1.00	37.37	6
ATOM	7266	C	ALA	E	87	63.510	34.959	29.255	1.00	41.61	6
ATOM	7267	O	ALA	E	87	64.583	34.372	29.288	1.00	42.91	8
ATOM	7268	N	ALA	E	88	62.989	35.550	30.323	1.00	41.72	7
ATOM	7269	CA	ALA	E	88	63.639	35.460	31.624	1.00	40.16	6
ATOM	7270	CB	ALA	E	88	63.259	36.638	32.480	1.00	38.02	6
ATOM	7271	C	ALA	E	88	63.154	34.168	32.261	1.00	41.60	6
ATOM	7272	O	ALA	E	88	62.028	34.089	32.740	1.00	43.75	8
ATOM	7273	N	TYR	E	89	64.008	33.152	32.245	1.00	43.12	7
ATOM	7274	CA	TYR	E	89	63.691	31.832	32.793	1.00	44.73	6
ATOM	7275	CB	TYR	E	89	64.970	31.010	32.900	1.00	47.55	6
ATOM	7276	CG	TYR	E	89	65.633	30.711	31.573	1.00	53.63	6
ATOM	7277	CD1	TYR	E	89	66.903	30.120	31.521	1.00	54.69	6
ATOM	7278	CE1	TYR	E	89	67.519	29.831	30.311	1.00	56.44	6
ATOM	7279	CD2	TYR	E	89	64.995	31.006	30.368	1.00	56.01	6
ATOM	7280	CE2	TYR	E	89	65.599	30.720	29.147	1.00	58.87	6
ATOM	7281	CZ	TYR	E	89	66.860	30.131	29.125	1.00	58.82	6
ATOM	7282	OH	TYR	E	89	67.437	29.821	27.908	1.00	64.15	8
ATOM	7283	C	TYR	E	89	62.959	31.792	34.138	1.00	44.61	6
ATOM	7284	O	TYR	E	89	62.113	30.920	34.362	1.00	43.17	8
ATOM	7285	N	ASN	E	90	63.275	32.723	35.036	1.00	43.58	7
ATOM	7286	CA	ASN	E	90	62.621	32.729	36.338	1.00	43.92	6
ATOM	7287	CB	ASN	E	90	63.658	32.682	37.469	1.00	41.30	6
ATOM	7288	CG	ASN	E	90	64.654	33.809	37.401	1.00	40.93	6
ATOM	7289	OD1	ASN	E	90	65.197	34.116	36.341	1.00	40.18	8
ATOM	7290	ND2	ASN	E	90	64.914	34.425	38.542	1.00	42.13	7
ATOM	7291	C	ASN	E	90	61.668	33.894	36.538	1.00	45.22	6
ATOM	7292	O	ASN	E	90	61.397	34.296	37.668	1.00	45.17	8
ATOM	7293	N	ALA	E	91	61.170	34.437	35.432	1.00	46.14	7
ATOM	7294	CA	ALA	E	91	60.207	35.526	35.482	1.00	44.27	6
ATOM	7295	CB	ALA	E	91	59.974	36.095	34.110	1.00	43.16	6
ATOM	7296	C	ALA	E	91	58.937	34.881	36.006	1.00	45.11	6
ATOM	7297	O	ALA	E	91	58.543	33.800	35.577	1.00	43.27	8
ATOM	7298	N	ILE	E	92	58.306	35.569	36.940	1.00	46.13	7
ATOM	7299	CA	ILE	E	92	57.111	35.100	37.611	1.00	45.40	6
ATOM	7300	CB	ILE	E	92	57.301	35.365	39.123	1.00	49.00	6
ATOM	7301	CG2	ILE	E	92	56.517	36.598	39.568	1.00	53.30	6
ATOM	7302	CG1	ILE	E	92	56.883	34.165	39.929	1.00	50.53	6
ATOM	7303	CD1	ILE	E	92	56.902	34.482	41.419	1.00	57.12	6
ATOM	7304	C	ILE	E	92	55.863	35.805	37.060	1.00	43.27	6
ATOM	7305	O	ILE	E	92	54.745	35.458	37.395	1.00	40.97	8
ATOM	7306	N	SER	E	93	56.078	36.806	36.216	1.00	42.51	7
ATOM	7307	CA	SER	E	93	55.001	37.573	35.599	1.00	41.03	6
ATOM	7308	CB	SER	E	93	54.765	38.864	36.362	1.00	40.45	6
ATOM	7309	OG	SER	E	93	55.849	39.756	36.170	1.00	40.42	8

ATOM	7310	C	SER	E	93	55.497	37.925	34.214	1.00	41.98	6
ATOM	7311	O	SER	E	93	56.686	37.781	33.932	1.00	43.61	8
ATOM	7312	N	LYS	E	94	54.617	38.380	33.333	1.00	41.47	7
ATOM	7313	CA	LYS	E	94	55.109	38.738	32.018	1.00	44.98	6
ATOM	7314	CB	LYS	E	94	54.037	38.561	30.942	1.00	44.95	6
ATOM	7315	CG	LYS	E	94	52.663	39.071	31.264	1.00	48.24	6
ATOM	7316	CD	LYS	E	94	51.659	38.499	30.255	1.00	50.47	6
ATOM	7317	CE	LYS	E	94	52.173	38.628	28.822	1.00	53.56	6
ATOM	7318	NZ	LYS	E	94	51.218	38.125	27.795	1.00	54.79	7
ATOM	7319	C	LYS	E	94	55.675	40.151	32.031	1.00	45.16	6
ATOM	7320	O	LYS	E	94	55.386	40.939	32.933	1.00	46.22	8
ATOM	7321	N	PRO	E	95	56.514	40.481	31.038	1.00	43.95	7
ATOM	7322	CD	PRO	E	95	56.973	39.633	29.926	1.00	42.19	6
ATOM	7323	CA	PRO	E	95	57.131	41.802	30.957	1.00	43.02	6
ATOM	7324	CB	PRO	E	95	58.076	41.671	29.768	1.00	42.81	6
ATOM	7325	CG	PRO	E	95	58.306	40.216	29.636	1.00	42.27	6
ATOM	7326	C	PRO	E	95	56.162	42.939	30.761	1.00	42.70	6
ATOM	7327	O	PRO	E	95	55.320	42.899	29.870	1.00	46.65	8
ATOM	7328	N	GLU	E	96	56.269	43.952	31.601	1.00	40.32	7
ATOM	7329	CA	GLU	E	96	55.424	45.115	31.446	1.00	41.45	6
ATOM	7330	CB	GLU	E	96	54.910	45.635	32.797	1.00	42.90	6
ATOM	7331	CG	GLU	E	96	53.911	46.797	32.674	1.00	47.98	6
ATOM	7332	CD	GLU	E	96	53.396	47.308	34.024	1.00	50.94	6
ATOM	7333	OE1	GLU	E	96	53.482	46.539	35.005	1.00	53.57	8
ATOM	7334	OE2	GLU	E	96	52.894	48.462	34.102	1.00	47.79	8
ATOM	7335	C	GLU	E	96	56.372	46.123	30.830	1.00	40.44	6
ATOM	7336	O	GLU	E	96	57.143	46.762	31.538	1.00	42.91	8
ATOM	7337	N	VAL	E	97	56.348	46.227	29.506	1.00	36.63	7
ATOM	7338	CA	VAL	E	97	57.200	47.165	28.800	1.00	34.15	6
ATOM	7339	CB	VAL	E	97	57.230	46.850	27.311	1.00	31.33	6
ATOM	7340	CG1	VAL	E	97	58.136	47.814	26.596	1.00	31.45	6
ATOM	7341	CG2	VAL	E	97	57.708	45.444	27.113	1.00	28.98	6
ATOM	7342	C	VAL	E	97	56.665	48.576	29.041	1.00	35.79	6
ATOM	7343	O	VAL	E	97	55.558	48.932	28.636	1.00	35.88	8
ATOM	7344	N	LEU	E	98	57.474	49.378	29.714	1.00	35.63	7
ATOM	7345	CA	LEU	E	98	57.091	50.725	30.086	1.00	36.41	6
ATOM	7346	CB	LEU	E	98	57.787	51.098	31.395	1.00	34.14	6
ATOM	7347	CG	LEU	E	98	57.676	50.176	32.598	1.00	33.56	6
ATOM	7348	CD1	LEU	E	98	58.694	50.570	33.602	1.00	31.56	6
ATOM	7349	CD2	LEU	E	98	56.306	50.248	33.190	1.00	33.37	6
ATOM	7350	C	LEU	E	98	57.400	51.793	29.058	1.00	36.97	6
ATOM	7351	O	LEU	E	98	56.969	52.936	29.203	1.00	38.13	8
ATOM	7352	N	THR	E	99	58.133	51.426	28.018	1.00	35.68	7
ATOM	7353	CA	THR	E	99	58.533	52.391	27.011	1.00	34.41	6
ATOM	7354	CB	THR	E	99	60.067	52.547	27.032	1.00	35.73	6
ATOM	7355	OG1	THR	E	99	60.683	51.265	26.850	1.00	39.59	8
ATOM	7356	CG2	THR	E	99	60.517	53.122	28.355	1.00	34.05	6
ATOM	7357	C	THR	E	99	58.098	52.084	25.589	1.00	33.50	6
ATOM	7358	O	THR	E	99	57.696	50.969	25.283	1.00	33.37	8
ATOM	7359	N	PRO	E	100	58.155	53.093	24.701	1.00	34.01	7
ATOM	7360	CD	PRO	E	100	58.424	54.514	24.975	1.00	36.06	6
ATOM	7361	CA	PRO	E	100	57.777	52.919	23.302	1.00	33.45	6
ATOM	7362	CB	PRO	E	100	58.227	54.223	22.669	1.00	31.60	6
ATOM	7363	CG	PRO	E	100	57.906	55.190	23.725	1.00	32.57	6
ATOM	7364	C	PRO	E	100	58.529	51.719	22.769	1.00	35.44	6
ATOM	7365	O	PRO	E	100	59.713	51.546	23.041	1.00	35.44	8
ATOM	7366	N	GLN	E	101	57.844	50.868	22.029	1.00	37.12	7
ATOM	7367	CA	GLN	E	101	58.514	49.701	21.516	1.00	38.35	6
ATOM	7368	CB	GLN	E	101	57.551	48.532	21.476	1.00	39.07	6
ATOM	7369	CG	GLN	E	101	57.398	47.921	22.845	1.00	43.00	6
ATOM	7370	CD	GLN	E	101	56.194	47.037	22.948	1.00	48.55	6

ATOM	7371	OE1	GLN	E	101	56.055	46.068	22.194	1.00	50.74	8
ATOM	7372	NE2	GLN	E	101	55.298	47.359	23.885	1.00	48.45	7
ATOM	7373	C	GLN	E	101	59.146	49.950	20.181	1.00	37.98	6
ATOM	7374	O	GLN	E	101	58.749	49.374	19.177	1.00	36.86	8
ATOM	7375	N	LEU	E	102	60.153	50.825	20.213	1.00	39.66	7
ATOM	7376	CA	LEU	E	102	60.936	51.230	19.046	1.00	38.89	6
ATOM	7377	CB	LEU	E	102	60.911	52.749	18.880	1.00	36.07	6
ATOM	7378	CG	LEU	E	102	59.545	53.416	18.766	1.00	36.30	6
ATOM	7379	CD1	LEU	E	102	59.712	54.906	18.615	1.00	37.57	6
ATOM	7380	CD2	LEU	E	102	58.809	52.853	17.571	1.00	37.42	6
ATOM	7381	C	LEU	E	102	62.374	50.791	19.207	1.00	37.90	6
ATOM	7382	O	LEU	E	102	62.909	50.784	20.312	1.00	40.06	8
ATOM	7383	N	ALA	E	103	62.995	50.408	18.102	1.00	37.36	7
ATOM	7384	CA	ALA	E	103	64.395	50.007	18.127	1.00	38.78	6
ATOM	7385	CB	ALA	E	103	64.577	48.634	17.504	1.00	37.72	6
ATOM	7386	C	ALA	E	103	65.193	51.039	17.351	1.00	38.02	6
ATOM	7387	O	ALA	E	103	64.645	51.890	16.666	1.00	38.29	8
ATOM	7388	N	ARG	E	104	66.500	50.969	17.469	1.00	40.78	7
ATOM	7389	CA	ARG	E	104	67.344	51.911	16.770	1.00	44.75	6
ATOM	7390	CB	ARG	E	104	68.258	52.612	17.771	1.00	44.40	6
ATOM	7391	CG	ARG	E	104	68.873	53.873	17.251	1.00	45.66	6
ATOM	7392	CD	ARG	E	104	67.868	54.956	16.983	1.00	43.79	6
ATOM	7393	NE	ARG	E	104	68.570	56.118	16.456	1.00	46.54	7
ATOM	7394	CZ	ARG	E	104	68.008	57.289	16.175	1.00	46.54	6
ATOM	7395	NH1	ARG	E	104	66.711	57.493	16.365	1.00	47.66	7
ATOM	7396	NH2	ARG	E	104	68.760	58.266	15.698	1.00	49.69	7
ATOM	7397	C	ARG	E	104	68.142	51.099	15.763	1.00	46.58	6
ATOM	7398	O	ARG	E	104	68.775	50.105	16.119	1.00	47.46	8
ATOM	7399	N	VAL	E	105	68.081	51.492	14.497	1.00	48.34	7
ATOM	7400	CA	VAL	E	105	68.808	50.761	13.475	1.00	49.67	6
ATOM	7401	CB	VAL	E	105	67.869	50.244	12.388	1.00	49.06	6
ATOM	7402	CG1	VAL	E	105	68.643	49.361	11.431	1.00	49.26	6
ATOM	7403	CG2	VAL	E	105	66.731	49.478	13.010	1.00	49.99	6
ATOM	7404	C	VAL	E	105	69.883	51.601	12.805	1.00	51.57	6
ATOM	7405	O	VAL	E	105	69.606	52.684	12.272	1.00	49.78	8
ATOM	7406	N	VAL	E	106	71.109	51.077	12.834	1.00	53.67	7
ATOM	7407	CA	VAL	E	106	72.265	51.738	12.232	1.00	55.11	6
ATOM	7408	CB	VAL	E	106	73.537	51.409	13.009	1.00	54.77	6
ATOM	7409	CG1	VAL	E	106	74.666	52.300	12.539	1.00	55.46	6
ATOM	7410	CG2	VAL	E	106	73.283	51.577	14.507	1.00	57.64	6
ATOM	7411	C	VAL	E	106	72.428	51.253	10.795	1.00	55.88	6
ATOM	7412	O	VAL	E	106	72.213	50.075	10.508	1.00	57.82	8
ATOM	7413	N	SER	E	107	72.812	52.153	9.897	1.00	55.80	7
ATOM	7414	CA	SER	E	107	72.972	51.812	8.486	1.00	55.14	6
ATOM	7415	CB	SER	E	107	73.610	52.984	7.740	1.00	55.20	6
ATOM	7416	OG	SER	E	107	74.708	53.503	8.470	1.00	58.75	8
ATOM	7417	C	SER	E	107	73.738	50.530	8.175	1.00	54.04	6
ATOM	7418	O	SER	E	107	73.578	49.966	7.096	1.00	52.93	8
ATOM	7419	N	ASP	E	108	74.558	50.062	9.105	1.00	53.77	7
ATOM	7420	CA	ASP	E	108	75.324	48.847	8.862	1.00	56.74	6
ATOM	7421	CB	ASP	E	108	76.691	48.938	9.548	1.00	58.54	6
ATOM	7422	CG	ASP	E	108	76.597	48.911	11.055	1.00	61.09	6
ATOM	7423	OD1	ASP	E	108	75.653	49.522	11.599	1.00	63.34	8
ATOM	7424	OD2	ASP	E	108	77.479	48.296	11.694	1.00	61.64	8
ATOM	7425	C	ASP	E	108	74.612	47.563	9.288	1.00	58.86	6
ATOM	7426	O	ASP	E	108	75.213	46.484	9.278	1.00	58.05	8
ATOM	7427	N	GLY	E	109	73.337	47.686	9.662	1.00	60.25	7
ATOM	7428	CA	GLY	E	109	72.559	46.528	10.072	1.00	60.49	6
ATOM	7429	C	GLY	E	109	72.581	46.229	11.563	1.00	61.38	6
ATOM	7430	O	GLY	E	109	72.031	45.211	12.011	1.00	60.99	8
ATOM	7431	N	GLU	E	110	73.215	47.100	12.342	1.00	61.69	7

ATOM	7432	CA	GLU	E	110	73.283	46.899	13.787	1.00 61.54	6
ATOM	7433	CB	GLU	E	110	74.432	47.720	14.391	1.00 64.16	6
ATOM	7434	CG	GLU	E	110	74.946	47.231	15.755	1.00 67.88	6
ATOM	7435	CD	GLU	E	110	75.559	45.828	15.684	1.00 72.22	6
ATOM	7436	OE1	GLU	E	110	75.936	45.401	14.554	1.00 72.61	8
ATOM	7437	OE2	GLU	E	110	75.676	45.165	16.758	1.00 70.57	8
ATOM	7438	C	GLU	E	110	71.948	47.368	14.347	1.00 60.20	6
ATOM	7439	O	GLU	E	110	71.421	48.418	13.949	1.00 59.08	8
ATOM	7440	N	VAL	E	111	71.403	46.581	15.266	1.00 57.63	7
ATOM	7441	CA	VAL	E	111	70.116	46.893	15.885	1.00 54.53	6
ATOM	7442	CB	VAL	E	111	69.065	45.797	15.557	1.00 53.43	6
ATOM	7443	CG1	VAL	E	111	67.728	46.159	16.178	1.00 53.30	6
ATOM	7444	CG2	VAL	E	111	68.932	45.631	14.053	1.00 52.07	6
ATOM	7445	C	VAL	E	111	70.231	47.017	17.406	1.00 52.96	6
ATOM	7446	O	VAL	E	111	70.846	46.170	18.066	1.00 52.11	8
ATOM	7447	N	LEU	E	112	69.641	48.070	17.961	1.00 50.09	7
ATOM	7448	CA	LEU	E	112	69.687	48.261	19.399	1.00 50.92	6
ATOM	7449	CB	LEU	E	112	70.546	49.468	19.770	1.00 55.28	6
ATOM	7450	CG	LEU	E	112	71.820	49.846	18.992	1.00 58.58	6
ATOM	7451	CD1	LEU	E	112	72.649	48.603	18.629	1.00 59.41	6
ATOM	7452	CD2	LEU	E	112	71.428	50.603	17.742	1.00 58.46	6
ATOM	7453	C	LEU	E	112	68.286	48.485	19.930	1.00 50.61	6
ATOM	7454	O	LEU	E	112	67.628	49.437	19.535	1.00 50.59	8
ATOM	7455	N	TYR	E	113	67.835	47.597	20.816	1.00 49.12	7
ATOM	7456	CA	TYR	E	113	66.514	47.690	21.420	1.00 46.39	6
ATOM	7457	CB	TYR	E	113	65.635	46.500	21.003	1.00 45.58	6
ATOM	7458	CG	TYR	E	113	64.235	46.491	21.610	1.00 44.58	6
ATOM	7459	CD1	TYR	E	113	63.453	47.650	21.655	1.00 45.06	6
ATOM	7460	CE1	TYR	E	113	62.162	47.632	22.177	1.00 44.35	6
ATOM	7461	CD2	TYR	E	113	63.684	45.318	22.105	1.00 43.68	6
ATOM	7462	CE2	TYR	E	113	62.395	45.287	22.629	1.00 45.23	6
ATOM	7463	CZ	TYR	E	113	61.633	46.444	22.663	1.00 46.53	6
ATOM	7464	OH	TYR	E	113	60.346	46.399	23.183	1.00 46.01	8
ATOM	7465	C	TYR	E	113	66.721	47.679	22.915	1.00 46.41	6
ATOM	7466	O	TYR	E	113	67.194	46.697	23.463	1.00 46.43	8
ATOM	7467	N	MET	E	114	66.363	48.774	23.572	1.00 46.91	7
ATOM	7468	CA	MET	E	114	66.539	48.880	25.011	1.00 48.35	6
ATOM	7469	CB	MET	E	114	67.635	49.889	25.315	1.00 51.44	6
ATOM	7470	CG	MET	E	114	68.053	49.906	26.737	1.00 56.27	6
ATOM	7471	SD	MET	E	114	68.981	51.368	27.017	1.00 65.32	16
ATOM	7472	CE	MET	E	114	70.586	50.862	26.425	1.00 63.97	6
ATOM	7473	C	MET	E	114	65.255	49.320	25.697	1.00 48.66	6
ATOM	7474	O	MET	E	114	65.095	50.494	26.036	1.00 50.19	8
ATOM	7475	N	PRO	E	115	64.325	48.383	25.920	1.00 48.19	7
ATOM	7476	CD	PRO	E	115	64.341	46.978	25.467	1.00 47.93	6
ATOM	7477	CA	PRO	E	115	63.056	48.702	26.572	1.00 46.04	6
ATOM	7478	CB	PRO	E	115	62.150	47.590	26.077	1.00 46.59	6
ATOM	7479	CG	PRO	E	115	63.080	46.411	26.083	1.00 45.01	6
ATOM	7480	C	PRO	E	115	63.184	48.685	28.080	1.00 44.33	6
ATOM	7481	O	PRO	E	115	63.997	47.940	28.619	1.00 44.22	8
ATOM	7482	N	SER	E	116	62.397	49.510	28.761	1.00 41.95	7
ATOM	7483	CA	SER	E	116	62.428	49.514	30.217	1.00 42.78	6
ATOM	7484	CB	SER	E	116	62.113	50.884	30.773	1.00 41.77	6
ATOM	7485	OG	SER	E	116	62.191	50.841	32.181	1.00 44.88	8
ATOM	7486	C	SER	E	116	61.344	48.533	30.643	1.00 43.69	6
ATOM	7487	O	SER	E	116	60.196	48.672	30.246	1.00 46.37	8
ATOM	7488	N	ILE	E	117	61.704	47.544	31.449	1.00 42.70	7
ATOM	7489	CA	ILE	E	117	60.751	46.534	31.851	1.00 40.36	6
ATOM	7490	CB	ILE	E	117	61.182	45.152	31.304	1.00 39.17	6
ATOM	7491	CG2	ILE	E	117	60.251	44.080	31.792	1.00 39.63	6
ATOM	7492	CG1	ILE	E	117	61.207	45.173	29.787	1.00 38.62	6

ATOM	7493	CD1	ILE	E	117	61.883	43.985	29.185	1.00 35.74	6
ATOM	7494	C	ILE	E	117	60.561	46.387	33.349	1.00 43.14	6
ATOM	7495	O	ILE	E	117	61.525	46.400	34.116	1.00 44.32	8
ATOM	7496	N	ARG	E	118	59.305	46.266	33.768	1.00 43.03	7
ATOM	7497	CA	ARG	E	118	59.014	46.009	35.170	1.00 42.46	6
ATOM	7498	CB	ARG	E	118	57.907	46.897	35.710	1.00 40.98	6
ATOM	7499	CG	ARG	E	118	57.537	46.484	37.113	1.00 39.32	6
ATOM	7500	CD	ARG	E	118	56.671	47.482	37.827	1.00 40.32	6
ATOM	7501	NE	ARG	E	118	56.321	46.985	39.155	1.00 40.46	7
ATOM	7502	CZ	ARG	E	118	55.762	47.717	40.108	1.00 38.25	6
ATOM	7503	NH1	ARG	E	118	55.485	48.991	39.899	1.00 41.07	7
ATOM	7504	NH2	ARG	E	118	55.486	47.175	41.273	1.00 37.40	7
ATOM	7505	C	ARG	E	118	58.552	44.557	35.140	1.00 41.73	6
ATOM	7506	O	ARG	E	118	57.738	44.185	34.309	1.00 41.59	8
ATOM	7507	N	GLN	E	119	59.071	43.731	36.036	1.00 42.60	7
ATOM	7508	CA	GLN	E	119	58.718	42.321	36.016	1.00 43.62	6
ATOM	7509	CB	GLN	E	119	59.460	41.671	34.842	1.00 41.24	6
ATOM	7510	CG	GLN	E	119	59.220	40.211	34.624	1.00 40.90	6
ATOM	7511	CD	GLN	E	119	59.795	39.749	33.304	1.00 40.75	6
ATOM	7512	OE1	GLN	E	119	60.829	40.227	32.879	1.00 41.44	8
ATOM	7513	NE2	GLN	E	119	59.126	38.807	32.654	1.00 44.30	7
ATOM	7514	C	GLN	E	119	59.085	41.658	37.337	1.00 44.85	6
ATOM	7515	O	GLN	E	119	60.030	42.059	38.006	1.00 44.93	8
ATOM	7516	N	ARG	E	120	58.326	40.649	37.724	1.00 46.59	7
ATOM	7517	CA	ARG	E	120	58.612	39.958	38.969	1.00 49.63	6
ATOM	7518	CB	ARG	E	120	57.327	39.657	39.722	1.00 52.24	6
ATOM	7519	CG	ARG	E	120	56.514	40.879	40.037	1.00 59.37	6
ATOM	7520	CD	ARG	E	120	55.730	40.641	41.301	1.00 65.41	6
ATOM	7521	NE	ARG	E	120	56.517	40.896	42.518	1.00 68.76	7
ATOM	7522	CZ	ARG	E	120	56.467	40.125	43.606	1.00 69.55	6
ATOM	7523	NH1	ARG	E	120	55.687	39.045	43.617	1.00 67.60	7
ATOM	7524	NH2	ARG	E	120	57.150	40.459	44.702	1.00 69.98	7
ATOM	7525	C	ARG	E	120	59.365	38.662	38.724	1.00 48.95	6
ATOM	7526	O	ARG	E	120	59.187	38.013	37.692	1.00 47.74	8
ATOM	7527	N	PHE	E	121	60.210	38.295	39.683	1.00 47.82	7
ATOM	7528	CA	PHE	E	121	60.996	37.085	39.563	1.00 46.24	6
ATOM	7529	CB	PHE	E	121	62.453	37.408	39.224	1.00 42.79	6
ATOM	7530	CG	PHE	E	121	62.620	38.238	38.001	1.00 43.16	6
ATOM	7531	CD1	PHE	E	121	62.431	39.605	38.052	1.00 42.55	6
ATOM	7532	CD2	PHE	E	121	62.945	37.651	36.793	1.00 41.67	6
ATOM	7533	CE1	PHE	E	121	62.559	40.372	36.924	1.00 44.29	6
ATOM	7534	CE2	PHE	E	121	63.074	38.406	35.667	1.00 39.85	6
ATOM	7535	CZ	PHE	E	121	62.881	39.770	35.725	1.00 43.74	6
ATOM	7536	C	PHE	E	121	60.991	36.243	40.812	1.00 46.96	6
ATOM	7537	O	PHE	E	121	60.663	36.708	41.902	1.00 44.85	8
ATOM	7538	N	SER	E	122	61.381	34.987	40.619	1.00 50.04	7
ATOM	7539	CA	SER	E	122	61.509	34.019	41.691	1.00 50.97	6
ATOM	7540	CB	SER	E	122	60.846	32.701	41.302	1.00 50.69	6
ATOM	7541	OG	SER	E	122	60.993	31.753	42.338	1.00 54.83	8
ATOM	7542	C	SER	E	122	63.007	33.817	41.838	1.00 51.59	6
ATOM	7543	O	SER	E	122	63.648	33.274	40.947	1.00 51.83	8
ATOM	7544	N	CYS	E	123	63.566	34.282	42.946	1.00 53.04	7
ATOM	7545	CA	CYS	E	123	65.000	34.155	43.186	1.00 55.64	6
ATOM	7546	C	CYS	E	123	65.301	34.247	44.680	1.00 58.47	6
ATOM	7547	O	CYS	E	123	64.390	34.401	45.501	1.00 58.89	8
ATOM	7548	CB	CYS	E	123	65.757	35.249	42.425	1.00 53.82	6
ATOM	7549	SG	CYS	E	123	65.215	36.927	42.881	1.00 56.41	16
ATOM	7550	N	ASP	E	124	66.581	34.151	45.033	1.00 61.78	7
ATOM	7551	CA	ASP	E	124	66.991	34.215	46.437	1.00 63.06	6
ATOM	7552	CB	ASP	E	124	68.406	33.650	46.620	1.00 63.79	6
ATOM	7553	CG	ASP	E	124	68.605	33.024	47.992	1.00 64.87	6

ATOM	7554	OD1	ASP	E	124	67.970	33.502	48.967	1.00	63.75	8
ATOM	7555	OD2	ASP	E	124	69.396	32.058	48.094	1.00	65.17	8
ATOM	7556	C	ASP	E	124	66.953	35.636	47.007	1.00	63.18	6
ATOM	7557	O	ASP	E	124	67.748	36.495	46.630	1.00	63.39	8
ATOM	7558	N	VAL	E	125	66.031	35.857	47.936	1.00	63.67	7
ATOM	7559	CA	VAL	E	125	65.869	37.152	48.586	1.00	63.68	6
ATOM	7560	CB	VAL	E	125	64.370	37.506	48.710	1.00	61.88	6
ATOM	7561	CG1	VAL	E	125	64.195	38.794	49.466	1.00	58.52	6
ATOM	7562	CG2	VAL	E	125	63.751	37.608	47.331	1.00	59.91	6
ATOM	7563	C	VAL	E	125	66.501	37.157	49.987	1.00	64.88	6
ATOM	7564	O	VAL	E	125	66.768	38.214	50.551	1.00	66.59	8
ATOM	7565	N	SER	E	126	66.745	35.975	50.544	1.00	64.96	7
ATOM	7566	CA	SER	E	126	67.335	35.870	51.874	1.00	64.47	6
ATOM	7567	CB	SER	E	126	67.672	34.410	52.185	1.00	62.82	6
ATOM	7568	OG	SER	E	126	68.617	33.901	51.267	1.00	61.35	8
ATOM	7569	C	SER	E	126	68.588	36.729	52.013	1.00	65.71	6
ATOM	7570	O	SER	E	126	69.494	36.690	51.165	1.00	65.59	8
ATOM	7571	N	GLY	E	127	68.632	37.519	53.082	1.00	66.30	7
ATOM	7572	CA	GLY	E	127	69.788	38.369	53.309	1.00	67.81	6
ATOM	7573	C	GLY	E	127	69.595	39.800	52.848	1.00	69.06	6
ATOM	7574	O	GLY	E	127	70.471	40.633	53.037	1.00	69.45	8
ATOM	7575	N	VAL	E	128	68.444	40.093	52.253	1.00	70.68	7
ATOM	7576	CA	VAL	E	128	68.179	41.438	51.771	1.00	72.21	6
ATOM	7577	CB	VAL	E	128	66.784	41.575	51.127	1.00	70.88	6
ATOM	7578	CG1	VAL	E	128	66.771	40.882	49.794	1.00	74.99	6
ATOM	7579	CG2	VAL	E	128	65.722	40.993	52.039	1.00	69.09	6
ATOM	7580	C	VAL	E	128	68.233	42.480	52.855	1.00	73.85	6
ATOM	7581	O	VAL	E	128	68.855	43.525	52.678	1.00	74.59	8
ATOM	7582	N	ASP	E	129	67.579	42.197	53.977	1.00	75.59	7
ATOM	7583	CA	ASP	E	129	67.506	43.170	55.046	1.00	77.34	6
ATOM	7584	CB	ASP	E	129	66.583	42.691	56.164	1.00	78.29	6
ATOM	7585	CG	ASP	E	129	65.952	43.864	56.939	1.00	80.26	6
ATOM	7586	OD1	ASP	E	129	64.733	43.805	57.257	1.00	82.07	8
ATOM	7587	OD2	ASP	E	129	66.674	44.848	57.231	1.00	78.55	8
ATOM	7588	C	ASP	E	129	68.825	43.625	55.628	1.00	78.37	6
ATOM	7589	O	ASP	E	129	68.852	44.624	56.362	1.00	78.49	8
ATOM	7590	N	THR	E	130	69.925	42.942	55.302	1.00	79.16	7
ATOM	7591	CA	THR	E	130	71.201	43.391	55.847	1.00	80.17	6
ATOM	7592	CB	THR	E	130	71.162	43.351	57.393	1.00	83.36	6
ATOM	7593	OG1	THR	E	130	70.028	42.564	57.803	1.00	84.91	8
ATOM	7594	CG2	THR	E	130	71.096	44.810	57.995	1.00	82.87	6
ATOM	7595	C	THR	E	130	72.505	42.731	55.445	1.00	78.82	6
ATOM	7596	O	THR	E	130	72.549	41.553	55.068	1.00	78.45	8
ATOM	7597	N	GLU	E	131	73.564	43.537	55.572	1.00	78.85	7
ATOM	7598	CA	GLU	E	131	74.961	43.153	55.353	1.00	78.23	6
ATOM	7599	CB	GLU	E	131	75.292	41.900	56.187	1.00	80.76	6
ATOM	7600	CG	GLU	E	131	75.507	42.176	57.686	1.00	82.62	6
ATOM	7601	CD	GLU	E	131	75.241	40.955	58.543	1.00	83.46	6
ATOM	7602	OE1	GLU	E	131	75.740	39.854	58.186	1.00	83.49	8
ATOM	7603	OE2	GLU	E	131	74.534	41.107	59.565	1.00	83.07	8
ATOM	7604	C	GLU	E	131	75.434	42.931	53.943	1.00	77.11	6
ATOM	7605	O	GLU	E	131	75.646	43.884	53.173	1.00	75.95	8
ATOM	7606	N	SER	E	132	75.658	41.652	53.650	1.00	76.20	7
ATOM	7607	CA	SER	E	132	76.107	41.200	52.352	1.00	75.57	6
ATOM	7608	CB	SER	E	132	76.773	39.831	52.501	1.00	75.40	6
ATOM	7609	OG	SER	E	132	75.896	38.911	53.122	1.00	73.45	8
ATOM	7610	C	SER	E	132	74.858	41.115	51.462	1.00	74.79	6
ATOM	7611	O	SER	E	132	74.926	40.722	50.288	1.00	76.37	8
ATOM	7612	N	GLY	E	133	73.719	41.484	52.048	1.00	72.67	7
ATOM	7613	CA	GLY	E	133	72.459	41.482	51.330	1.00	69.80	6
ATOM	7614	C	GLY	E	133	72.127	40.179	50.631	1.00	67.70	6

ATOM	7615	O	GLY	E	133	72.686	39.128	50.934	1.00	67.31	8
ATOM	7616	N	ALA	E	134	71.205	40.256	49.681	1.00	66.03	7
ATOM	7617	CA	ALA	E	134	70.799	39.081	48.931	1.00	64.43	6
ATOM	7618	CB	ALA	E	134	69.275	38.990	48.879	1.00	64.83	6
ATOM	7619	C	ALA	E	134	71.363	39.108	47.512	1.00	63.34	6
ATOM	7620	O	ALA	E	134	71.825	40.148	47.014	1.00	61.70	8
ATOM	7621	N	THR	E	135	71.339	37.944	46.875	1.00	61.78	7
ATOM	7622	CA	THR	E	135	71.813	37.817	45.515	1.00	61.48	6
ATOM	7623	CB	THR	E	135	73.108	37.043	45.446	1.00	62.04	6
ATOM	7624	OG1	THR	E	135	74.093	37.715	46.237	1.00	63.94	8
ATOM	7625	CG2	THR	E	135	73.590	36.970	44.012	1.00	63.05	6
ATOM	7626	C	THR	E	135	70.741	37.102	44.718	1.00	61.03	6
ATOM	7627	O	THR	E	135	70.522	35.886	44.839	1.00	59.53	8
ATOM	7628	N	CYS	E	136	70.049	37.901	43.919	1.00	59.40	7
ATOM	7629	CA	CYS	E	136	68.975	37.422	43.083	1.00	57.62	6
ATOM	7630	C	CYS	E	136	69.530	37.254	41.669	1.00	56.65	6
ATOM	7631	O	CYS	E	136	69.990	38.220	41.054	1.00	54.61	8
ATOM	7632	CB	CYS	E	136	67.843	38.442	43.129	1.00	55.65	6
ATOM	7633	SG	CYS	E	136	66.510	38.178	41.946	1.00	55.99	16
ATOM	7634	N	ARG	E	137	69.517	36.016	41.180	1.00	56.36	7
ATOM	7635	CA	ARG	E	137	70.025	35.717	39.853	1.00	57.23	6
ATOM	7636	CB	ARG	E	137	70.861	34.437	39.871	1.00	58.80	6
ATOM	7637	CG	ARG	E	137	72.068	34.513	40.774	1.00	62.70	6
ATOM	7638	CD	ARG	E	137	72.482	33.125	41.241	1.00	66.89	6
ATOM	7639	NE	ARG	E	137	73.230	33.182	42.500	1.00	70.82	7
ATOM	7640	CZ	ARG	E	137	74.469	33.659	42.633	1.00	71.90	6
ATOM	7641	NH1	ARG	E	137	75.134	34.130	41.578	1.00	70.38	7
ATOM	7642	NH2	ARG	E	137	75.042	33.674	43.832	1.00	71.22	7
ATOM	7643	C	ARG	E	137	68.863	35.545	38.894	1.00	56.91	6
ATOM	7644	O	ARG	E	137	67.909	34.822	39.177	1.00	56.92	8
ATOM	7645	N	ILE	E	138	68.970	36.215	37.754	1.00	54.63	7
ATOM	7646	CA	ILE	E	138	67.966	36.175	36.716	1.00	51.98	6
ATOM	7647	CB	ILE	E	138	67.432	37.587	36.468	1.00	51.76	6
ATOM	7648	CG2	ILE	E	138	66.432	37.573	35.333	1.00	49.89	6
ATOM	7649	CG1	ILE	E	138	66.817	38.137	37.757	1.00	50.16	6
ATOM	7650	CD1	ILE	E	138	66.476	39.606	37.681	1.00	47.06	6
ATOM	7651	C	ILE	E	138	68.611	35.655	35.434	1.00	52.26	6
ATOM	7652	O	ILE	E	138	69.557	36.261	34.933	1.00	52.12	8
ATOM	7653	N	LYS	E	139	68.105	34.542	34.901	1.00	52.70	7
ATOM	7654	CA	LYS	E	139	68.656	33.961	33.667	1.00	53.32	6
ATOM	7655	CB	LYS	E	139	68.877	32.455	33.822	1.00	53.63	6
ATOM	7656	CG	LYS	E	139	69.732	32.075	35.013	1.00	57.59	6
ATOM	7657	CD	LYS	E	139	70.150	30.612	34.967	1.00	59.76	6
ATOM	7658	CE	LYS	E	139	71.183	30.363	33.869	1.00	62.51	6
ATOM	7659	NZ	LYS	E	139	71.624	28.928	33.787	1.00	63.48	7
ATOM	7660	C	LYS	E	139	67.738	34.187	32.480	1.00	52.42	6
ATOM	7661	O	LYS	E	139	66.572	33.826	32.527	1.00	52.75	8
ATOM	7662	N	ILE	E	140	68.264	34.770	31.410	1.00	52.23	7
ATOM	7663	CA	ILE	E	140	67.449	35.013	30.229	1.00	51.67	6
ATOM	7664	CB	ILE	E	140	66.995	36.513	30.165	1.00	50.77	6
ATOM	7665	CG2	ILE	E	140	66.543	36.974	31.546	1.00	51.60	6
ATOM	7666	CG1	ILE	E	140	68.136	37.434	29.766	1.00	52.08	6
ATOM	7667	CD1	ILE	E	140	67.815	38.915	30.060	1.00	55.62	6
ATOM	7668	C	ILE	E	140	68.145	34.594	28.935	1.00	51.13	6
ATOM	7669	O	ILE	E	140	69.295	34.917	28.710	1.00	49.59	8
ATOM	7670	N	GLY	E	141	67.434	33.840	28.102	1.00	52.11	7
ATOM	7671	CA	GLY	E	141	67.985	33.382	26.833	1.00	51.58	6
ATOM	7672	C	GLY	E	141	66.884	33.089	25.826	1.00	51.56	6
ATOM	7673	O	GLY	E	141	65.709	33.125	26.186	1.00	52.84	8
ATOM	7674	N	SER	E	142	67.245	32.807	24.573	1.00	49.52	7
ATOM	7675	CA	SER	E	142	66.241	32.514	23.553	1.00	46.89	6

ATOM	7676	CB	SER	E	142	66.883	32.177	22.214	1.00	44.37	6
ATOM	7677	OG	SER	E	142	65.913	31.657	21.329	1.00	40.29	8
ATOM	7678	C	SER	E	142	65.386	31.346	23.997	1.00	47.72	6
ATOM	7679	O	SER	E	142	65.880	30.376	24.584	1.00	48.09	8
ATOM	7680	N	TRP	E	143	64.097	31.439	23.701	1.00	47.51	7
ATOM	7681	CA	TRP	E	143	63.165	30.406	24.101	1.00	46.17	6
ATOM	7682	CB	TRP	E	143	61.780	31.025	24.327	1.00	45.01	6
ATOM	7683	CG	TRP	E	143	60.808	30.096	24.968	1.00	42.92	6
ATOM	7684	CD2	TRP	E	143	60.799	29.697	26.337	1.00	41.62	6
ATOM	7685	CE2	TRP	E	143	59.721	28.803	26.505	1.00	39.45	6
ATOM	7686	CE3	TRP	E	143	61.601	30.008	27.442	1.00	42.26	6
ATOM	7687	CD1	TRP	E	143	59.764	29.448	24.371	1.00	41.66	6
ATOM	7688	NE1	TRP	E	143	59.106	28.669	25.288	1.00	41.08	7
ATOM	7689	CZ2	TRP	E	143	59.423	28.216	27.736	1.00	39.02	6
ATOM	7690	CZ3	TRP	E	143	61.305	29.426	28.662	1.00	40.87	6
ATOM	7691	CH2	TRP	E	143	60.223	28.540	28.799	1.00	41.01	6
ATOM	7692	C	TRP	E	143	63.067	29.281	23.097	1.00	46.14	6
ATOM	7693	O	TRP	E	143	62.816	28.147	23.467	1.00	47.72	8
ATOM	7694	N	THR	E	144	63.277	29.579	21.821	1.00	46.28	7
ATOM	7695	CA	THR	E	144	63.141	28.539	20.808	1.00	44.88	6
ATOM	7696	CB	THR	E	144	61.961	28.863	19.859	1.00	42.99	6
ATOM	7697	OG1	THR	E	144	62.131	30.174	19.308	1.00	42.03	8
ATOM	7698	CG2	THR	E	144	60.655	28.824	20.609	1.00	40.32	6
ATOM	7699	C	THR	E	144	64.378	28.276	19.969	1.00	46.55	6
ATOM	7700	O	THR	E	144	64.434	27.294	19.243	1.00	46.91	8
ATOM	7701	N	HIS	E	145	65.367	29.151	20.060	1.00	48.37	7
ATOM	7702	CA	HIS	E	145	66.576	28.973	19.275	1.00	50.06	6
ATOM	7703	CB	HIS	E	145	66.937	30.265	18.541	1.00	49.35	6
ATOM	7704	CG	HIS	E	145	65.947	30.669	17.492	1.00	49.26	6
ATOM	7705	CD2	HIS	E	145	65.676	30.143	16.275	1.00	49.17	6
ATOM	7706	ND1	HIS	E	145	65.112	31.756	17.634	1.00	47.03	7
ATOM	7707	CE1	HIS	E	145	64.371	31.883	16.548	1.00	48.38	6
ATOM	7708	NE2	HIS	E	145	64.694	30.917	15.708	1.00	50.40	7
ATOM	7709	C	HIS	E	145	67.754	28.529	20.125	1.00	51.77	6
ATOM	7710	O	HIS	E	145	68.096	29.153	21.129	1.00	50.03	8
ATOM	7711	N	HIS	E	146	68.371	27.427	19.710	1.00	55.46	7
ATOM	7712	CA	HIS	E	146	69.530	26.886	20.418	1.00	57.69	6
ATOM	7713	CB	HIS	E	146	69.654	25.377	20.162	1.00	56.07	6
ATOM	7714	CG	HIS	E	146	69.679	25.019	18.715	1.00	56.24	6
ATOM	7715	CD2	HIS	E	146	70.477	25.442	17.707	1.00	55.97	6
ATOM	7716	ND1	HIS	E	146	68.798	24.121	18.157	1.00	58.10	7
ATOM	7717	CE1	HIS	E	146	69.053	24.005	16.863	1.00	58.23	6
ATOM	7718	NE2	HIS	E	146	70.068	24.797	16.566	1.00	57.28	7
ATOM	7719	C	HIS	E	146	70.801	27.612	19.971	1.00	58.37	6
ATOM	7720	O	HIS	E	146	70.775	28.455	19.064	1.00	59.37	8
ATOM	7721	N	SER	E	147	71.908	27.269	20.618	1.00	60.00	7
ATOM	7722	CA	SER	E	147	73.218	27.872	20.356	1.00	60.54	6
ATOM	7723	CB	SER	E	147	74.268	27.134	21.185	1.00	60.36	6
ATOM	7724	OG	SER	E	147	74.082	25.728	21.071	1.00	61.90	8
ATOM	7725	C	SER	E	147	73.690	27.960	18.897	1.00	60.61	6
ATOM	7726	O	SER	E	147	74.491	28.837	18.553	1.00	60.32	8
ATOM	7727	N	ARG	E	148	73.197	27.072	18.041	1.00	59.60	7
ATOM	7728	CA	ARG	E	148	73.611	27.083	16.646	1.00	60.89	6
ATOM	7729	CB	ARG	E	148	73.307	25.722	15.996	1.00	66.00	6
ATOM	7730	CG	ARG	E	148	73.902	24.527	16.756	1.00	74.00	6
ATOM	7731	CD	ARG	E	148	73.462	23.177	16.169	1.00	79.80	6
ATOM	7732	NE	ARG	E	148	73.749	22.052	17.077	1.00	85.45	7
ATOM	7733	CZ	ARG	E	148	74.973	21.680	17.475	1.00	86.76	6
ATOM	7734	NH1	ARG	E	148	76.045	22.338	17.046	1.00	87.13	7
ATOM	7735	NH2	ARG	E	148	75.130	20.650	18.306	1.00	86.87	7
ATOM	7736	C	ARG	E	148	72.942	28.189	15.847	1.00	59.62	6

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ATOM   7737  O   ARG E 148      73.418  28.564  14.766  1.00 58.11   8
ATOM   7738  N   GLU E 149      71.836  28.707  16.384  1.00 58.68   7
ATOM   7739  CA  GLU E 149      71.067  29.756  15.716  1.00 56.72   6
ATOM   7740  CB  GLU E 149      69.598  29.337  15.630  1.00 55.99   6
ATOM   7741  CG  GLU E 149      69.435  27.854  15.335  1.00 57.25   6
ATOM   7742  CD  GLU E 149      67.992  27.402  15.239  1.00 57.65   6
ATOM   7743  OE1 GLU E 149      67.166  27.825  16.075  1.00 58.97   8
ATOM   7744  OE2 GLU E 149      67.684  26.606  14.332  1.00 56.32   8
ATOM   7745  C   GLU E 149      71.214  31.073  16.463  1.00 55.95   6
ATOM   7746  O   GLU E 149      71.423  32.122  15.852  1.00 54.41   8
ATOM   7747  N   ILE E 150      71.109  31.012  17.787  1.00 55.27   7
ATOM   7748  CA  ILE E 150      71.265  32.202  18.600  1.00 54.72   6
ATOM   7749  CB  ILE E 150      69.922  32.686  19.227  1.00 54.60   6
ATOM   7750  CG2 ILE E 150      70.190  33.711  20.339  1.00 51.29   6
ATOM   7751  CG1 ILE E 150      69.051  33.354  18.167  1.00 53.90   6
ATOM   7752  CD1 ILE E 150      67.738  33.855  18.709  1.00 52.06   6
ATOM   7753  C   ILE E 150      72.238  31.954  19.728  1.00 55.47   6
ATOM   7754  O   ILE E 150      72.226  30.898  20.361  1.00 54.39   8
ATOM   7755  N   SER E 151      73.083  32.948  19.962  1.00 56.26   7
ATOM   7756  CA  SER E 151      74.055  32.898  21.035  1.00 59.09   6
ATOM   7757  CB  SER E 151      75.478  32.752  20.471  1.00 59.25   6
ATOM   7758  OG  SER E 151      75.826  33.853  19.653  1.00 59.55   8
ATOM   7759  C   SER E 151      73.904  34.226  21.770  1.00 59.98   6
ATOM   7760  O   SER E 151      73.793  35.283  21.139  1.00 59.94   8
ATOM   7761  N   VAL E 152      73.878  34.172  23.096  1.00 60.88   7
ATOM   7762  CA  VAL E 152      73.739  35.380  23.900  1.00 62.73   6
ATOM   7763  CB  VAL E 152      72.628  35.233  24.956  1.00 61.31   6
ATOM   7764  CG1 VAL E 152      71.339  34.777  24.294  1.00 58.78   6
ATOM   7765  CG2 VAL E 152      73.067  34.241  26.034  1.00 62.59   6
ATOM   7766  C   VAL E 152      75.054  35.633  24.612  1.00 64.27   6
ATOM   7767  O   VAL E 152      75.743  34.687  24.994  1.00 63.76   8
ATOM   7768  N   ASP E 153      75.393  36.904  24.805  1.00 66.67   7
ATOM   7769  CA  ASP E 153      76.650  37.261  25.456  1.00 70.32   6
ATOM   7770  CB  ASP E 153      77.713  37.471  24.381  1.00 70.77   6
ATOM   7771  CG  ASP E 153      77.832  36.272  23.433  1.00 74.19   6
ATOM   7772  OD1 ASP E 153      78.483  35.261  23.803  1.00 75.87   8
ATOM   7773  OD2 ASP E 153      77.265  36.331  22.319  1.00 73.45   8
ATOM   7774  C   ASP E 153      76.531  38.533  26.304  1.00 72.18   6
ATOM   7775  O   ASP E 153      75.835  39.481  25.922  1.00 72.90   8
ATOM   7776  N   PRO E 154      77.187  38.561  27.478  1.00 73.33   7
ATOM   7777  CD  PRO E 154      77.671  37.398  28.243  1.00 72.54   6
ATOM   7778  CA  PRO E 154      77.123  39.755  28.332  1.00 75.06   6
ATOM   7779  CB  PRO E 154      77.749  39.279  29.642  1.00 74.00   6
ATOM   7780  CG  PRO E 154      77.389  37.823  29.676  1.00 74.05   6
ATOM   7781  C   PRO E 154      77.911  40.901  27.688  1.00 77.63   6
ATOM   7782  O   PRO E 154      78.502  40.717  26.620  1.00 78.05   8
ATOM   7783  N   THR E 155      77.940  42.066  28.338  1.00 81.26   7
ATOM   7784  CA  THR E 155      78.638  43.230  27.781  1.00 85.03   6
ATOM   7785  CB  THR E 155      77.623  44.147  27.020  1.00 83.83   6
ATOM   7786  OG1 THR E 155      76.717  44.749  27.956  1.00 81.33   8
ATOM   7787  CG2 THR E 155      76.815  43.341  26.020  1.00 83.47   6
ATOM   7788  C   THR E 155      79.417  44.101  28.803  1.00 88.40   6
ATOM   7789  O   THR E 155      79.900  43.592  29.825  1.00 88.82   8
ATOM   7790  N   THR E 156      79.527  45.405  28.487  1.00 91.48   7
ATOM   7791  CA  THR E 156      80.206  46.443  29.288  1.00 93.55   6
ATOM   7792  CB  THR E 156      79.615  47.854  29.002  1.00 93.31   6
ATOM   7793  OG1 THR E 156      79.697  48.136  27.596  1.00 92.71   8
ATOM   7794  CG2 THR E 156      80.376  48.925  29.813  1.00 92.25   6
ATOM   7795  C   THR E 156      80.165  46.249  30.803  1.00 95.69   6
ATOM   7796  O   THR E 156      79.173  46.584  31.476  1.00 95.92   8
ATOM   7797  N   GLU E 157      81.264  45.733  31.340  1.00 97.89   7
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ATOM	7798	CA	GLU	E	157	81.365	45.481	32.776	1.00	100.21	6
ATOM	7799	CB	GLU	E	157	82.361	44.343	33.018	1.00	101.17	6
ATOM	7800	CG	GLU	E	157	82.198	43.190	32.046	1.00	103.80	6
ATOM	7801	CD	GLU	E	157	83.222	42.107	32.296	1.00	105.78	6
ATOM	7802	OE1	GLU	E	157	84.423	42.466	32.375	1.00	105.64	8
ATOM	7803	OE2	GLU	E	157	82.828	40.907	32.410	1.00	107.35	8
ATOM	7804	C	GLU	E	157	81.817	46.729	33.550	1.00	100.48	6
ATOM	7805	O	GLU	E	157	81.869	46.719	34.798	1.00	100.82	8
ATOM	7806	N	ASN	E	158	82.151	47.793	32.818	1.00	99.54	7
ATOM	7807	CA	ASN	E	158	82.620	49.011	33.461	1.00	98.41	6
ATOM	7808	CB	ASN	E	158	83.235	49.953	32.426	1.00	100.23	6
ATOM	7809	CG	ASN	E	158	84.338	49.283	31.604	1.00	101.57	6
ATOM	7810	OD1	ASN	E	158	85.334	48.768	32.152	1.00	100.21	8
ATOM	7811	ND2	ASN	E	158	84.165	49.286	30.274	1.00	102.69	7
ATOM	7812	C	ASN	E	158	81.456	49.701	34.156	1.00	96.86	6
ATOM	7813	O	ASN	E	158	81.185	49.443	35.341	1.00	96.41	8
ATOM	7814	N	SER	E	159	80.791	50.578	33.395	1.00	94.72	7
ATOM	7815	CA	SER	E	159	79.624	51.349	33.834	1.00	91.39	6
ATOM	7816	CB	SER	E	159	78.465	51.087	32.858	1.00	91.87	6
ATOM	7817	OG	SER	E	159	78.391	49.705	32.499	1.00	92.44	8
ATOM	7818	C	SER	E	159	79.169	51.080	35.269	1.00	88.56	6
ATOM	7819	O	SER	E	159	78.823	49.947	35.614	1.00	89.22	8
ATOM	7820	N	ASP	E	160	79.171	52.119	36.102	1.00	85.19	7
ATOM	7821	CA	ASP	E	160	78.744	51.966	37.495	1.00	81.21	6
ATOM	7822	CB	ASP	E	160	78.527	53.327	38.157	1.00	80.51	6
ATOM	7823	CG	ASP	E	160	78.005	53.194	39.574	1.00	79.98	6
ATOM	7824	OD1	ASP	E	160	77.424	54.174	40.079	1.00	80.37	8
ATOM	7825	OD2	ASP	E	160	78.184	52.104	40.178	1.00	78.39	8
ATOM	7826	C	ASP	E	160	77.426	51.202	37.525	1.00	78.59	6
ATOM	7827	O	ASP	E	160	76.427	51.669	36.959	1.00	77.98	8
ATOM	7828	N	ASP	E	161	77.427	50.043	38.185	1.00	75.05	7
ATOM	7829	CA	ASP	E	161	76.233	49.203	38.283	1.00	71.67	6
ATOM	7830	CB	ASP	E	161	76.473	48.017	39.226	1.00	70.39	6
ATOM	7831	CG	ASP	E	161	77.428	46.994	38.641	1.00	70.69	6
ATOM	7832	OD1	ASP	E	161	77.389	46.782	37.416	1.00	70.97	8
ATOM	7833	OD2	ASP	E	161	78.211	46.386	39.400	1.00	71.91	8
ATOM	7834	C	ASP	E	161	74.968	49.931	38.732	1.00	70.49	6
ATOM	7835	O	ASP	E	161	73.864	49.439	38.514	1.00	71.58	8
ATOM	7836	N	SER	E	162	75.099	51.093	39.356	1.00	68.11	7
ATOM	7837	CA	SER	E	162	73.903	51.792	39.785	1.00	66.58	6
ATOM	7838	CB	SER	E	162	73.771	51.731	41.308	1.00	66.49	6
ATOM	7839	OG	SER	E	162	74.786	52.478	41.938	1.00	64.63	8
ATOM	7840	C	SER	E	162	73.856	53.237	39.319	1.00	65.96	6
ATOM	7841	O	SER	E	162	73.250	54.088	39.972	1.00	64.77	8
ATOM	7842	N	GLU	E	163	74.475	53.514	38.178	1.00	65.61	7
ATOM	7843	CA	GLU	E	163	74.474	54.872	37.676	1.00	67.53	6
ATOM	7844	CB	GLU	E	163	75.582	55.051	36.631	1.00	70.35	6
ATOM	7845	CG	GLU	E	163	75.237	54.661	35.213	1.00	72.94	6
ATOM	7846	CD	GLU	E	163	76.338	55.083	34.225	1.00	76.12	6
ATOM	7847	OE1	GLU	E	163	77.424	54.448	34.241	1.00	77.12	8
ATOM	7848	OE2	GLU	E	163	76.118	56.054	33.445	1.00	76.02	8
ATOM	7849	C	GLU	E	163	73.108	55.271	37.113	1.00	66.26	6
ATOM	7850	O	GLU	E	163	72.873	56.442	36.800	1.00	64.91	8
ATOM	7851	N	TYR	E	164	72.211	54.292	36.990	1.00	66.34	7
ATOM	7852	CA	TYR	E	164	70.848	54.539	36.496	1.00	65.02	6
ATOM	7853	CB	TYR	E	164	70.555	53.716	35.235	1.00	64.40	6
ATOM	7854	CG	TYR	E	164	71.386	54.109	34.051	1.00	64.81	6
ATOM	7855	CD1	TYR	E	164	72.237	53.191	33.437	1.00	64.72	6
ATOM	7856	CE1	TYR	E	164	73.040	53.559	32.351	1.00	65.69	6
ATOM	7857	CD2	TYR	E	164	71.350	55.413	33.559	1.00	67.21	6
ATOM	7858	CE2	TYR	E	164	72.154	55.805	32.471	1.00	67.79	6

ATOM	7859	CZ	TYR	E	164	72.994	54.867	31.867	1.00	67.33	6
ATOM	7860	OH	TYR	E	164	73.744	55.230	30.765	1.00	67.72	8
ATOM	7861	C	TYR	E	164	69.831	54.174	37.574	1.00	63.42	6
ATOM	7862	O	TYR	E	164	68.642	54.458	37.442	1.00	62.96	8
ATOM	7863	N	PHE	E	165	70.309	53.552	38.646	1.00	60.43	7
ATOM	7864	CA	PHE	E	165	69.428	53.139	39.717	1.00	59.92	6
ATOM	7865	CB	PHE	E	165	70.208	52.378	40.776	1.00	58.36	6
ATOM	7866	CG	PHE	E	165	69.347	51.515	41.645	1.00	58.01	6
ATOM	7867	CD1	PHE	E	165	68.674	50.427	41.110	1.00	55.31	6
ATOM	7868	CD2	PHE	E	165	69.189	51.802	42.994	1.00	58.36	6
ATOM	7869	CE1	PHE	E	165	67.858	49.642	41.904	1.00	56.74	6
ATOM	7870	CE2	PHE	E	165	68.368	51.016	43.804	1.00	57.34	6
ATOM	7871	CZ	PHE	E	165	67.703	49.939	43.260	1.00	57.55	6
ATOM	7872	C	PHE	E	165	68.732	54.324	40.356	1.00	60.15	6
ATOM	7873	O	PHE	E	165	69.321	55.390	40.504	1.00	62.59	8
ATOM	7874	N	SER	E	166	67.466	54.148	40.718	1.00	59.42	7
ATOM	7875	CA	SER	E	166	66.724	55.222	41.357	1.00	57.86	6
ATOM	7876	CB	SER	E	166	65.241	54.869	41.503	1.00	56.65	6
ATOM	7877	OG	SER	E	166	64.513	55.951	42.064	1.00	53.76	8
ATOM	7878	C	SER	E	166	67.325	55.425	42.733	1.00	56.88	6
ATOM	7879	O	SER	E	166	67.712	54.472	43.407	1.00	55.76	8
ATOM	7880	N	GLN	E	167	67.406	56.677	43.142	1.00	56.96	7
ATOM	7881	CA	GLN	E	167	67.955	57.010	44.443	1.00	58.28	6
ATOM	7882	CB	GLN	E	167	68.547	58.423	44.401	1.00	60.41	6
ATOM	7883	CG	GLN	E	167	67.549	59.465	43.941	1.00	64.41	6
ATOM	7884	CD	GLN	E	167	68.198	60.780	43.599	1.00	66.50	6
ATOM	7885	OE1	GLN	E	167	68.795	61.433	44.458	1.00	67.54	8
ATOM	7886	NE2	GLN	E	167	68.089	61.184	42.330	1.00	68.48	7
ATOM	7887	C	GLN	E	167	66.880	56.924	45.532	1.00	57.21	6
ATOM	7888	O	GLN	E	167	67.196	56.835	46.720	1.00	56.91	8
ATOM	7889	N	TYR	E	168	65.613	56.932	45.133	1.00	54.47	7
ATOM	7890	CA	TYR	E	168	64.550	56.877	46.111	1.00	53.18	6
ATOM	7891	CB	TYR	E	168	63.399	57.760	45.649	1.00	53.95	6
ATOM	7892	CG	TYR	E	168	63.881	59.125	45.249	1.00	53.27	6
ATOM	7893	CD1	TYR	E	168	64.102	59.439	43.913	1.00	54.37	6
ATOM	7894	CE1	TYR	E	168	64.625	60.672	43.541	1.00	56.01	6
ATOM	7895	CD2	TYR	E	168	64.190	60.077	46.208	1.00	52.09	6
ATOM	7896	CE2	TYR	E	168	64.711	61.304	45.856	1.00	55.52	6
ATOM	7897	CZ	TYR	E	168	64.929	61.599	44.522	1.00	57.20	6
ATOM	7898	OH	TYR	E	168	65.458	62.815	44.177	1.00	59.36	8
ATOM	7899	C	TYR	E	168	64.072	55.470	46.431	1.00	52.65	6
ATOM	7900	O	TYR	E	168	63.131	55.282	47.189	1.00	53.48	8
ATOM	7901	N	SER	E	169	64.735	54.479	45.861	1.00	51.93	7
ATOM	7902	CA	SER	E	169	64.387	53.093	46.117	1.00	53.34	6
ATOM	7903	CB	SER	E	169	65.191	52.167	45.201	1.00	53.89	6
ATOM	7904	OG	SER	E	169	64.945	50.807	45.514	1.00	50.40	8
ATOM	7905	C	SER	E	169	64.686	52.726	47.567	1.00	54.98	6
ATOM	7906	O	SER	E	169	65.636	53.225	48.162	1.00	54.67	8
ATOM	7907	N	ARG	E	170	63.875	51.844	48.131	1.00	56.35	7
ATOM	7908	CA	ARG	E	170	64.075	51.404	49.500	1.00	56.22	6
ATOM	7909	CB	ARG	E	170	62.869	50.568	49.963	1.00	57.55	6
ATOM	7910	CG	ARG	E	170	61.832	51.361	50.724	1.00	59.10	6
ATOM	7911	CD	ARG	E	170	60.436	50.785	50.587	1.00	63.93	6
ATOM	7912	NE	ARG	E	170	60.309	49.382	50.992	1.00	67.80	7
ATOM	7913	CZ	ARG	E	170	59.897	48.405	50.181	1.00	68.39	6
ATOM	7914	NH1	ARG	E	170	59.577	48.664	48.916	1.00	66.05	7
ATOM	7915	NH2	ARG	E	170	59.784	47.163	50.637	1.00	71.45	7
ATOM	7916	C	ARG	E	170	65.342	50.563	49.577	1.00	56.43	6
ATOM	7917	O	ARG	E	170	65.878	50.334	50.666	1.00	57.41	8
ATOM	7918	N	PHE	E	171	65.833	50.115	48.423	1.00	54.16	7
ATOM	7919	CA	PHE	E	171	67.011	49.265	48.403	1.00	53.05	6

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ATOM   7920  CB  PHE E 171      66.665  47.926  47.747  1.00 51.94      6
ATOM   7921  CG  PHE E 171      65.392  47.326  48.259  1.00 52.21      6
ATOM   7922  CD1 PHE E 171      64.157  47.848  47.876  1.00 54.72      6
ATOM   7923  CD2 PHE E 171      65.416  46.288  49.180  1.00 52.12      6
ATOM   7924  CE1 PHE E 171      62.963  47.346  48.412  1.00 54.00      6
ATOM   7925  CE2 PHE E 171      64.233  45.781  49.719  1.00 52.15      6
ATOM   7926  CZ  PHE E 171      63.008  46.313  49.334  1.00 53.26      6
ATOM   7927  C   PHE E 171      68.181  49.909  47.698  1.00 54.03      6
ATOM   7928  O   PHE E 171      68.056  50.993  47.137  1.00 55.23      8
ATOM   7929  N   GLU E 172      69.328  49.245  47.749  1.00 55.00      7
ATOM   7930  CA  GLU E 172      70.520  49.755  47.106  1.00 56.51      6
ATOM   7931  CB  GLU E 172      71.385  50.513  48.120  1.00 58.70      6
ATOM   7932  CG  GLU E 172      71.906  49.691  49.299  1.00 63.76      6
ATOM   7933  CD  GLU E 172      72.716  50.527  50.300  1.00 66.16      6
ATOM   7934  OE1 GLU E 172      73.450  51.439  49.861  1.00 67.90      8
ATOM   7935  OE2 GLU E 172      72.635  50.266  51.526  1.00 67.48      8
ATOM   7936  C   GLU E 172      71.288  48.596  46.490  1.00 57.61      6
ATOM   7937  O   GLU E 172      71.161  47.451  46.917  1.00 57.07      8
ATOM   7938  N   ILE E 173      72.077  48.891  45.470  1.00 58.83      7
ATOM   7939  CA  ILE E 173      72.844  47.850  44.802  1.00 60.44      6
ATOM   7940  CB  ILE E 173      72.863  48.063  43.274  1.00 60.05      6
ATOM   7941  CG2 ILE E 173      73.751  47.016  42.617  1.00 60.65      6
ATOM   7942  CG1 ILE E 173      71.439  47.999  42.722  1.00 60.27      6
ATOM   7943  CD1 ILE E 173      71.357  48.283  41.245  1.00 60.88      6
ATOM   7944  C   ILE E 173      74.289  47.760  45.275  1.00 60.89      6
ATOM   7945  O   ILE E 173      75.011  48.752  45.342  1.00 60.64      8
ATOM   7946  N   LEU E 174      74.715  46.555  45.595  1.00 62.24      7
ATOM   7947  CA  LEU E 174      76.079  46.360  46.019  1.00 63.64      6
ATOM   7948  CB  LEU E 174      76.152  45.176  46.968  1.00 62.78      6
ATOM   7949  CG  LEU E 174      75.126  45.262  48.086  1.00 63.68      6
ATOM   7950  CD1 LEU E 174      75.212  44.013  48.952  1.00 63.39      6
ATOM   7951  CD2 LEU E 174      75.367  46.538  48.896  1.00 62.58      6
ATOM   7952  C   LEU E 174      76.908  46.093  44.760  1.00 65.84      6
ATOM   7953  O   LEU E 174      77.891  46.787  44.480  1.00 67.17      8
ATOM   7954  N   ASP E 175      76.494  45.102  43.979  1.00 67.20      7
ATOM   7955  CA  ASP E 175      77.227  44.772  42.763  1.00 67.40      6
ATOM   7956  CB  ASP E 175      78.496  43.999  43.148  1.00 68.39      6
ATOM   7957  CG  ASP E 175      79.385  43.673  41.961  1.00 67.83      6
ATOM   7958  OD1 ASP E 175      79.754  44.600  41.192  1.00 66.66      8
ATOM   7959  OD2 ASP E 175      79.727  42.477  41.821  1.00 67.72      8
ATOM   7960  C   ASP E 175      76.358  43.960  41.803  1.00 67.16      6
ATOM   7961  O   ASP E 175      75.405  43.291  42.216  1.00 66.38      8
ATOM   7962  N   VAL E 176      76.692  44.044  40.520  1.00 66.77      7
ATOM   7963  CA  VAL E 176      75.974  43.329  39.477  1.00 67.34      6
ATOM   7964  CB  VAL E 176      75.077  44.283  38.643  1.00 67.70      6
ATOM   7965  CG1 VAL E 176      74.430  43.524  37.479  1.00 66.11      6
ATOM   7966  CG2 VAL E 176      74.009  44.902  39.537  1.00 66.22      6
ATOM   7967  C   VAL E 176      76.979  42.692  38.541  1.00 66.94      6
ATOM   7968  O   VAL E 176      77.894  43.354  38.078  1.00 65.94      8
ATOM   7969  N   THR E 177      76.796  41.407  38.265  1.00 68.37      7
ATOM   7970  CA  THR E 177      77.682  40.671  37.362  1.00 70.46      6
ATOM   7971  CB  THR E 177      78.677  39.794  38.142  1.00 69.65      6
ATOM   7972  OG1 THR E 177      77.962  38.938  39.041  1.00 68.82      8
ATOM   7973  CG2 THR E 177      79.630  40.667  38.938  1.00 70.26      6
ATOM   7974  C   THR E 177      76.870  39.778  36.420  1.00 72.02      6
ATOM   7975  O   THR E 177      75.849  39.202  36.813  1.00 72.47      8
ATOM   7976  N   GLN E 178      77.327  39.669  35.175  1.00 73.21      7
ATOM   7977  CA  GLN E 178      76.642  38.861  34.173  1.00 74.06      6
ATOM   7978  CB  GLN E 178      76.151  39.744  33.035  1.00 75.43      6
ATOM   7979  CG  GLN E 178      75.865  41.187  33.442  1.00 77.78      6
ATOM   7980  CD  GLN E 178      74.935  41.901  32.464  1.00 79.93      6
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ATOM	7981	OE1	GLN	E	178	75.139	41.862	31.236	1.00	82.06	8
ATOM	7982	NE2	GLN	E	178	73.909	42.565	33.002	1.00	78.21	7
ATOM	7983	C	GLN	E	178	77.608	37.840	33.610	1.00	74.50	6
ATOM	7984	O	GLN	E	178	78.661	38.205	33.086	1.00	74.89	8
ATOM	7985	N	LYS	E	179	77.248	36.563	33.703	1.00	75.28	7
ATOM	7986	CA	LYS	E	179	78.107	35.482	33.209	1.00	75.34	6
ATOM	7987	CB	LYS	E	179	78.666	34.692	34.391	1.00	77.30	6
ATOM	7988	CG	LYS	E	179	79.186	35.600	35.515	1.00	81.23	6
ATOM	7989	CD	LYS	E	179	79.593	34.805	36.763	1.00	83.79	6
ATOM	7990	CE	LYS	E	179	79.779	35.727	37.981	1.00	82.73	6
ATOM	7991	NZ	LYS	E	179	78.496	36.431	38.332	1.00	82.45	7
ATOM	7992	C	LYS	E	179	77.274	34.554	32.353	1.00	74.24	6
ATOM	7993	O	LYS	E	179	76.409	33.850	32.882	1.00	74.20	8
ATOM	7994	N	LYS	E	180	77.528	34.533	31.045	1.00	72.18	7
ATOM	7995	CA	LYS	E	180	76.747	33.674	30.155	1.00	70.93	6
ATOM	7996	CB	LYS	E	180	77.062	34.017	28.694	1.00	71.21	6
ATOM	7997	CG	LYS	E	180	78.412	33.558	28.187	1.00	67.95	6
ATOM	7998	CD	LYS	E	180	78.327	32.136	27.630	1.00	67.85	6
ATOM	7999	CE	LYS	E	180	77.429	32.041	26.394	1.00	66.39	6
ATOM	8000	NZ	LYS	E	180	78.005	32.722	25.197	1.00	67.24	7
ATOM	8001	C	LYS	E	180	77.014	32.199	30.429	1.00	69.92	6
ATOM	8002	O	LYS	E	180	77.803	31.876	31.303	1.00	70.33	8
ATOM	8003	N	ASN	E	181	76.335	31.310	29.711	1.00	69.75	7
ATOM	8004	CA	ASN	E	181	76.570	29.881	29.878	1.00	70.27	6
ATOM	8005	CB	ASN	E	181	76.563	29.495	31.362	1.00	69.84	6
ATOM	8006	CG	ASN	E	181	75.395	30.060	32.112	1.00	70.39	6
ATOM	8007	OD1	ASN	E	181	74.255	30.006	31.648	1.00	75.03	8
ATOM	8008	ND2	ASN	E	181	75.659	30.587	33.299	1.00	70.26	7
ATOM	8009	C	ASN	E	181	75.658	28.932	29.097	1.00	71.10	6
ATOM	8010	O	ASN	E	181	74.438	28.918	29.276	1.00	72.53	8
ATOM	8011	N	SER	E	182	76.266	28.121	28.236	1.00	71.98	7
ATOM	8012	CA	SER	E	182	75.518	27.161	27.427	1.00	73.38	6
ATOM	8013	CB	SER	E	182	76.437	26.566	26.343	1.00	74.44	6
ATOM	8014	OG	SER	E	182	75.712	25.791	25.388	1.00	77.56	8
ATOM	8015	C	SER	E	182	74.984	26.054	28.345	1.00	73.19	6
ATOM	8016	O	SER	E	182	75.527	25.836	29.428	1.00	73.57	8
ATOM	8017	N	VAL	E	183	73.936	25.350	27.914	1.00	72.44	7
ATOM	8018	CA	VAL	E	183	73.341	24.295	28.738	1.00	71.01	6
ATOM	8019	CB	VAL	E	183	72.582	24.906	29.956	1.00	69.59	6
ATOM	8020	CG1	VAL	E	183	71.892	26.184	29.555	1.00	67.54	6
ATOM	8021	CG2	VAL	E	183	71.534	23.922	30.470	1.00	69.87	6
ATOM	8022	C	VAL	E	183	72.366	23.391	27.986	1.00	71.36	6
ATOM	8023	O	VAL	E	183	71.508	23.867	27.234	1.00	71.74	8
ATOM	8024	N	THR	E	184	72.490	22.087	28.202	1.00	71.66	7
ATOM	8025	CA	THR	E	184	71.586	21.134	27.551	1.00	73.71	6
ATOM	8026	CB	THR	E	184	72.339	19.902	26.988	1.00	72.73	6
ATOM	8027	OG1	THR	E	184	73.243	20.327	25.957	1.00	72.08	8
ATOM	8028	CG2	THR	E	184	71.353	18.897	26.392	1.00	71.99	6
ATOM	8029	C	THR	E	184	70.547	20.656	28.565	1.00	75.19	6
ATOM	8030	O	THR	E	184	70.862	20.458	29.740	1.00	75.50	8
ATOM	8031	N	TYR	E	185	69.307	20.495	28.110	1.00	76.63	7
ATOM	8032	CA	TYR	E	185	68.234	20.054	28.992	1.00	77.67	6
ATOM	8033	CB	TYR	E	185	67.084	21.074	29.004	1.00	78.57	6
ATOM	8034	CG	TYR	E	185	67.547	22.482	29.285	1.00	78.26	6
ATOM	8035	CD1	TYR	E	185	68.203	23.218	28.304	1.00	77.24	6
ATOM	8036	CE1	TYR	E	185	68.666	24.506	28.559	1.00	79.16	6
ATOM	8037	CD2	TYR	E	185	67.361	23.065	30.544	1.00	79.06	6
ATOM	8038	CE2	TYR	E	185	67.822	24.359	30.817	1.00	79.31	6
ATOM	8039	CZ	TYR	E	185	68.472	25.075	29.819	1.00	79.42	6
ATOM	8040	OH	TYR	E	185	68.919	26.357	30.067	1.00	80.13	8
ATOM	8041	C	TYR	E	185	67.725	18.723	28.516	1.00	77.68	6

ATOM	8042	O	TYR	E	185	67.578	18.509	27.314	1.00	76.95	8
ATOM	8043	N	SER	E	186	67.460	17.831	29.463	1.00	79.15	7
ATOM	8044	CA	SER	E	186	66.968	16.497	29.134	1.00	80.95	6
ATOM	8045	CB	SER	E	186	66.593	15.755	30.423	1.00	81.59	6
ATOM	8046	OG	SER	E	186	65.784	16.580	31.254	1.00	83.29	8
ATOM	8047	C	SER	E	186	65.770	16.594	28.192	1.00	81.27	6
ATOM	8048	O	SER	E	186	65.612	15.764	27.291	1.00	81.31	8
ATOM	8049	N	CYS	E	187	64.948	17.624	28.402	1.00	82.15	7
ATOM	8050	CA	CYS	E	187	63.753	17.876	27.583	1.00	83.38	6
ATOM	8051	C	CYS	E	187	64.119	18.104	26.143	1.00	83.62	6
ATOM	8052	O	CYS	E	187	63.463	17.631	25.206	1.00	82.88	8
ATOM	8053	CB	CYS	E	187	63.043	19.179	27.993	1.00	83.49	6
ATOM	8054	SG	CYS	E	187	63.980	20.757	27.703	1.00	86.50	16
ATOM	8055	N	CYS	E	188	65.204	18.841	25.993	1.00	84.35	7
ATOM	8056	CA	CYS	E	188	65.589	19.318	24.701	1.00	84.60	6
ATOM	8057	C	CYS	E	188	67.013	18.991	24.213	1.00	84.20	6
ATOM	8058	O	CYS	E	188	68.012	19.334	24.874	1.00	84.71	8
ATOM	8059	CB	CYS	E	188	65.319	20.833	24.759	1.00	85.11	6
ATOM	8060	SG	CYS	E	188	63.808	21.349	25.731	1.00	88.15	16
ATOM	8061	N	PRO	E	189	67.108	18.340	23.025	1.00	83.48	7
ATOM	8062	CD	PRO	E	189	65.864	18.064	22.267	1.00	82.84	6
ATOM	8063	CA	PRO	E	189	68.292	17.878	22.267	1.00	81.51	6
ATOM	8064	CB	PRO	E	189	67.738	17.666	20.853	1.00	82.30	6
ATOM	8065	CG	PRO	E	189	66.345	17.173	21.119	1.00	82.79	6
ATOM	8066	C	PRO	E	189	69.547	18.782	22.249	1.00	79.46	6
ATOM	8067	O	PRO	E	189	70.592	18.398	22.785	1.00	79.36	8
ATOM	8068	N	GLU	E	190	69.450	19.961	21.629	1.00	76.55	7
ATOM	8069	CA	GLU	E	190	70.592	20.878	21.529	1.00	74.34	6
ATOM	8070	CB	GLU	E	190	70.358	21.881	20.401	1.00	76.82	6
ATOM	8071	CG	GLU	E	190	69.520	21.352	19.239	1.00	80.12	6
ATOM	8072	CD	GLU	E	190	70.336	20.533	18.231	1.00	81.75	6
ATOM	8073	OE1	GLU	E	190	71.471	20.965	17.884	1.00	81.85	8
ATOM	8074	OE2	GLU	E	190	69.836	19.472	17.775	1.00	80.52	8
ATOM	8075	C	GLU	E	190	70.822	21.663	22.815	1.00	71.33	6
ATOM	8076	O	GLU	E	190	70.095	21.489	23.791	1.00	71.05	8
ATOM	8077	N	ALA	E	191	71.826	22.543	22.798	1.00	68.78	7
ATOM	8078	CA	ALA	E	191	72.142	23.390	23.957	1.00	67.15	6
ATOM	8079	CB	ALA	E	191	73.651	23.536	24.108	1.00	65.15	6
ATOM	8080	C	ALA	E	191	71.502	24.787	23.836	1.00	65.83	6
ATOM	8081	O	ALA	E	191	71.379	25.340	22.730	1.00	64.00	8
ATOM	8082	N	TYR	E	192	71.097	25.355	24.971	1.00	64.83	7
ATOM	8083	CA	TYR	E	192	70.487	26.678	24.964	1.00	65.12	6
ATOM	8084	CB	TYR	E	192	69.025	26.613	25.450	1.00	63.81	6
ATOM	8085	CG	TYR	E	192	68.096	25.953	24.462	1.00	63.14	6
ATOM	8086	CD1	TYR	E	192	67.939	24.564	24.442	1.00	64.40	6
ATOM	8087	CE1	TYR	E	192	67.146	23.934	23.468	1.00	64.53	6
ATOM	8088	CD2	TYR	E	192	67.435	26.705	23.493	1.00	62.60	6
ATOM	8089	CE2	TYR	E	192	66.642	26.094	22.521	1.00	64.04	6
ATOM	8090	CZ	TYR	E	192	66.505	24.710	22.512	1.00	64.71	6
ATOM	8091	OH	TYR	E	192	65.744	24.101	21.538	1.00	66.46	8
ATOM	8092	C	TYR	E	192	71.262	27.694	25.795	1.00	65.22	6
ATOM	8093	O	TYR	E	192	71.181	27.699	27.026	1.00	67.13	8
ATOM	8094	N	GLU	E	193	72.010	28.557	25.112	1.00	65.61	7
ATOM	8095	CA	GLU	E	193	72.792	29.606	25.773	1.00	64.70	6
ATOM	8096	CB	GLU	E	193	73.643	30.372	24.749	1.00	66.19	6
ATOM	8097	CG	GLU	E	193	74.722	29.522	24.074	1.00	69.50	6
ATOM	8098	CD	GLU	E	193	75.625	30.345	23.144	1.00	72.29	6
ATOM	8099	OE1	GLU	E	193	76.083	31.435	23.584	1.00	71.70	8
ATOM	8100	OE2	GLU	E	193	75.881	29.898	21.985	1.00	73.48	8
ATOM	8101	C	GLU	E	193	71.890	30.600	26.498	1.00	63.08	6
ATOM	8102	O	GLU	E	193	70.747	30.828	26.095	1.00	64.03	8

ATOM	8103	N	ASP	E	194	72.418	31.187	27.566	1.00 62.00	7
ATOM	8104	CA	ASP	E	194	71.683	32.168	28.340	1.00 60.31	6
ATOM	8105	CB	ASP	E	194	70.644	31.480	29.235	1.00 62.01	6
ATOM	8106	CG	ASP	E	194	71.268	30.749	30.413	1.00 64.58	6
ATOM	8107	OD1	ASP	E	194	71.200	29.504	30.448	1.00 66.44	8
ATOM	8108	OD2	ASP	E	194	71.824	31.415	31.314	1.00 64.95	8
ATOM	8109	C	ASP	E	194	72.637	32.989	29.193	1.00 59.18	6
ATOM	8110	O	ASP	E	194	73.715	32.515	29.570	1.00 59.24	8
ATOM	8111	N	VAL	E	195	72.238	34.223	29.484	1.00 56.73	7
ATOM	8112	CA	VAL	E	195	73.029	35.121	30.311	1.00 55.51	6
ATOM	8113	CB	VAL	E	195	73.019	36.555	29.763	1.00 53.92	6
ATOM	8114	CG1	VAL	E	195	73.686	37.498	30.752	1.00 53.41	6
ATOM	8115	CG2	VAL	E	195	73.738	36.595	28.431	1.00 55.34	6
ATOM	8116	C	VAL	E	195	72.453	35.145	31.715	1.00 56.03	6
ATOM	8117	O	VAL	E	195	71.270	35.400	31.907	1.00 56.70	8
ATOM	8118	N	GLU	E	196	73.292	34.868	32.702	1.00 57.06	7
ATOM	8119	CA	GLU	E	196	72.834	34.870	34.077	1.00 57.01	6
ATOM	8120	CB	GLU	E	196	73.402	33.673	34.821	1.00 57.41	6
ATOM	8121	CG	GLU	E	196	72.908	33.555	36.238	1.00 61.42	6
ATOM	8122	CD	GLU	E	196	73.533	32.383	36.968	1.00 62.69	6
ATOM	8123	OE1	GLU	E	196	73.377	31.235	36.493	1.00 64.88	8
ATOM	8124	OE2	GLU	E	196	74.184	32.604	38.013	1.00 64.76	8
ATOM	8125	C	GLU	E	196	73.315	36.160	34.715	1.00 57.51	6
ATOM	8126	O	GLU	E	196	74.518	36.427	34.755	1.00 60.16	8
ATOM	8127	N	VAL	E	197	72.375	36.969	35.192	1.00 55.54	7
ATOM	8128	CA	VAL	E	197	72.712	38.226	35.829	1.00 54.09	6
ATOM	8129	CB	VAL	E	197	71.853	39.380	35.278	1.00 50.90	6
ATOM	8130	CG1	VAL	E	197	72.241	40.685	35.932	1.00 47.64	6
ATOM	8131	CG2	VAL	E	197	72.030	39.471	33.782	1.00 49.59	6
ATOM	8132	C	VAL	E	197	72.473	38.067	37.325	1.00 56.97	6
ATOM	8133	O	VAL	E	197	71.414	37.614	37.748	1.00 58.03	8
ATOM	8134	N	SER	E	198	73.476	38.409	38.125	1.00 58.05	7
ATOM	8135	CA	SER	E	198	73.338	38.300	39.562	1.00 58.55	6
ATOM	8136	CB	SER	E	198	74.550	37.584	40.174	1.00 58.65	6
ATOM	8137	OG	SER	E	198	74.556	36.209	39.811	1.00 60.87	8
ATOM	8138	C	SER	E	198	73.182	39.685	40.155	1.00 58.53	6
ATOM	8139	O	SER	E	198	74.049	40.549	40.004	1.00 59.57	8
ATOM	8140	N	LEU	E	199	72.060	39.895	40.823	1.00 58.51	7
ATOM	8141	CA	LEU	E	199	71.803	41.176	41.434	1.00 59.74	6
ATOM	8142	CB	LEU	E	199	70.361	41.612	41.186	1.00 59.28	6
ATOM	8143	CG	LEU	E	199	69.921	42.861	41.953	1.00 58.45	6
ATOM	8144	CD1	LEU	E	199	70.758	44.059	41.543	1.00 57.64	6
ATOM	8145	CD2	LEU	E	199	68.466	43.127	41.669	1.00 57.53	6
ATOM	8146	C	LEU	E	199	72.039	41.084	42.917	1.00 61.63	6
ATOM	8147	O	LEU	E	199	71.226	40.500	43.640	1.00 64.16	8
ATOM	8148	N	ASN	E	200	73.163	41.637	43.366	1.00 61.69	7
ATOM	8149	CA	ASN	E	200	73.486	41.658	44.780	1.00 58.91	6
ATOM	8150	CB	ASN	E	200	74.981	41.477	44.994	1.00 61.22	6
ATOM	8151	CG	ASN	E	200	75.355	41.522	46.454	1.00 63.36	6
ATOM	8152	OD1	ASN	E	200	74.686	40.916	47.295	1.00 64.82	8
ATOM	8153	ND2	ASN	E	200	76.426	42.235	46.770	1.00 64.37	7
ATOM	8154	C	ASN	E	200	73.048	43.026	45.280	1.00 56.95	6
ATOM	8155	O	ASN	E	200	73.610	44.056	44.905	1.00 58.64	8
ATOM	8156	N	PHE	E	201	72.018	43.030	46.109	1.00 54.18	7
ATOM	8157	CA	PHE	E	201	71.474	44.260	46.650	1.00 52.16	6
ATOM	8158	CB	PHE	E	201	70.257	44.688	45.844	1.00 50.83	6
ATOM	8159	CG	PHE	E	201	69.065	43.780	46.028	1.00 47.47	6
ATOM	8160	CD1	PHE	E	201	67.923	44.233	46.681	1.00 47.04	6
ATOM	8161	CD2	PHE	E	201	69.107	42.458	45.601	1.00 44.93	6
ATOM	8162	CE1	PHE	E	201	66.843	43.382	46.911	1.00 45.49	6
ATOM	8163	CE2	PHE	E	201	68.043	41.608	45.829	1.00 43.88	6

ATOM	8164	CZ	PHE	E	201	66.905	42.072	46.488	1.00	43.86	6
ATOM	8165	C	PHE	E	201	71.029	43.977	48.066	1.00	53.50	6
ATOM	8166	O	PHE	E	201	71.001	42.823	48.504	1.00	53.30	8
ATOM	8167	N	ARG	E	202	70.650	45.032	48.770	1.00	55.04	7
ATOM	8168	CA	ARG	E	202	70.195	44.915	50.146	1.00	57.24	6
ATOM	8169	CB	ARG	E	202	71.399	44.898	51.084	1.00	59.58	6
ATOM	8170	CG	ARG	E	202	72.078	46.254	51.130	1.00	64.26	6
ATOM	8171	CD	ARG	E	202	73.337	46.278	51.951	1.00	65.59	6
ATOM	8172	NE	ARG	E	202	73.935	47.606	51.908	1.00	67.13	7
ATOM	8173	CZ	ARG	E	202	75.140	47.891	52.386	1.00	68.53	6
ATOM	8174	NH1	ARG	E	202	75.870	46.930	52.942	1.00	69.03	7
ATOM	8175	NH2	ARG	E	202	75.612	49.129	52.303	1.00	68.11	7
ATOM	8176	C	ARG	E	202	69.321	46.121	50.499	1.00	57.27	6
ATOM	8177	O	ARG	E	202	69.370	47.167	49.839	1.00	56.88	8
ATOM	8178	N	LYS	E	203	68.528	45.974	51.551	1.00	56.76	7
ATOM	8179	CA	LYS	E	203	67.689	47.063	52.011	1.00	57.10	6
ATOM	8180	CB	LYS	E	203	66.755	46.583	53.109	1.00	58.42	6
ATOM	8181	CG	LYS	E	203	65.904	47.682	53.702	1.00	60.29	6
ATOM	8182	CD	LYS	E	203	65.112	47.157	54.883	1.00	64.62	6
ATOM	8183	CE	LYS	E	203	64.222	48.241	55.471	1.00	67.46	6
ATOM	8184	NZ	LYS	E	203	63.171	48.696	54.504	1.00	70.79	7
ATOM	8185	C	LYS	E	203	68.623	48.101	52.603	1.00	56.53	6
ATOM	8186	O	LYS	E	203	69.715	47.769	53.060	1.00	58.18	8
ATOM	8187	N	LYS	E	204	68.190	49.352	52.629	1.00	53.82	7
ATOM	8188	CA	LYS	E	204	69.021	50.392	53.207	1.00	52.45	6
ATOM	8189	CB	LYS	E	204	68.545	51.766	52.731	1.00	50.86	6
ATOM	8190	CG	LYS	E	204	68.852	52.110	51.279	1.00	44.94	6
ATOM	8191	CD	LYS	E	204	68.253	53.462	50.970	1.00	45.54	6
ATOM	8192	CE	LYS	E	204	68.744	54.050	49.669	1.00	46.91	6
ATOM	8193	NZ	LYS	E	204	68.388	53.268	48.463	1.00	48.94	7
ATOM	8194	C	LYS	E	204	68.991	50.317	54.747	1.00	54.01	6
ATOM	8195	O	LYS	E	204	68.119	49.668	55.329	1.00	54.82	8
ATOM	8196	N	GLY	E	205	69.958	50.969	55.394	1.00	53.51	7
ATOM	8197	CA	GLY	E	205	70.025	50.987	56.848	1.00	52.96	6
ATOM	8198	C	GLY	E	205	69.747	52.400	57.344	1.00	54.24	6
ATOM	8199	OT1	GLY	E	205	69.326	53.224	56.507	1.00	53.02	8
ATOM	8200	OT2	GLY	E	205	69.937	52.697	58.551	1.00	54.73	8
ATOM	8201	OH2	WAT	W	1	42.707	26.844	16.535	1.00	50.04	8
ATOM	8202	OH2	WAT	W	2	46.115	22.922	8.819	1.00	33.72	8
ATOM	8203	OH2	WAT	W	3	49.921	22.962	13.240	1.00	27.71	8
ATOM	8204	OH2	WAT	W	4	48.219	24.526	9.434	1.00	48.75	8
ATOM	8205	OH2	WAT	W	5	27.826	41.690	17.095	1.00	41.54	8
ATOM	8206	OH2	WAT	W	6	24.872	36.589	8.613	1.00	51.20	8
ATOM	8207	OH2	WAT	W	7	36.046	60.034	17.934	1.00	33.21	8
ATOM	8208	OH2	WAT	W	8	35.043	57.811	16.418	1.00	28.29	8
ATOM	8209	OH2	WAT	W	9	55.882	56.455	16.997	1.00	31.72	8
ATOM	8210	OH2	WAT	W	10	55.717	62.292	9.132	1.00	41.99	8
ATOM	8211	OH2	WAT	W	11	54.077	57.638	15.628	1.00	35.89	8
ATOM	8212	OH2	WAT	W	12	60.807	36.700	17.893	1.00	31.22	8
ATOM	8213	OH2	WAT	W	13	66.541	42.748	13.082	1.00	52.94	8
ATOM	8214	OH2	WAT	W	14	64.752	41.327	9.587	1.00	53.75	8
ATOM	8215	CA+2	CA2	I	1	56.450	11.097	37.999	1.00	76.79	20
ATOM	8216	CL-1	CL1	I	2	37.092	21.684	12.754	1.00	43.91	17
ATOM	8217	CA+2	CA2	I	3	17.667	23.110	38.506	1.00	80.38	20
ATOM	8218	CL-1	CL1	I	4	20.502	44.774	13.190	1.00	62.37	17
ATOM	8219	CA+2	CA2	I	5	16.762	64.154	38.299	1.00	85.82	20
ATOM	8220	CL-1	CL1	I	6	37.412	67.363	13.067	1.00	45.17	17
ATOM	8221	CA+2	CA2	I	7	55.038	76.858	37.301	1.00	71.00	20
ATOM	8222	CL-1	CL1	I	8	64.026	57.746	12.334	1.00	69.47	17
ATOM	8223	CA+2	CA2	I	9	79.499	45.067	37.836	1.00	85.28	20
ATOM	8224	CL-1	CL1	I	10	64.286	29.844	12.440	1.00	48.05	17

ATOM	8225	C1	HEP	L	1	31.694	22.169	23.679	1.00109.78	6
ATOM	8226	C2	HEP	L	1	32.042	22.822	25.000	1.00106.01	6
ATOM	8227	C3	HEP	L	1	33.258	20.667	25.468	1.00 99.68	6
ATOM	8228	C4	HEP	L	1	34.107	19.901	26.462	1.00 97.90	6
ATOM	8229	C5	HEP	L	1	33.049	21.220	28.203	1.00 99.77	6
ATOM	8230	C6	HEP	L	1	32.154	21.953	27.266	1.00101.85	6
ATOM	8231	C7	HEP	L	1	34.051	19.067	28.833	1.00 98.50	6
ATOM	8232	C8	HEP	L	1	35.030	19.802	29.773	1.00 97.76	6
ATOM	8233	O4	HEP	L	1	34.441	19.860	31.064	1.00 96.20	8
ATOM	8234	N1	HEP	L	1	32.880	22.043	25.968	1.00103.11	7
ATOM	8235	S1	HEP	L	1	31.207	23.336	22.418	1.00113.66	16
ATOM	8236	O1	HEP	L	1	31.826	22.878	21.182	1.00113.59	8
ATOM	8237	O2	HEP	L	1	31.477	24.685	22.941	1.00111.64	8
ATOM	8238	O3	HEP	L	1	29.701	23.322	22.307	1.00111.51	8
ATOM	8239	N2	HEP	L	1	33.333	19.839	27.737	1.00 98.16	7
ATOM	8240	C1	HEP	L	2	19.833	49.708	24.248	1.00108.88	6
ATOM	8241	C2	HEP	L	2	20.653	49.684	25.518	1.00104.63	6
ATOM	8242	C3	HEP	L	2	19.090	47.814	26.172	1.00100.27	6
ATOM	8243	C4	HEP	L	2	18.728	46.788	27.241	1.00 98.30	6
ATOM	8244	C5	HEP	L	2	19.702	48.326	28.859	1.00100.12	6
ATOM	8245	C6	HEP	L	2	20.022	49.380	27.845	1.00101.78	6
ATOM	8246	C7	HEP	L	2	18.080	46.646	29.663	1.00 97.02	6
ATOM	8247	C8	HEP	L	2	19.186	46.065	30.550	1.00 96.36	6
ATOM	8248	O4	HEP	L	2	19.161	46.714	31.805	1.00 95.77	8
ATOM	8249	N1	HEP	L	2	20.281	48.676	26.560	1.00102.78	7
ATOM	8250	S1	HEP	L	2	20.640	50.530	22.892	1.00112.59	16
ATOM	8251	O1	HEP	L	2	20.348	49.765	21.697	1.00113.24	8
ATOM	8252	O2	HEP	L	2	22.024	50.791	23.309	1.00111.25	8
ATOM	8253	O3	HEP	L	2	20.059	51.924	22.770	1.00111.32	8
ATOM	8254	N2	HEP	L	2	18.478	47.544	28.507	1.00 98.39	7
ATOM	8255	C1	HEP	L	3	42.028	70.369	23.900	1.00109.55	6
ATOM	8256	C2	HEP	L	3	42.091	69.312	25.003	1.00104.54	6
ATOM	8257	C3	HEP	L	3	40.178	70.594	25.988	1.00 97.17	6
ATOM	8258	C4	HEP	L	3	39.192	70.688	27.124	1.00 96.78	6
ATOM	8259	C5	HEP	L	3	40.844	69.540	28.502	1.00 98.62	6
ATOM	8260	C6	HEP	L	3	41.854	69.476	27.408	1.00100.28	6
ATOM	8261	C7	HEP	L	3	39.103	70.891	29.639	1.00 97.37	6
ATOM	8262	C8	HEP	L	3	38.600	69.616	30.336	1.00 97.34	6
ATOM	8263	O4	HEP	L	3	39.310	69.466	31.552	1.00 95.42	8
ATOM	8264	N1	HEP	L	3	41.104	69.418	26.123	1.00100.25	7
ATOM	8265	S1	HEP	L	3	42.851	69.897	22.390	1.00113.40	16
ATOM	8266	O1	HEP	L	3	41.999	70.352	21.301	1.00112.83	8
ATOM	8267	O2	HEP	L	3	43.216	68.464	22.535	1.00111.97	8
ATOM	8268	O3	HEP	L	3	44.208	70.580	22.342	1.00111.22	8
ATOM	8269	N2	HEP	L	3	39.982	70.756	28.394	1.00 97.91	7
ATOM	8270	C1	HEP	L	4	67.843	54.529	23.109	1.00109.23	6
ATOM	8271	C2	HEP	L	4	67.696	54.053	24.549	1.00105.70	6
ATOM	8272	C3	HEP	L	4	67.448	56.488	25.071	1.00101.29	6
ATOM	8273	C4	HEP	L	4	67.199	57.526	26.150	1.00 99.73	6
ATOM	8274	C5	HEP	L	4	68.223	55.960	27.701	1.00100.32	6
ATOM	8275	C6	HEP	L	4	68.526	54.948	26.646	1.00101.68	6
ATOM	8276	C7	HEP	L	4	68.126	58.362	28.296	1.00 99.92	6
ATOM	8277	C8	HEP	L	4	67.284	58.007	29.528	1.00100.01	6
ATOM	8278	O4	HEP	L	4	68.179	57.751	30.594	1.00100.41	8
ATOM	8279	N1	HEP	L	4	67.472	55.082	25.609	1.00103.08	7
ATOM	8280	S1	HEP	L	4	67.556	53.252	21.895	1.00112.53	16
ATOM	8281	O1	HEP	L	4	66.829	53.860	20.813	1.00112.71	8
ATOM	8282	O2	HEP	L	4	67.011	52.080	22.599	1.00111.24	8
ATOM	8283	O3	HEP	L	4	68.908	52.765	21.423	1.00111.51	8
ATOM	8284	N2	HEP	L	4	68.258	57.354	27.169	1.00 99.66	7
ATOM	8285	C1	HEP	L	5	62.836	24.327	23.511	1.00108.64	6

ATOM	8286	C2	HEP	L	5	62.164	25.268	24.495	1.00104.37	6
ATOM	8287	C3	HEP	L	5	64.426	25.352	25.555	1.00 99.26	6
ATOM	8288	C4	HEP	L	5	65.270	25.934	26.676	1.00 98.50	6
ATOM	8289	C5	HEP	L	5	63.215	26.126	27.960	1.00 99.10	6
ATOM	8290	C6	HEP	L	5	62.366	25.505	26.903	1.00100.20	6
ATOM	8291	C7	HEP	L	5	65.381	26.089	29.165	1.00 98.56	6
ATOM	8292	C8	HEP	L	5	65.085	27.500	29.708	1.00 98.97	6
ATOM	8293	O4	HEP	L	5	64.379	27.406	30.942	1.00 98.36	8
ATOM	8294	N1	HEP	L	5	63.001	25.830	25.594	1.00101.58	7
ATOM	8295	S1	HEP	L	5	61.935	24.146	21.985	1.00112.71	16
ATOM	8296	O1	HEP	L	5	62.912	24.120	20.912	1.00112.36	8
ATOM	8297	O2	HEP	L	5	60.852	25.151	22.006	1.00111.63	8
ATOM	8298	O3	HEP	L	5	61.166	22.846	22.024	1.00111.95	8
ATOM	8299	N2	HEP	L	5	64.610	25.582	27.957	1.00 98.40	7
END										

Atom Type	Residue	#	X	Y	Z	OCC	B

Table 1: Structural coordinates of AChBP

"Atom type" refers to the element whoose coordinate are measured. The first letter in the column defines the element.

"Residue" refers to the amino acid in the AChBP protein sequence, using the standard three letter abbreviations known in the art.

"#" refers to the residue number.

"X, Y, Z" crystallographically define the atomic position, in three-dimensional space, of the element measured.

"OCC" is the occupancy volume.

"B" is a thermal factor that measures movement of the atom around its atomic center.

Claims

1. A water-soluble protein derived from a mollusc being capable of binding a ligand of a ligand-gated receptor.

2. The protein of claim 1, wherein the ligand is acetylcholine, gamma-amino-butyric acid (GABA), glycine or serotonin.

3. The protein of claim 2, wherein said protein is a acetylcholine-binding protein (AChBP).

4. The protein of any one of claim 1 to 3 which is capable of forming multimers.

5. The protein of any one of claims 1 to 4 which is derived form a Pulmonata species, preferably from a Basommatophora species.

6. The protein of any one of claims 1 to 5 comprising an amino acid sequence selected from the group consisting of:
   (a) an amino acid sequence as depicted in any one of SEQ ID Nos. 2, 4, 6 or 8 or a functional equivalent thereof, or a fragment of at least 5 continuous amino acids thereof;
   (b) an amino acid sequence having at least 30% amino acid identity to the amino acid sequence of any one of SEQ ID Nos. 2, 4, 6 or 8.

7. A water-soluble ligand binding protein capable of binding a ligand of a ligand-gated receptor and comprising at least 5 continuous amino acids of the aminoacid sequence depicted in any one of SEQ ID Nos. 2, 4, 6 or 8 and/or said protein is detectable by a monoclonal or polyclonal antibody which recognises, preferably with a binding affinity of at least 10^{-7}M, a protein of any one of claims 1 to 6.

8. A water-soluble protein being capable of binding a ligand of a ligand-gated receptor comprising
   (a) at least the amino acids of the water-soluble protein of any one of claims 1 to 6 determining solubility of said protein, in the same or corresponding positions as in said protein; and
   (b) at least 4 amino acids determining binding to said ligand.

9. The protein of claim 7 or 8 which is capable of forming multimers.

10. The protein of any one of claims 7 to 9 comprising 200-240 amino acids.

11. The protein of any one of claims 7 to 10, wherein the ligand is acetylcholine, nicotine, lophotoxin, d-tubocurarine, carbamylcholine, galanthamine or epibatidine.

12. The protein of any one of claims 1 to 11 , wherein said ligand-gated receptor is derived from an arthropod (preferably insect), a plant (preferably a higher plant, most preferably a seed plant) or a chordate (preferably a mammalian, most preferably human).

13. The protein of any one of claims 7 to 12, wherein said ligand-gated receptor is a nicotinic acetylcholine receptor.

14. The protein of any one of claims 7 to 13, wherein said amino acids determining solubility are in the same positions as in the AChBP having the amino acid sequence as depicted in any one of SEQ ID Nos. 2, 4, 6 or 8; preferably in which said solubility-determining amino acids comprise solvent accessible regions in the crystal structure according to Figure 10.

15. The protein of any one of claims 7 to 14 comprising an amino acid sequence having at least 40% amino acid identity to the amino acid sequence 20-223 of any one of SEQ ID Nos. 2, 4, 6 or 8, in which the ligand binding amino acids have been replaced with the corresponding amino acids of a ligand-gated receptor.

16. The protein of any one of claims 7 to 15, in which said solubility-determining amino acids (a) comprise hydrophilic amino acids (Asp, Glu, Arg, Lys) from the sequences 20-44, 73-81, 86-92, 112-120, 135-152, 166-189, 196-20, 209-213, and/or 219-227 of SEQ ID No. 2.

17. The protein of claim 16, in which said solubility determining amino acids (a) comprise amino acids Asp(36), Asp(68), Glu(115), Arg(137), Asp(143), Asp(148), Glu(150), Arg(167), Arg(189), Glu(215) of SEQ ID No.2, wherein

Asp may be exchanged for Glu and vice versa and Lys may be exchanged for Arg and vice versa.

18. The protein of any one of claims 7 to 17 which further comprises the amino acids Cys(142), Thr(149), Ala(153), Thr(154), Cys(155), Arg(156), Ile(157) and/or Lys(158) of SEQ ID No. 2.

19. The protein of any one of claims 7 to 17 which comprises the amino acids (b) Pro(39), Trp(77), Trp(101), Pro(103), Asp(194), and/or Ser(161) of SEQ ID No. 2.

20. The protein of any one of claims 7 to 19 in which the amino acid sequences 165-169 and/or 200-203 of SEQ ID No. 2 have been exchanged with the corresponding sequence of the ligand-gated receptor.

21. The protein of any one of claims 7 to 20 which is capable of binding a ligand of an acetylcholine receptor, in which at least one of the amino acid sequences Trp(101) - Tyr(T08), Trp(162) - His(164) and Tyr(204) - Tyr(211) of SEQ ID No. 2 have been exchanged with the corresponding sequence of the acetylcholine receptor.

22. A method for the production of a water-soluble ligand-gated receptor or a corresponding ligand-binding domain or for improving the water solubility and accessibility to crystallization of such a receptor or domain, said method comprising altering the amino acid sequence of the extracellular domain of a ligand-gated receptor by way of substituting, adding, deleting or modifying at least one amino acid at a position corresponding to an amino acid determining or contributing to the water-solubility of the protein of any one of claims 1 to 21.

23. The method of claim 22, wherein the ligand-gated receptor is defined as in any one of claims 1 to 21.

24. The method of claim 22 or 23, wherein at least one amino acid is altered to the corresponding amino acid of the amino acid sequence depicted in any one of SEQ ID Nos. 2, 4, 6 or 8, or to a an equivalent amino acid, preferably

in which said solubility-determining amino acids comprise solvent accessible regions in the crystal structure according to Figure 10.

25. The method of any one of claims 22 to 24, wherein loop Cys123-Cys136 of SEQ ID No. 2 is inserted into the corresponding region of the ligand binding domain of the ligand-gated receptor.

26. The method of any one of claims 22 to 25 further comprising

(a) culturing a host cell transfected with and capable of expressing a polynucleotide comprising a nucleotide sequence encoding the altered amino acid sequence; and optionally

(b) recovering said water-soluble ligand-gated receptor or corresponding ligand-binding domain from the culture.

27. A water-soluble ligand-gated receptor or ligand-binding domain obtainable by the method of any one of claims 22 to 26.

28. The protein of any one of claims 1 to 21 or 27 further comprising a spacer sequence allowing coupling with a carrier body.

29. A fusion protein comprising the water-soluble ligand-binding protein of any one of claims 1 to 21, 27 or 28, or a binding fragment thereof and a fragment of a ligand-gated receptor

30. A dimer or pentamer consisting of at least one monomer comprising a protein of any one of claims 1 to 21 or 27 to 29.

31. A ligand-gated ion channel comprising a protein of any one of claims 1 to 21 or 27 to 29 or the dimer or pentamer of claim 30.

32. One or more polynucleotides encoding the protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30 or the ligand-gated ion channel of claim 31.

33. The polynucleotide(s) of claim 32 which comprise(s)

(a) a nucleotide sequence having at least 15 continuous nucleotides of the nucleotide sequence depicted in any one of SEQ ID Nos. 1, 3, 5 or 7 or a degenerated sequence thereof; or

(b) a nucleotide sequence capable of hybridizing to a nucleotide sequence of (a) under stringent hybridisation conditions.

34. The polynucleotide(s) of claim 32 or 33 which is(are) operatively linked to heterologous expression control sequences allowing expression inprokaryotic or eukaryotic cells.

35. One or more vector(s) containing the polynucleotide(s) of any one of claims 32 to 34.

36. A host cell genetically engineered with the polynucleotide(s) of any one claims 32 to 34 or with the vector(s) of claim 35.

37. An antigen comprising an epitope of at least 5 continuous amino acids of the amino acid sequence depicted in any one of SEQ ID Nos. 2, 4, 6 or 8 and/or said epitope is detectable by a monoclonal or polyclonal antibody which recognises, preferably with a binding affinity of at least 10^{-7}M, a protein of any one of claims 1 to 6.

38. An antibody specifically recognizing the protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30, the ligand-gated ion channel of claim 31 or the antigen of claim 37.

39. An oligonucleotide probe comprising a nucleotide sequence having at least 15 continuous nucleotides of a polynucleotide of any one claims 32 to 34 or encoding the antigen of claim 37.

40. A composition comprising the protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30, the ligand-gated ion channel of claim 31, the polynucleotide(s) of any one claims 32 to 34, the vector(s) of claim 35, the host cell of claim 36, the antigen of claim 37, the antibody of claim 38, or an oligonucleotide probe of claim 39; and optionally suitable means for detection or performing a ligand-receptor binding assay.

41. A method for identifying an agonist/activator or antagonist/inhibitor of a ligand-gated receptor comprising the steps of:

(a) contacting the water-soluble ligand-binding protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30, the ligand-gated ion channel of claim 31 or a cell expressing said protein in the presence of components capable of providing a detectable signal in response to ligand binding with a compound to be screened under conditions that permit binding of said compound to the ligand-binding protein; and

(b) detecting the presence or absence of a signal generated from the binding activity of the ligand-binding protein, wherein the presence/increase and absence/decrease of the signal is indicative for an agonist/activator and antagonist/inhibitor, respectively, of a ligand-gated receptor.

42. A crystal of a protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30 or the ligand-gated ion channel of claim 31.

43. A crystal of a protein-ligand complex comprising a protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30 or the ligand-gated ion channel of claim 31; and a ligand.

44. The crystal of claim 43, wherein the ligand comprises an N-alkylated hydroxyalkyl and/or a quaternary ammonium ion.

45. The crystal of claim 43, wherein the ligand comprises 4-(2-Hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES), B-bippinatin, lophotoxin, d-tubocurarine, carbamylcholine, galanthamine, epibatidine or alpha-bungarotoxin.

46. The crystal of any one of claims 42 to 45, wherein the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the protein or protein-ligand complex to a resolution of greater than 5.0, preferably greater than 4.0 Angstroms.

47. The crystal of any one claims 42 to 46, wherein the protein has an amino acid sequence of amino acids 20 to 223 of SEQ ID No. 2, or an amino acid

sequence that differs from amino acid 20 to 223 of SEQ ID No. 2 by only having conservative substitutions.

48. The crystal of claim 47, wherein the ligand is HEPES.

49. The crystal of claim 46 having (1) a space group of $P2_12_12_1$ and a unit cell of dimensions of a=120.6Å, b=137.0Å and c=161.5Å; (2) a space group of $P4_22_12$ and a unit cell of dimensions of a=b=141.6Å and c=120.8Å or (3) a space group of $P2_1$ and a unit cell of dimensions of a=121.1Å, b=162.1Å, c=139.4Å, ß=90.1°.

50. The crystal of any one of claims 42 to 49, wherein the protein has secondary structural elements that include .alpha.-helix and antiparallel .beta.-sheets as shown in Figure 7, 10, 11 and/or 12.

51. The crystal of any one claims 42 to 50 having a three-dimensional structure as defined by atomic coordinates shown in Table 1.

52. The crystal of any one of claims 42 to 51 having a binding cavity as shown in Figure 6, 8, 9 and/or 13.

53. A method of using the crystal of any one of claims 42 to 52 in a drug screening assay comprising:

(a) selecting a potential ligand by performing structure assisted drug design with the three-dimensional structure determined for the crystal, wherein said selecting is performed in conjunction with computer modeling; optionally

(b) contacting the potential ligand with the ligand binding domain of the ligand-gated receptor in an in vitro or in vivo assay; and

(c) detecting the binding of the potential ligand for the ligand binding domain.

54. The method of claim 53, wherein the ligand-gated receptor is a nicotinic acetylcholine receptor.

55. The method of claim 53 or 54 further comprising:

(d) forming a supplemental crystal of a protein-ligand complex by co-crystallization or soaking the crystal of the water-soluble ligand-binding protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30 or the ligand-gated ion channel of claim 31, with a potential drug, wherein the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the protein-ligand complex to a resolution of greater than 5.0, preferably greater than 4.0 Angstroms, more preferably greater than 3;

(e) determining the three-dimensional structure of the supplemental crystal;

(f) selecting a candidate drug by performing a structure assisted drug design with the three-dimensional structure determined for the supplemental crystal, wherein said selecting is performed in conjunction with computer modeling; optionally

(g) contacting the candidate drug with a cell that expresses the ligand-gated receptor; and

(h) detecting a cell response; wherein a candidate drug is identified as a drug when the cell response is altered compared to a cell that has not been contacted with the candidate compound.

56. The method of any one of claims 53 to 55 further comprising an initial step that precedes step (a) wherein said initial step consists of determining the three-dimensional structure of a crystal comprising a protein-ligand complex formed between the water-soluble ligand-binding protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30 or the ligand-gated ion channel of claim 31, and the ligand of the ligand-gated receptor, wherein the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the protein-ligand complex to a resolution of greater than 5.0, preferably greater than 4.0 Angstroms.

57. A method of growing a crystal of a protein-ligand complex comprising:

(a) contacting the water-soluble ligand-binding protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30 or the ligand-gated ion channel of claim 31 with a ligand of a ligand-gated receptor, wherein the water-soluble ligand-binding protein forms a protein-ligand complex with the ligand; and

(b) growing the crystal of the protein-ligand complex; wherein the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the protein-ligand complex to a resolution of greater than 5.0, preferably greater than 4.0 Angstroms.

58. A drug screening assay comprising soaking the crystal of any one of claims 42 to 52 in a solution of compounds to be screened and detecting the binding of the compound to the ligand-binding protein.

59. The method of claim 57 or 58, wherein said ligand comprises an alkylated nitrogen and/or quaternary ammonium ion.

60. A method of increasing or decreasing the affinity of a drug to a ligand-gated receptor, comprising

(a) performing structure assisted drug design with the three-dimensional structure determined for the crystal of any one of claims 42 to 52, wherein said drug design is performed in conjunction with computer modeling; and

(b) modifying said drug to alter or eliminate a portion thereof suspected of interacting with a binding site of the binding cavity or with a non-specific binding site of the protein in the crystal.

61. The method of claim 60, wherein step (a) further comprises the steps of a method of any one of claims 53 to 59.

62. The method of claim 60 or 61, further comprising after step (b), the additional step of :

(c) repeating the method used to perform structure assisted drug design according to step (a) using the modified drug according to step (b).

63. A method of drug design comprising the step of using the structural coordinates of a water-soluble ligand-binding protein crystal comprising the coordinates of Table 1, to computationally evaluate a chemical entity for associating with the ligand-binding site or a non-specific binding site of a ligand-binding protein.

64. The method of any one of claims 53 to 63, wherein the identified drug prevents or promotes correct assembly of a ligand-gated ion channel.

65. The method of any one of claims 53 to 63, wherein the identified drug binds to a non-specific binding site of a ligand-gated ion channel.

66. The method of any one of claims 53 to 65 further comprising synthesizing the drug in a therapeutically effective amount.

67. A drug produced by the method of claim 66 or a pro-drug thereof.

68. The drug of claim 67 which interacts with a ligand-gated receptor comprising a pentamer of claim 30 with monomers A to E, wherein the drug binds to one or more primary contact regions of a monomer (residues from A contacting B) defined by amino acid residues 15 to 21, 44 to 47, 85 to 87, 91 to 94, 122 to 124, 143 to 146, 149, 185 to 187 of the mature protein of SEQ ID No. 2 and/or to one or more of the complementary contact regions of the other monomer (from B contacting A, (identical to residues on A contacting E) defined by amino acid residues 3 to 4, 7 to 8, 11, 37 to 39, 53, 75 to 77, 96 to 104, 114 to 118 and 163-170 of the mature protein of SEQ ID No. 2; or to the contact regions as identified in Figure 14; or to the corresponding contact regions of the monomers of a ligand-gated ion channel.

69. The drug of claim 68, wherein the ligand-gated ion channel is the nicotinic acetylcholine receptor and the order of the monomers is $\alpha\gamma\alpha\beta\delta$.

70. A computer readable medium comprising a nucleotide sequence of the polynucleotide(s) of any one of claims 32 to 34, an amino acid sequence of a protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30 or the ligand-gated ion channel of claim 31, or the structural coordinates of a crystal of any one of claims 40 to 50.

71. A device comprising the computer readable medium of claim 70.

72. Use of the computer readable medium of claim 70 or the device of claim 71 for modeling an antagonist/inhibitor or agonist/activator of a ligand-gated receptor.

73. Use of the crystal of any one of claims 42 to 52 or its structural coordinates as a template for modeling the 3D structure of a ligand-gated ion channel.

74. Use of the polynucleotide(s) of any one of claims 32 to 34, the protein of any one of claims 1 to 21 or 27 to 29, the dimer or pentamer of claim 30, the ligand-gated ion channel of claim 31, the vector(s) of claim 35, the host cell of claim 36, the antigen of claim 37, the antibody of claim 38, an oligonucleotide probe of claim 39, the crystal of any one of claims 42 to 52 or a method of any one of claims 53 to 66 for screening or profiling putative ligands of ligand-gated receptors.

75. Use of an antagonist/inhibitor or agonist/activator identified according to a method of any one of claims 53 to 66 for the preparation of a pharmaceutical composition for the treatment of a ligand-gated ion channel mediated or related disorder.

76. The use of claim 75, wherein the antagonist/inhibitor is or is derived from the protein of any one of claims 1 to 21 or 27 to 29, an antigen of claim 37, an antibody of claim 38 or from a toxin of the ligand-gated ion channel.

77. The use of claim 75, wherein the agonist/activator is or is derived from a the protein of any one of claims 1 to 21 or 27 to 29, an antigen of claim 37, an antibody of claim 38 or from epibatidine, acetylcholine, choline, nicotine, carbachol, serotonin or GABA.

78. The use of any one claims 75 to 77, wherein the ligand-gated ion channel is the nicotinic acetylcholine receptor and said mediated or related disorder is Tourette's syndrome, Alzheimer's disease, addiction to nicotine or schizophrenia.

79. Use of ligand of a ligand-gated receptor for identifying and isolating a water-soluble ligand-binding protein from a mollusc.

80. The use of claim 79, wherein said ligand is α-bungarotoxin.

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```
L-AChBP_T1.      --MRRNIFCLACLWIVQACLSLDRADILYNIRQTSRPDVIPTQRDRPVAVSVSLKFINIL
L-AChBP_T2.      --MRRNIFCLACLWIVQGCLSLDRADILYNIRQTSRPDVIPTQRDRPVAVSVSLKFINIL
B-AChBP_T1.      MAELRRIILLLCTIAFHVSHGQIRWTLLNQITGES--DVIPLSNNTPLNVSLNFKLMNIV
B-AChBP_T2.      MAELRGIILLLCTIAFHVSHGQIRWTLLNQITGES--DVIPLSNNTPLNVSLNFKLMNIL
                     * *: * *   .: . .  *  :* :*   *  **** ..: *: **:.:*::**:

L-AChBP_T1.      EVNEITNEVDVVFWQQTTWSDRTLA-WNSSHSPDQVSVPISSLWVPDLAAYNAISKPEVL
L-AChBP_T2.      EVNEITNEVDVVFWQQTTWSDRTLA-WNSSHSPDQVSVPISSLWVPDLAAYNAISKPEVL
B-AChBP_T1.      EADTEKDQVEVVLWTQASWKVPYYSSLLSSSSLDQVSLPVSKMWTPDLSFYNAIAAPELL
B-AChBP_T2.      EADTEKDQVEVVLWTQASWKVPYYSSLLSSSSLDQVSLPASKMWTPDLSFYNAIAAPELL
                 *.:  .::*:**:* *::*.    :   ** * ****:* *.:*.***: ****: **:*

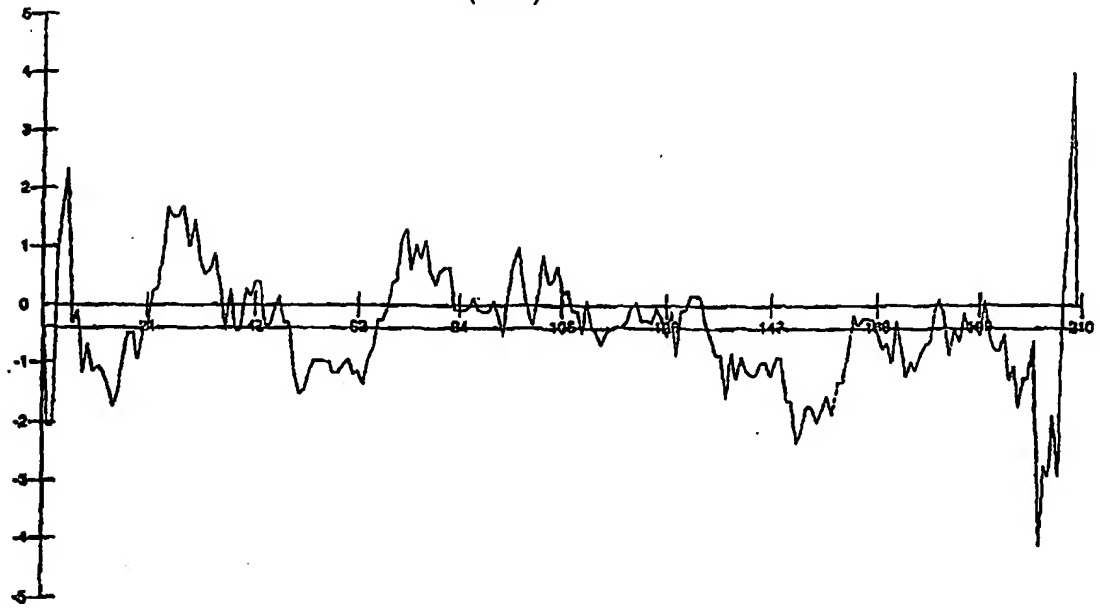
L-AChBP_T1.      TPQLARVVSDGEVLYMPSIRQRFSCDVSGVDTESGATCRIKIGSWTHHSREISVDPTTE-
L-AChBP_T2.      TPQLARVVSDGEVLYMPSIRQRFSCDVSGVDTESGATCRIKIGSWTHHSGEISVDPTTE-
B-AChBP_T1.      SADRVVVSKDGSVIYVPSQRVRFTCDLINVDTEPGATCRIKVGSWTHDNKQFALITGEEG
B-AChBP_T2.      STDRVVVSKDGSVIYVPSQRVRFTCDLINVDTEPGATCRIKVGSWTFDNKQLALITGEEG
                 :.: . * .**.*:*:** * **:**: .****.*******:****... :::: .  *

L-AChBP_T1.      NSDDSEYFSQYSRFEILDVTQKKNSVTYSCCPEAYEDVEVSLNFRKKGRSEIL
L-AChBP_T2.      NSDDSEYFSQYSRFEILDVTQKKNSVIYSCCPEAYEDVEVSLNFRKKGRSEIL
B-AChBP_T1.      VVNIAEYFDS-PKFDLLSATQSLNRKKYSCCENMYDDIEITFAFRKK------
B-AChBP_T2.      VVNIAEYFDS-PKYDLLSATQSLNRKKYRCCENMYEDIEITFAFRKK------
                   : :***.. .::::*..**. *   * **.: *:*:*::: ****
```

Figure 1

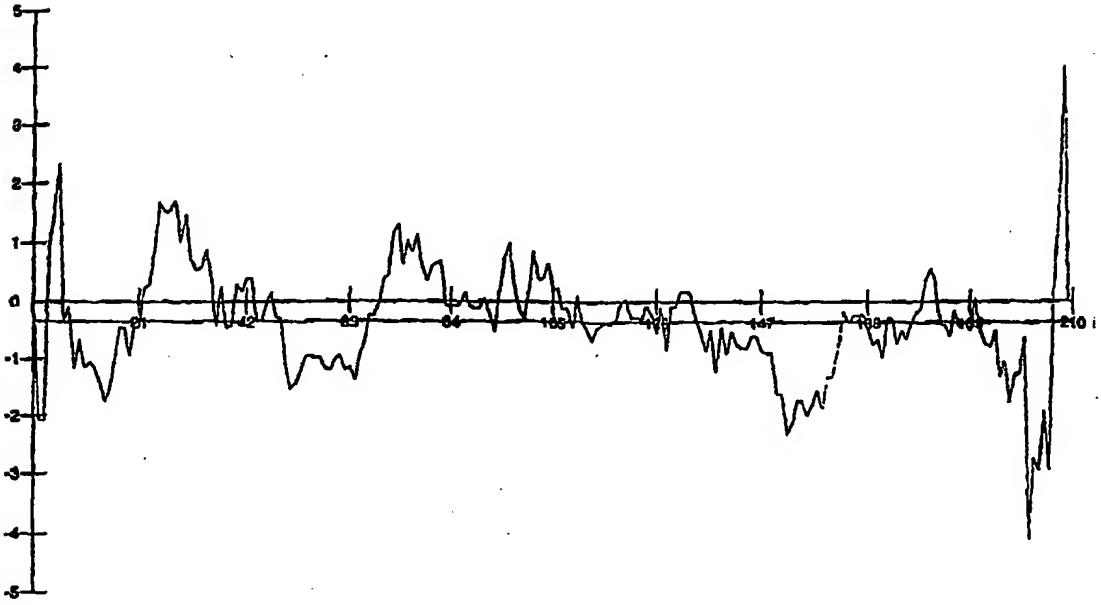
(2/19)

2A



Average Hydrophobicity = -,394

2B



Average Hydrophobicity = -,350

Figure 2

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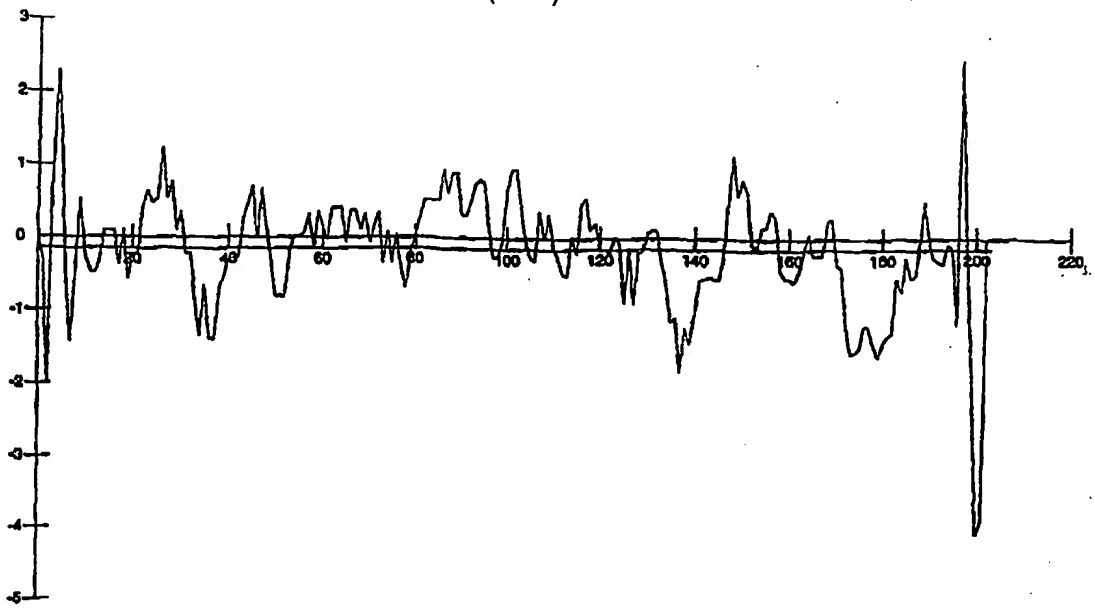
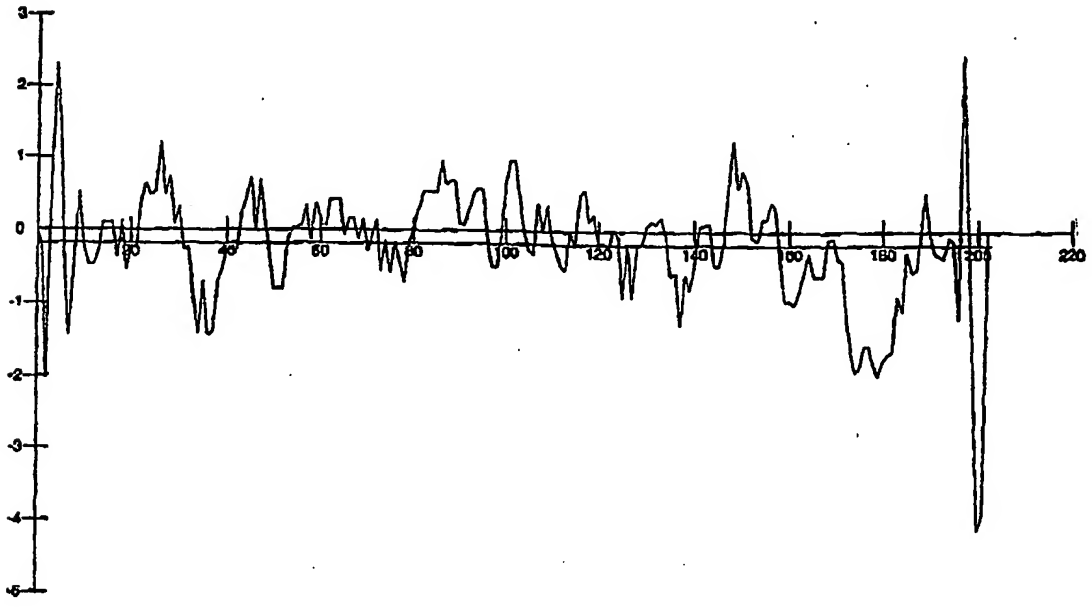
2C



Average Hydrophobicity = -,159

2D



Average Hydrophobicity = -,189

Figure 2 (continued)

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```
L-AChBP_T1      ------------------------------------LDRADILYNIRQTSRPDVIPT
L-AChBP_T2      ------------------------------------LDRADILYNIRQTSRPDVIPT
B-AChBP_T1      ------------------------------------QIRWTLLNQITGES--DVIPL
B-AChBP_T2      ------------------------------------QIRWTLLNQITGES--DVIPL
h_nAChR_A7      ---------MRCSPGGVWLALAASLLHV-------SLQGEFQRKLYKELVKNYNPLERPV
h_5HT3          --------MLLWVQQALLALLLPTLLAQGEARRSRNTTRPALLRLSDYLLTNYRKGVRPV
h_GlyR_a1       -MYSFNTLRLYLSGAIVFFSLAASKEAEAARSATKPMSPSDFLDKLMGRTSGYDARIRPN
h_GABAA_b1      MRKSPGLSDCLWAWILLLSTLTGRSYGQPSLQDELKDNTTVFTRILDRLLDGYDNRLRPG
                                                                        *

L-AChBP_T1      QRDR-PVAVSVSLKFINILEVNEITNEVDVVFWQQTTWSDRTLA--WNSSHSPDQVSVPI
L-AChBP_T2      QRDR-PVAVSVSLKFINILEVNEITNEVDVVFWQQTTWSDRTLA--WNSSHSPDQVSVPI
B-AChBP_T1      SNNT-PLNVSLNFKLMNIVEADTEKDQVEVVLWTQASWKVPYYSS-LLSSSSLDQVSLPV
B-AChBP_T2      SNNT-PLNVSLNFKLMNILEADTEKDQVEVVLWTQASWKVPYYSS-LLSSSSLDQVSLPA
h_nAChR_A7      ANDSQPLTVYFSLSLLQIMDVDEKNQVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPD
h_5HT3          RDWRKPTTVSIDVIVYAILNVDEKNQVLTTYIWYRQYWTDEFLQWNPEDFDNITKLSIPT
h_GlyR_a1       FKGP-PVNVSCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLAYNEYPDDSLDLDPSML
h_GABAA_b1      LGER-VTEVKTDIFVTSFGPVSDHDMEYTIDVFFRQSWKDERLKF-KGPMTVLRLNNLMA
                        *  .. .  :              .: :  *.

L-AChBP_T1      SSLWVPDLAAYNAISK-PEVLTPQ--LARVVSDGEVLYMPSIRQRFSCDVSG-VDTESGA
L-AChBP_T2      SSLWVPDLAAYNAISK-PEVLTPQ--LARVVSDGEVLYMPSIRQRFSCDVSG-VDTESGA
B-AChBP_T1      SKMWTPDLSFYNAIAA-PELLSAD--RVVVSKDGSVIYVPSQRVRFTCDLIN-VDTEPGA
B-AChBP_T2      SKMWTPDLSFYNAIAA-PELLSTD--RVVVSKDGSVIYVPSQRVRFTCDLIN-VDTEPGA
h_nAChR_A7      GQIWKPDILLYNSADERFDATFHT--NVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQ
h_5HT3          DSIWVPDILINEFVDV-GKSPNIP--YVYIRHQGEVQNYKPLQVVTACSLDIYNFPFDVQ
h_GlyR_a1       DSIWKPDLFFANEKGAHFHEITTDNKLLRISRNGNVLYSIRITLTLACPMDLKNFPMDVQ
h_GABAA_b1      SKIRTPDTFFHNGKKSVAHNMTMPNKLLRITEDGTLLYTMRLTVRAECPMHLEDFPMDAH
                ..:  **    :      .          : .*             * :     .

L-AChBP_T1      TCRIKIGSWTHHSREISVDPT---TE-NSDDSEYFSQYSRFEILDVTQKKNSVTYSCCPE
L-AChBP_T2      TCRIKIGSWTHHSGEISVDPT---TE-NSDDSEYFSQYSRFEILDVTQKKNSVIYSCCPE
B-AChBP_T1      TCRIKVGSWTHDNKQFALITG---EEGVVNIAEYFDS-PKFDLLSATQSLNRKKYSCCEN
B-AChBP_T2      TCRIKVGSWTFDNKQLALITG---EEGVVNIAEYFDS-PKYDLLSATQSLNRKKYRCCEN
h_nAChR_A7      HCKLKFGSWSYGGWSLDLQMQ---EA---DISGYIPN-GEWDLVGIPGKRSERFYECCKE
h_5HT3          NCSLTFTSWLHTIQDINISLWRLPEKVKSDRSVFMNQ-GEWELLGVLPYFREFSMESS-N
h_GlyR_a1       TCIMQLESFGYTMNDLIFEWQ---EQGAVQVADGLTL-PQFILKEEKDLRYCTKHYNT-G
h_GABAA_b1      ACPLKFGSYAYTRAEVVYEWTR-EPARSVVVAEDGSRLNQYDLLG--QTVDSGIVQSSTG
                 * : . *: .   ..                :       .: :

L-AChBP_T1      AYEDVEVSLNFRKKGRSEIL
L-AChBP_T2      AYEDVEVSLNFRKKGRSEIL
B-AChBP_T1      MYDDIEITFAFRKK------
B-AChBP_T2      MYEDIEITFAFRKK------
h_nAChR_A7      PYPDVTFTVTMRRRTLYYGL
h_5HT3          YYAEMKFYVVIRRRPLFYVV
h_GlyR_a1       KFTCIEARFHLERQMGYYLI
h_GABAA_b1      EYVVMTTHFHLKRKIGYFVI
                 :  :   . :.::
```

Figure 3

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```
nAChR_h-A2      MGPSCPVFLSFTKLSLWWLLLTPAGGEEAKRPPPRAPGDP---LSSPSPTALPQGGSHTE
nAChR_h-A4      ----------------------MELGGPGAPRLLP-----P---LLLLLGTGLLRASSHVE
nAChR_h-A5      ----------------------MAARGSGPRALRLLLLVQLVAGRCGLAGAAGGAQRGLSEPS
nAChR_h-A3      ----------------MALAALAAPGAVAPRLLL--------LLLSLLP--VAR---ASE
nAChR_h-A6      ------------------MLTSKGQGFLHGGLCL--------WLCVFTP--FFKGCVGCA
nAChR_h-A1      --------------------------MEPWPLLL---------LFSLCSAGLVLG---SE
nAChR_h-A7      ------------------MRCSPGGVWLALAASL--------LHVSLQG-EFQR------
nAChR_h-A9      ------------------CISFCWIYFAASRLR---------AAETADG-KYAQ------
B-AChBP_T1      --------------------MAELRRIILLLCT---------IAFHVSHG-QIR------
B-AChBP_T2      --------------------MAELRGIILLLCT---------IAFHVSHG-QIR------
L-AChBP_T1      ----------------------MRRNIFCLACL---------WIVQACLS-LDR------
L-AChBP_T2      ----------------------MRRNIFCLACL---------WIVQGCLS-LDR------

nAChR_h-A2      T----EDRLFKHLFRGYNRWARPVPNTSDVVIVRFGLSIAQLIDVDEKNQMMTTNVWLKQ
nAChR_h-A4      TRAHAEERLLKKLFSGYNKWSRPVANISDVVLVRFGLSIAQLIDVDEKNQMMTTNVWVKQ
nAChR_h-A5      SIAKHEDSLLKDLFQDYERWVRPVEHLNDKIKIKFGLAISQLVDVDEKNQLMTTNVWLKQ
nAChR_h-A3      A----EHRLFERLFEDYNEIIRPVANVSDPVIIHFEVSMSQLVKVDEVNQIMETNLWLKQ
nAChR_h-A6      T----EERLFHKLFSHYNQFIRPVENVSDPVTVHFEVAITQLANVDEVNQIMETNLWLRH
nAChR_h-A1      H----ETRLVAKLFKDYSSVVRPVEDHRQVVEVTVGLQLIQLINVDEVNQIVTTNVRLKQ
nAChR_h-A7      -------KLYKELVKNYNPLERPVANDSQPLTVYFSLSLLQIMDVDEKNQVLTTNIWLQM
nAChR_h-A9      -------KLFNDLFEDYSNALRPVEDTDKVLNVTLQITLSQIKDMDERNQILTAYLWIRQ
B-AChBP_T1      ------WTLLNQITGES--DVIPLSN-NTPLNVSLNFKLMNIVEADTEKDQVEVVLWTQA
B-AChBP_T2      ------WTLLNQITGES--DVIPLSN-NTPLNVSLNFKLMNILEADTEKDQVEVVLWTQA
L-AChBP_T1      ------ADILYNIRQTSRPDVIPTQR-DRPVAVSVSLKFINILEVNEITNEVDVVFWQQT
L-AChBP_T2      ------ADILYNIRQTSRPDVIPTQR-DRPVAVSVSLKFINILEVNEITNEVDVVFWQQT
                      .   :   :         *       : : . . : :: . .:  .: : . .  :

nAChR_h-A2      EWSDYKLRWNPTDFGNITSLRVPSEMIWIPDIVLYNNADGEFAVTHMTKAHLFSTGTVHW
nAChR_h-A4      EWHDYKLRWDPADYENVTSIRIPSELIWRPDIVLYNNADGDFAVTHLTKAHLFHDGRVQW
nAChR_h-A5      EWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRFEGTS-TKTVIRYNGTVTW
nAChR_h-A3      IWNDYKLKWNPSDYGGAEFMRVPAQKIWKPDIVLYNNAVGDFQVDDKTKALLKYTGEVTW
nAChR_h-A6      IWNDYKLRWDPMEYDGIETLRVPADKIWKPDIVLYNNAVGDFQVEGKTKALLKYNGMITW
nAChR_h-A1      QWVDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITW
nAChR_h-A7      SWTDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFHTNVLVNSSGHCQY
nAChR_h-A9      IWHDAYLTWDRDQYDGLDSIRIPSDLVWRPDIVLYNKADDESSEPVNTNVVLRYDGLITW
B-AChBP_T1      SWKVPYYSS-LLSSSSLDQVSLPVSKMWTPDLSFYN-AIAAPELLSADRVVVSKDGSVIY
B-AChBP_T2      SWKVPYYSS-LLSSSSLDQVSLPASKMWTPDLSFYN-AIAAPELLSTDRVVVSKDGSVIY
L-AChBP_T1      TWSDRTLA--WNSSHSPDQVSVPISSLWVPDLAAYN-AISKPEVLTPQLARVVSDGEVLY
L-AChBP_T2      TWSDRTLA--WNSSHSPDQVSVPISSLWVPDLAAYN-AISKPEVLTPQLARVVSDGEVLY
                 *          .  .   : .*   :* **:  :: *           . :   *   :

nAChR_h-A2      VPPAIYKSSCSIDVTFFPFDQQNCKMKFGSWTYDKAKIDLEQMEQ-TVDLKDYWES-GEW
nAChR_h-A4      TPPAIYKSSCSIDVTFFPFDQQNCTMKFGSWTYDKAKIDLVNMHS-RVDQLDFWES-GEW
nAChR_h-A5      TPPANYKSSCTIDVTFFPFDLQNCSMKFGSWTYDGSQVDIILEDQ-DVDKRDFFDN-GEW
nAChR_h-A3      IPPAIFKSSCKIDVTYFPFDYQNCTMKFGSWSYDKAKIDLVLIGS-SMNLKDYWES-GEW
nAChR_h-A6      TPPAIFKSSCPMDITFFPFDHQNCSLKFGSWTYDKAEIDLLIIGS-KVDMNDFWEN-SEW
nAChR_h-A1      TPPAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESD-QPDLSNFMES-GEW
nAChR_h-A7      LPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQM--Q-EADISGYIPN-GEW
nAChR_h-A9      DAPAITKSSCVVDVTYFPFDNQQCNLTFGSWTYNGNQVDIFNALD-SGDLSDFIED-VEW
B-AChBP_T1      VPSQRVRFTCDLINVDTEPG-ATCRIKVGSWTHDNKQFALITGEEGVVNIAEYFDS-PKF
B-AChBP_T2      VPSQRVRFTCDLINVDTEPG-ATCRIKVGSWTFDNKQLALITGEEGVVNIAEYFDS-PKY
L-AChBP_T1      MPSIRQRFSCDVSGVDTESG-ATCRIKIGSWTHHSREISVDPTTE-NSDDSEYFSQYSRF
L-AChBP_T2      MPSIRQRFSCDVSGVDTESG-ATCRIKIGSWTHHSGEISVDPTTE-NSDDSEYFSQYSRF
                 ..   :  * :       .   * :..*:*:.    . :    .   :   : . .:
```

Figure 4

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```
nAChR_h-A2      AIVNATGTYNSKKYDCCAE-IYPDVTYAFVIRRLPLFYTINLIIPCLLISCLTVLVFYLP
nAChR_h-A4      VIVDAVGTYNTRKYECCAE-IYPDITYAFVIRRLPLFYTINLIIPCLLISCLTVLVFYLP
nAChR_h-A5      EIVSATGSKGNRTDSCC---WYPYVTYSFVIKRLPLFYTLFLIIPCIGLSFLTVLVFYLP
nAChR_h-A3      AIIKAPGYKHDIKYNCCEE-IYPDITYSLYIRRLPLFYTINLIIPCLLISFLTVLVFYLP
nAChR_h-A6      EIIDASGYKHDIKYNCCEE-IYTDITYSFYIRRLPMFYTINLIIPCLFISFLTVLVFYLP
nAChR_h-A1      VIKESRGWKHSVTYSCCPDTPYLDITYHFVMQRLPLYFIVNVIIPCLLFSFLTGLVFYLP
nAChR_h-A7      DLVGIPGKRSERFYECCKE-PYPDVTFTVTMRRRTLYYGLNLLIPCVLISALALLVFLLP
nAChR_h-A9      EVHGMPAVKNVISYGCCSE-PYPDVTFTLLLKRRSSFYIVNLLIPCVLISFLAPLSFYLP
B-AChBP_T1      DLLSATQSLNRKKYSCCEN-MYDDIEITFAFRKK--------------------------
B-AChBP_T2      DLLSATQSLNRKKYRCCEN-MYEDIEITFAFRKK--------------------------
L-AChBP_T1      EILDVTQKKNSVTYSCCPE-AYEDVEVSLNFRKKGRSEIL--------------------
L-AChBP_T2      EILDVTQKKNSVIYSCCPE-AYEDVEVSLNFRKKGRSEIL--------------------
                 :             **    *  :   . :::

nAChR_h-A2      SDCGEKITLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVL
nAChR_h-A4      SECGEKITLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVL
nAChR_h-A5      SNEGEKICLCTSVLVSLTVFLLVIEEIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAI
nAChR_h-A3      SDCGEKVTLCISVLLSLTVFLLVITETIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFVL
nAChR_h-A6      SDCGEKVTLCISVLLSLTVFLLVITETIPSTSLVVPLVGEYLLFTMIFVTLSIVVTVFVL
nAChR_h-A1      TDSGEKMTLSISVLLSLTVFLLVIVELIPSTSSAVPLIGKYMLFTMVFVIASIIITVIVI
nAChR_h-A7      ADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVIVL
nAChR_h-A9      AASGEKVSLGVTILLAMTVFQLMVAEIMP-ASENVPLIGKYYIATMALITASTALTIMVM
B-AChBP_T1      ------------------------------------------------------------
B-AChBP_T2      ------------------------------------------------------------
L-AChBP_T1      ------------------------------------------------------------
L-AChBP_T2      ------------------------------------------------------------

nAChR_h-A2      NVHHRSPSTH-TMPHWVRGALLGCVPRWLLMNRP--------------------------
nAChR_h-A4      NVHHRSPRTH-TMPTWVRRVFLDIVPRLLLMKRPSVVKDNCRRLIESMHKMASAPRFWPE
nAChR_h-A5      NIHHRSSSTHNAMAPLVRKIFLHTLPKLLCMRSH--------------------------
nAChR_h-A3      NVHYRTPTTH-TMPSWVKTVFLNLLPRVMFMTRP--------------------------
nAChR_h-A6      NIHYRTPTTH-TMPRWVKTVFLKLLPQVLLMRWP--------------------------
nAChR_h-A1      NTHHRSPSTH-VMPNWVRKVFIDTIPNIMFFSTMK--------------------------
nAChR_h-A7      QYHHHDPDGG-KMPKWTRVILLNWCAWFLRMKRPG--------------------------
nAChR_h-A9      NIHFCGAEAR-PVPHWARVVILKYMSRVLFVYDVG--------------------------
B-AChBP_T1      ------------------------------------------------------------
B-AChBP_T2      ------------------------------------------------------------
L-AChBP_T1      ------------------------------------------------------------
L-AChBP_T2      ------------------------------------------------------------

nAChR_h-A2      ---------------PPPVELCHPLRLKLSPSYHWLESN--------VDAEEREVVVEEE
nAChR_h-A4      PEGEPPATSGTQSLHPPSPSFCVPLDVPAEPGPSCKSPSDQLPPQQPLEAEKASPHPSPG
nAChR_h-A5      ------------------------------------------------VDR----------
nAChR_h-A3      ---------------TSNEGNAQKPRPLYGAELSNLNCFS------RAESKGCKEGYPCQ
nAChR_h-A6      ---------------LDKTRGTGSDAVPRGLARR------------PAKGKLASHGEPRH
nAChR_h-A1      ----------------------RPSREK--------------------QDKK--------
nAChR_h-A7      ----------------EDKVRPACQHKQRRCSLAS-------------VEMSAVAPPPASN
nAChR_h-A9      ----------------ESCLSPHHSRER-D-----------------HLTKVYSKLPESN
B-AChBP_T1      ------------------------------------------------------------
B-AChBP_T2      ------------------------------------------------------------
L-AChBP_T1      ------------------------------------------------------------
L-AChBP_T2      ------------------------------------------------------------
```

Figure 4 (continued)

(7/19)

```
nAChR_h-A2      DRWACAGHVAP--------SVGTLCSHGHLHSG--------------------ASGPKA
nAChR_h-A4      PCRPPHGTQAPGLAKARSLSVQHMSSPGEAVEGGVRCRSRSIQYCVPRDDAAPEADGQAA
nAChR_h-A5      ----------------------YFTQKEETESG----------------------SGPKS
nAChR_h-A3      DGMCGYCHHRR---IK---ISNFSANLTRSSSS--------------------ESVDA
nAChR_h-A6      LKECFHCHK-----------SNELATSKRRLSH---------------------QPLQW
nAChR_h-A1      --------------------IFTEDIDISDISG--------------------KPGPPP
nAChR_h-A7      GNLLYIGFRGLDG------VHCVPTPDSGVVCG-----------------RMACSPTHD
nAChR_h-A9      LKAARNKDLSR---------KKDMNKRLKNDLG--------------------CQGKNP
B-AChBP_T1      ------------------------------------------------------------
B-AChBP_T2      ------------------------------------------------------------
L-AChBP_T1      ------------------------------------------------------------
L-AChBP_T2      ------------------------------------------------------------

nAChR_h-A2      EALLQE-------------------------------------------GELLLSPHMQKA
nAChR_h-A4      GALASRNTHSAELPPPDQPSPCKCTCKKEPSSVSPSATVKTRSTKAPPPHLPLSPALTRA
nAChR_h-A5      ----SR-------------------------------------------------NTLEAA
nAChR_h-A3      VLSLSA-------------------------------------------------LSPEIKEA
nAChR_h-A6      VVENSE-------------------------------------------------HSPEVEDV
nAChR_h-A1      MGFHSP-------------------------------------------LIKHPEVKSA
nAChR_h-A7      EHLLHGG-----------------------------------------QPPEGDPDLAKI
nAChR_h-A9      QEAESY-------------------------------------------------CAQYKVL
B-AChBP_T1      ------------------------------------------------------------
B-AChBP_T2      ------------------------------------------------------------
L-AChBP_T1      ------------------------------------------------------------
L-AChBP_T2      ------------------------------------------------------------

nAChR_h-A2      LEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFLWLFIIVCFLGTIGLFLP---PFLA
nAChR_h-A4      VEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLWMFIIVCLLGTVGLFLP---PWLA
nAChR_h-A5      LDSIRYITRHIMKENDVREVVEDWKFIAQVLDRMFLWTFLFVSIVGSLGLFVPVIYKWAN
nAChR_h-A3      IQSVKYIAENMKAQNEAKEIQDDWKYVAMVIDRIFLWVFTLVCILGTAGLFLQ---PLMA
nAChR_h-A6      INSVQFIAENMKSHNETKEVEDDWKYVAMVVDRVFLWVFIIVCVFGTAGLFLQ---PLLG
nAChR_h-A1      IEGIKYIAETMKSDQESNNAAAEWKYVAMVMDHILLGVFMLVCIIGTLAVFAG---RLIE
nAChR_h-A7      LEEVRYIANRFRCQDESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAP-NFVE
nAChR_h-A9      TRNIEYIAKCLKDHKATNSKGSEWKKVAKVIDRFFMWIFFIMVFVMTILIIA--------
B-AChBP_T1      ------------------------------------------------------------
B-AChBP_T2      ------------------------------------------------------------
L-AChBP_T1      ------------------------------------------------------------
L-AChBP_T2      ------------------------------------------------------------

nAChR_h-A2      GMI---------
nAChR_h-A4      GMI---------
nAChR_h-A5      ILIPVHIGNANK
nAChR_h-A3      REDA--------
nAChR_h-A6      NTGKS-------
nAChR_h-A1      LNQQG-------
nAChR_h-A7      AVSKDFA-----
nAChR_h-A9      ------------
B-AChBP_T1      ------------
B-AChBP_T2      ------------
L-AChBP_T1      ------------
L-AChBP_T2      ------------
```

Figure 4 (continued)

(8/19)

```
B-AChBP_T1.     -MAELRRIILLLCTIAFHVSHG-QIRWTLLNQITGES--DVIPLSNNT-PLNVSLNFKLM
B-AChBP_T2.     -MAELRGIILLLCTIAFHVSHG-QIRWTLLNQITGES--DVIPLSNNT-PLNVSLNFKLM
L-AChBP_T1.     ---MRRNIFCLACLWIVQACLS-LDRADILYNIRQTSRPDVIPTQRDR-PVAVSVSLKFI
L-AChBP_T2.     ---MRRNIFCLACLWIVQGCLS-LDRADILYNIRQTSRPDVIPTQRDR-PVAVSVSLKFI
A1_human        --MEPWPLLLLFSLCSAGLVLGSEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTVGLQLI
A7_human        MRCSPGGVWLGLAASLLHVSLQGEFQRKLYKELVKNYNPLERPVANDSQPLTVYFSLSLL
                       :   .           . : ::        *   .   : * ..:.::

B-AChBP_T1.     NIVEADTEKDQVEVVLWTQASWKVPYYSS-LLSSSSLDQVSLPVSKMWTPDLSFYN-AIA
B-AChBP_T2.     NILEADTEKDQVEVVLWTQASWKVPYYSS-LLSSSSLDQVSLPASKMWTPDLSFYN-AIA
L-AChBP_T1.     NILEVNEITNEVDVVFWQQTTWSDRTLA--WNSSHSPDQVSVPISSLWVPDLAAYN-AIS
L-AChBP_T2.     NILEVNEITNEVDVVFWQQTTWSDRTLA--WNSSHSPDQVSVPISSLWVPDLAAYN-AIS
A1_human        QLINVDEVNQIVTTNVRLKQQWVDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADG
A7_human        QIMDVDEKNQVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADE
                :::::.:  .: : . .  :  *          .  . . : .*  .:* **:  ** *

B-AChBP_T1.     APELLSADRVVVSKDGSVIYVPSQRVRFTCDLINVDTEPG-ATCRIKVGSWTHDNKQFAL
B-AChBP_T2.     APELLSTDRVVVSKDGSVIYVPSQRVRFTCDLINVDTEPG-ATCRIKVGSWTFDNKQLAL
L-AChBP_T1.     KPEVLTPQLARVVSDGEVLYMPSIRQRFSCDVSGVDTESG-ATCRIKIGSWTHHSREISV
L-AChBP_T2.     KPEVLTPQLARVVSDGEVLYMPSIRQRFSCDVSGVDTESG-ATCRIKIGSWTHHSGEISV
A1_human        DFAIVKFTKVLLQYTGHITWTPPAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAI
A7_human        RFDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGG--WSL
                          . :   *   : *.   :  * :       .   * :*.*:*:. .   ::

B-AChBP_T1.     ITGEEGVVNIAEYFDS-PKFDLLSATQSLNRKKYSCC-ENMYDDIEITFAFRKK------
B-AChBP_T2.     ITGEEGVVNIAEYFDS-PKYDLLSATQSLNRKKYRCC-ENMYEDIEITFAFRKK------
L-AChBP_T1.     DPTTE-NSDDSEYFSQYSRFEILDVTQKKNSVTYSCC-PEAYEDVEVSLNFRKKGRSEIL
L-AChBP_T2.     DPTTE-NSDDSEYFSQYSRFEILDVTQKKNSVIYSCC-PEAYEDVEVSLNFRKKGRSEIL
A1_human        NPESD-QPDLSNFMES-GEWVIKESRGWKHSVTYSCCPDTPYLDITYHFVMQRLPLYFIV
A7_human        DLQMQ-EADISGYIPN-GEWDLVGIPGKRSERFYECC-KEPYPDVTFTVTMRRRTLYYGL
                    :   : : :: .  .: :           * **    * *:   . :::

B-AChBP_T1.     ------------------------------------------------------------
B-AChBP_T2.     ------------------------------------------------------------
L-AChBP_T1.     ------------------------------------------------------------
L-AChBP_T2.     ------------------------------------------------------------
A1_human        NVIIPCLLFSFLTGLVFYLPTDSGEKMTLSISVLLSLTVFLLVIVELIPSTSSAVPLIGK
A7_human        NLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQ

B-AChBP_T1.     ------------------------------------------------------------
B-AChBP_T2.     ------------------------------------------------------------
L-AChBP_T1.     ------------------------------------------------------------
L-AChBP_T2.     ------------------------------------------------------------
A1_human        YMLFTMVFVIASIIITVIVINTHHRSPSTHVMPNWVRKVFIDTIPNIMFFSTMKRPSREK
A7_human        YFASTMIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLN---WCAWFLRMKRPGEDK

B-AChBP_T1.     ------------------------------------------------------------
B-AChBP_T2.     ------------------------------------------------------------
L-AChBP_T1.     ------------------------------------------------------------
L-AChBP_T2.     ------------------------------------------------------------
A1_human        Q-------DKKIFTEDIDISDISGKPGP-------------------PPMG--------
A7_human        VRPACQHKQRRCSLASVEMSAVGPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMAC
```

Figure 5

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```
B-AChBP_T1.     ------------------------------------------------------------
B-AChBP_T2.     ------------------------------------------------------------
L-AChBP_T1.     ------------------------------------------------------------
L-AChBP_T2.     ------------------------------------------------------------
A1_human        --------FHS--PLIKHPEVKSAIEGIKYIAETMKSDQESNNAAAEWKYVAMVMDHILL
A7_human        SPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQDESEAVCSEWKFAACVVDRLCL

B-AChBP_T1.     ----------------------------
B-AChBP_T2.     ----------------------------
L-AChBP_T1.     ----------------------------
L-AChBP_T2.     ----------------------------
A1_human        GVFMLVCIIGTLAVFAGR--LIELNQQG---
A7_human        MAFSVFTIICTIGILMSAPNFVEAVSKDFAZ
```

Figure 5 (continued)

(10/19)

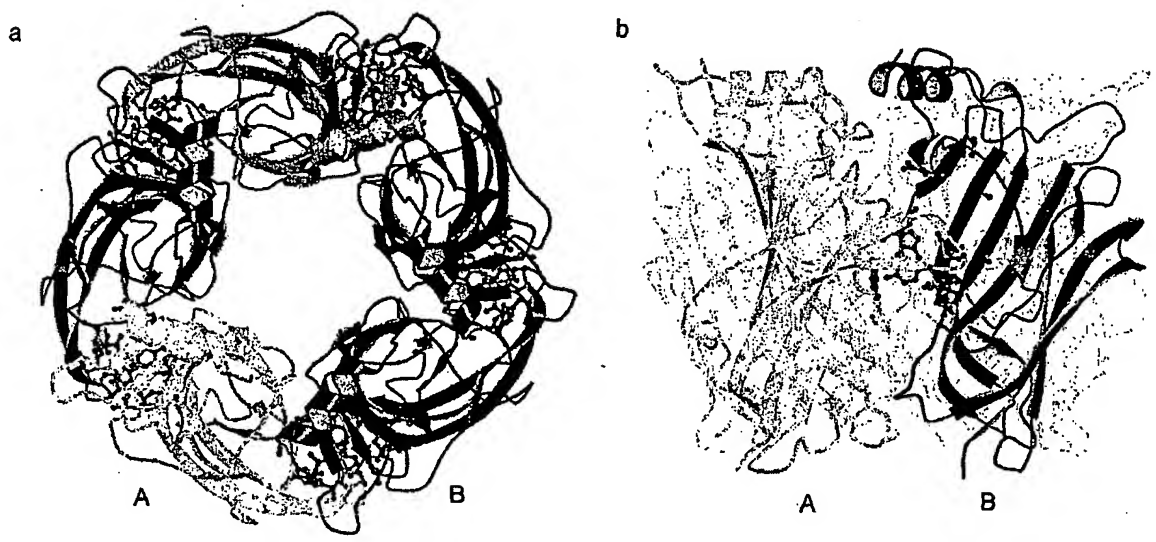


Figure 6

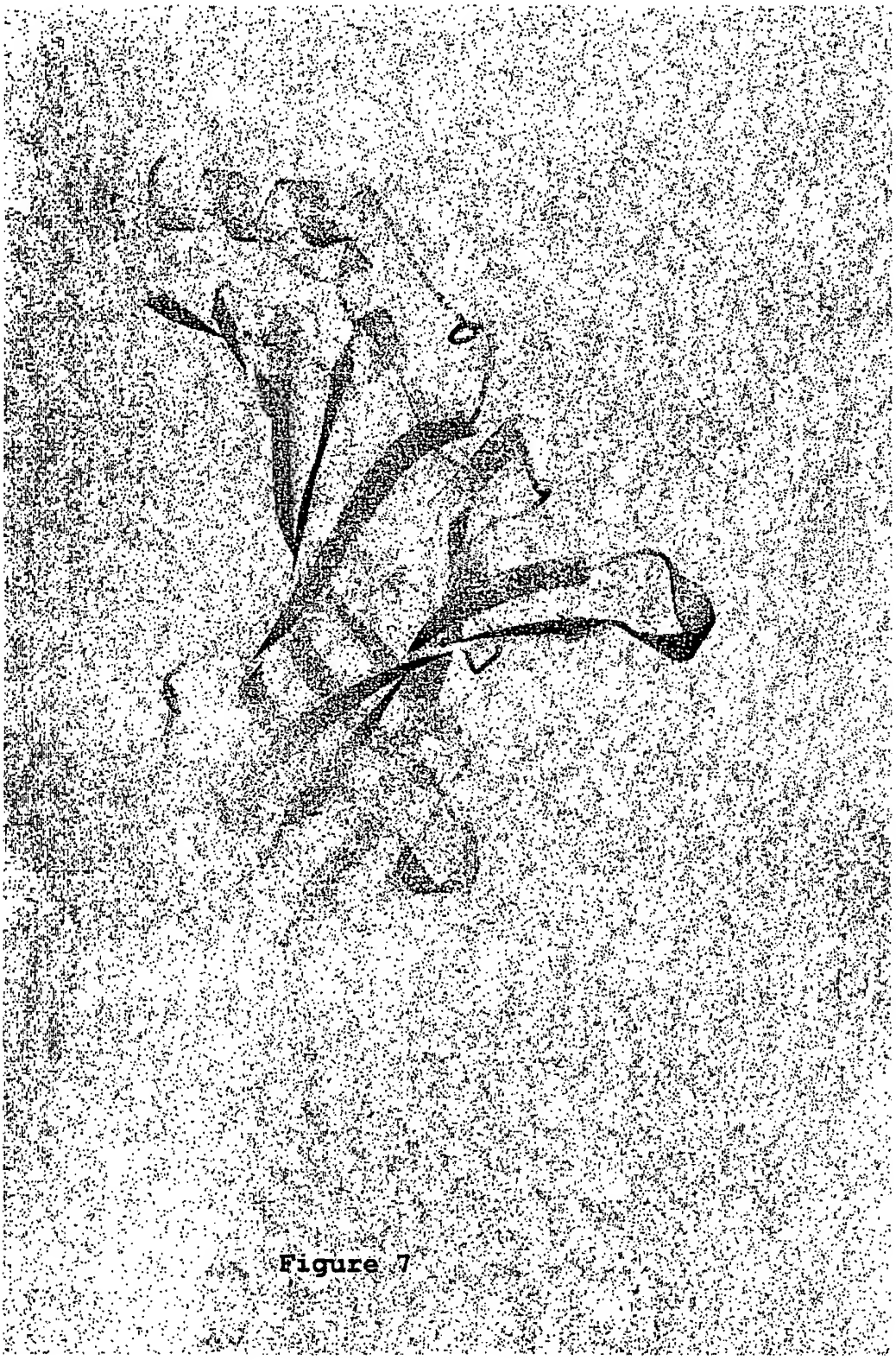


Figure 7

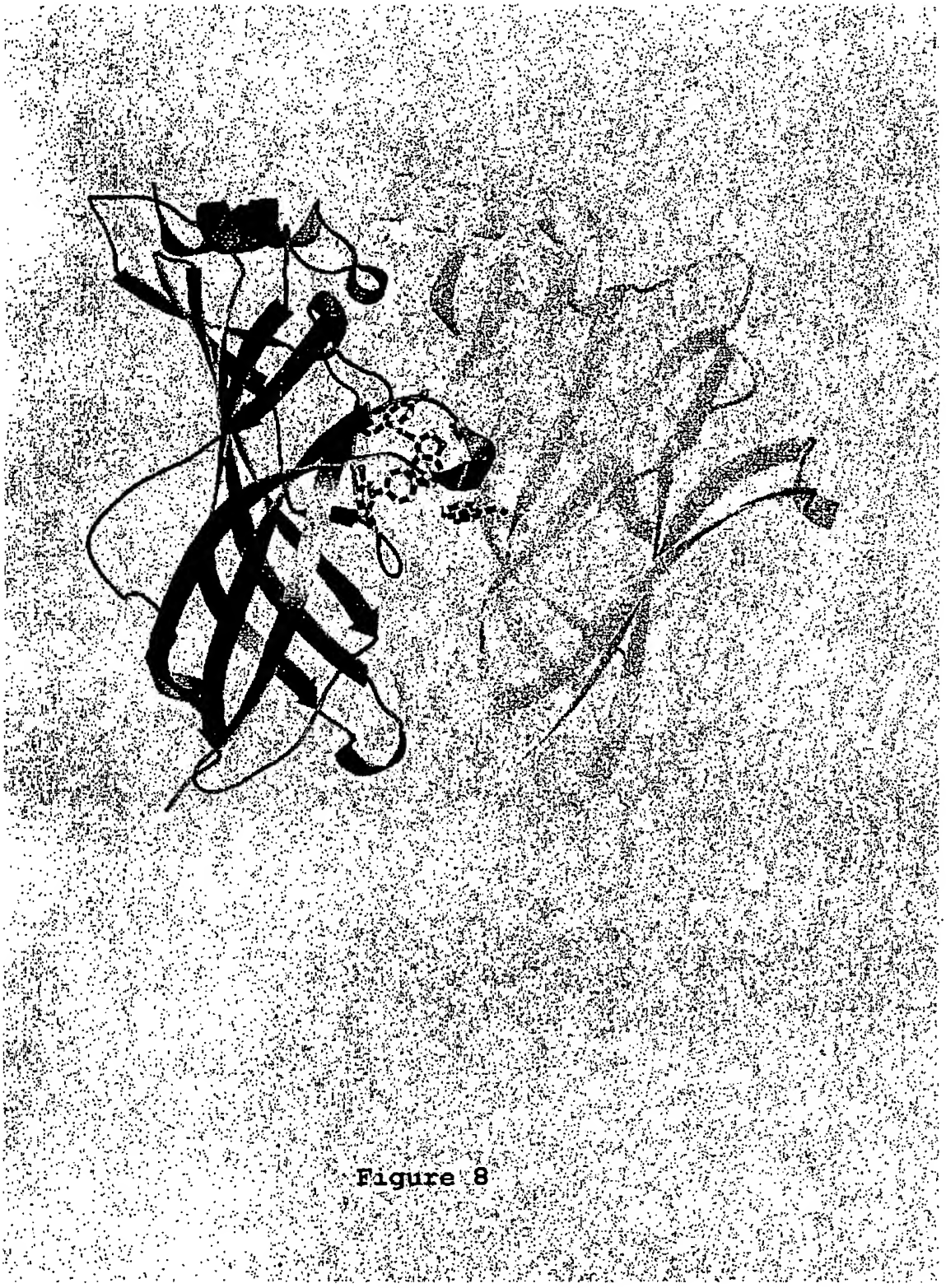


Figure 8

(13/19)

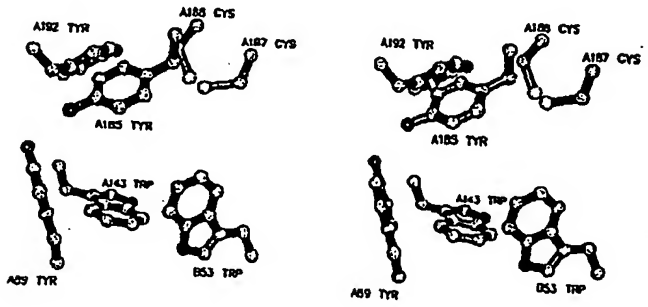


Figure 9

(14/19)

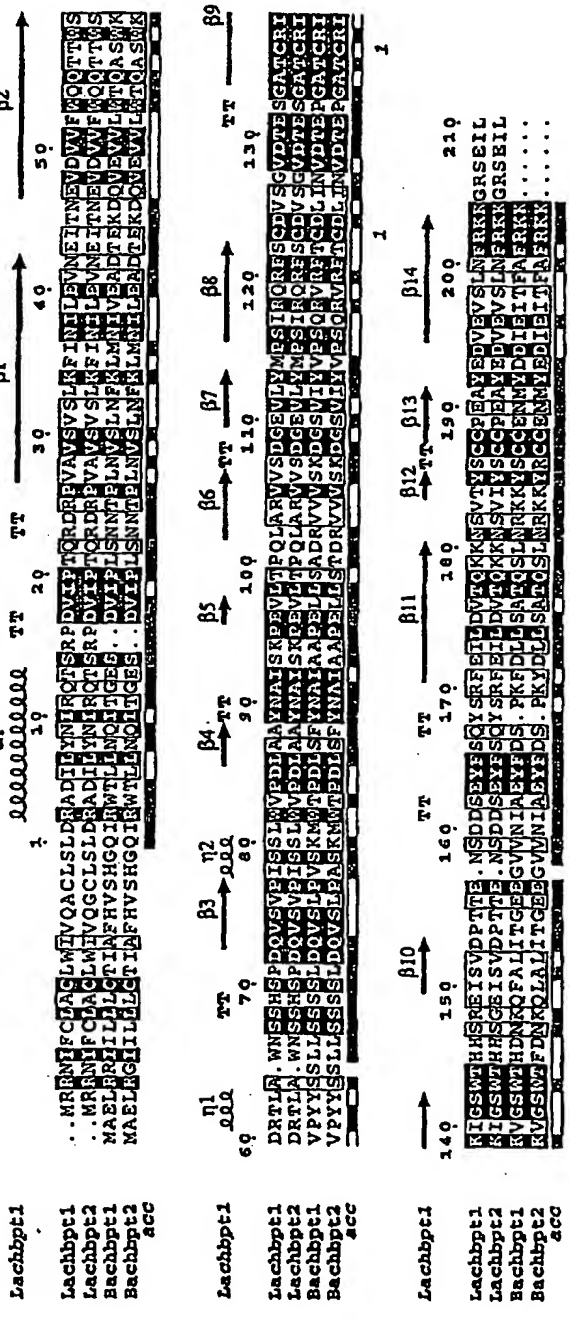


Figure 10

(15/19)

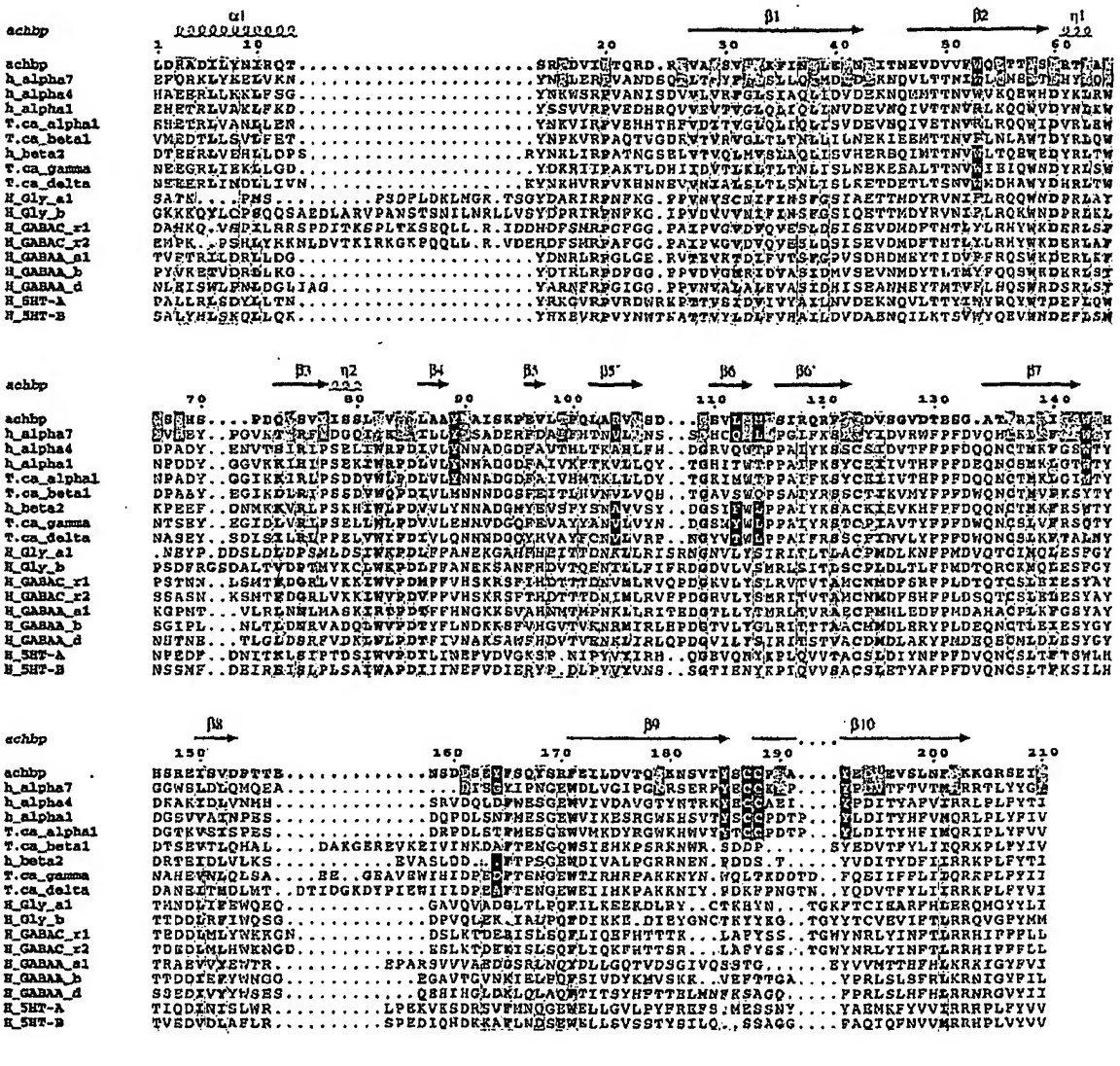


Figure 11

(16/19)

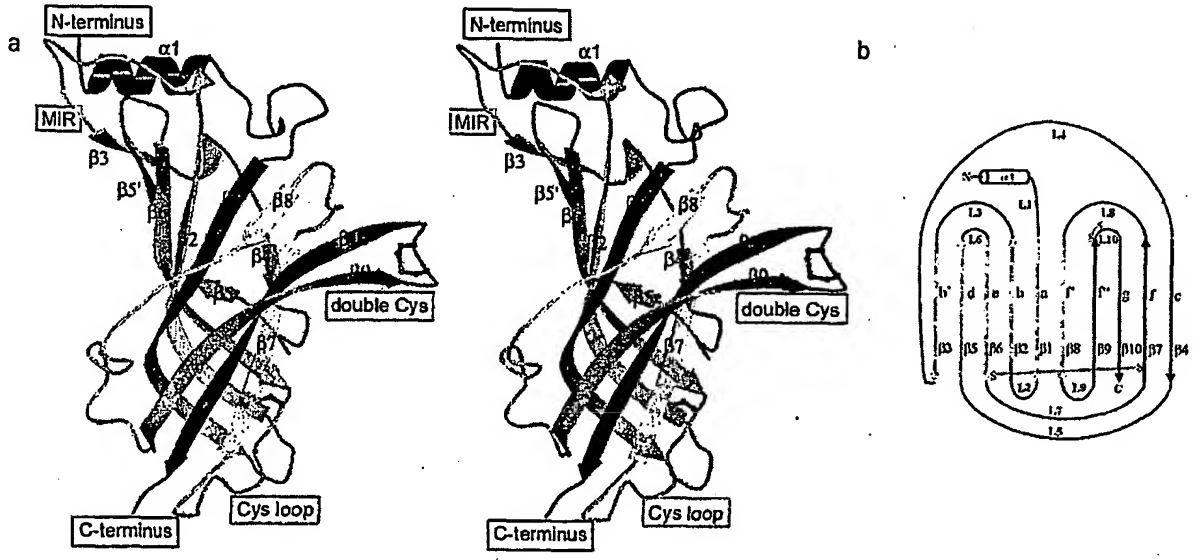


Figure 12

(17/19)

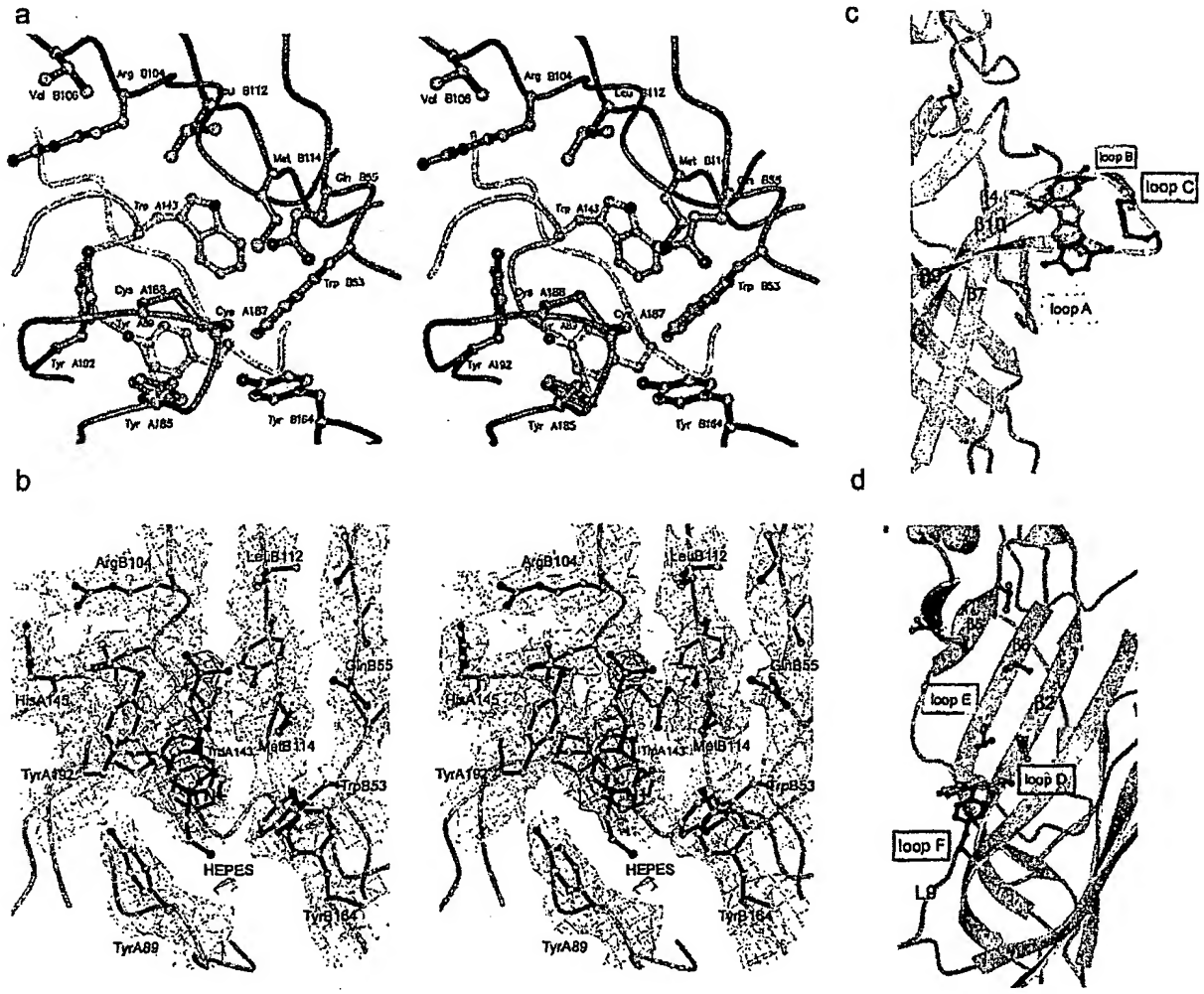
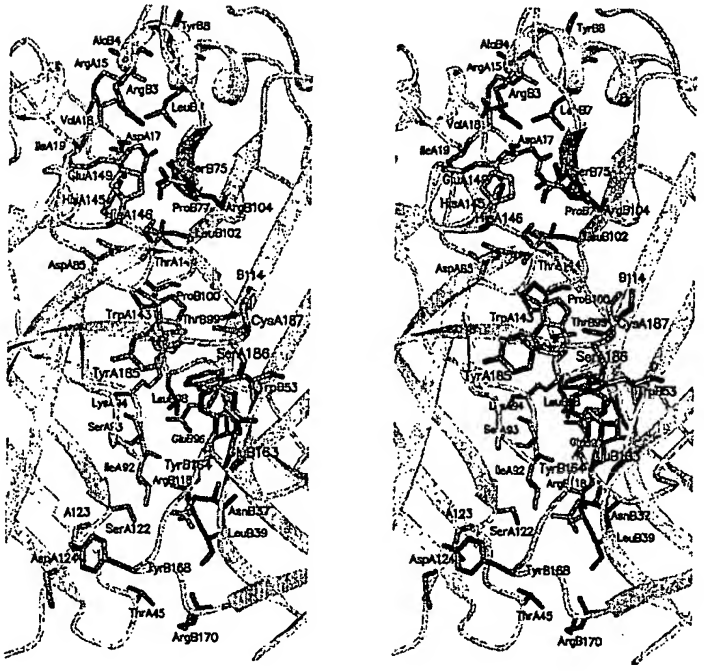


Figure 13

(18/19)

a



b

Plus side	Minus side
L1 (ArgA15, AspA17, ValA18, IleA19)	α1, β3 (ArgB3, AlaB4, LeuB7, TyrB8, ProB77)
L2 (ThrA45)	L9 (ArgB170)
L4 (AspA85)	β5 (ProB100, LeuB102)
L5 (IleA92, SerA93, LysA94)	β1, β5, β6 (LeuB39, GluB98, LeuB98, ArgB118)
L7 (SerA122, A123, AspA124)	β1, L9 (AsnB37, TyrB168)
L8 (TrpA143, ThrA144, HisA145, HisA146, GluA149)	α1, β2, β3, β5, β6 (ArgB3, TrpB53, SerB75, ThrB99, ArgB104, B114)
L10 (TyrA185, SerA186, CysA187)	L9 (GluB163, TyrB164)

Figure 14

(19/19)

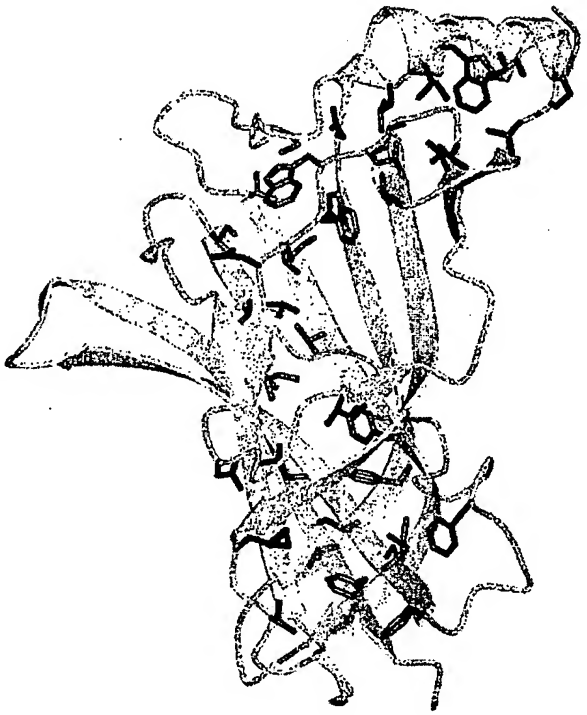


Figure 15

(1/20)

SEQUENCE LISTING

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(2/20)

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aat gaa gtg gac gtg gtc ttt tgg cag cag acg aca tgg tcg gac agg   240
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acc ctc gcc tgg aac agt tct cac tca cca gat cag gtt tcc gtg cca   288
Thr Leu Ala Trp Asn Ser Ser His Ser Pro Asp Gln Val Ser Val Pro
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Ile Ser Ser Leu Trp Val Pro Asp Leu Ala Ala Tyr Asn Ala Ile Ser
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aaa cct gaa gtc ctt aca ccg caa ctg gcc agg gtc gta tcc gat ggt   384
Lys Pro Glu Val Leu Thr Pro Gln Leu Ala Arg Val Val Ser Asp Gly
     95                  100                 105

gaa gtg ctg tac atg ccg agt atc cgc cag cgg ttc tcc tgc gat gta   432
Glu Val Leu Tyr Met Pro Ser Ile Arg Gln Arg Phe Ser Cys Asp Val
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Ser Gly Val Asp Thr Glu Ser Gly Ala Thr Cys Arg Ile Lys Ile Gly
                130                 135                 140

tcc tgg acc cac cac agt aga gag att tct gta gat ccc acg aca gaa   528
Ser Trp Thr His His Ser Arg Glu Ile Ser Val Asp Pro Thr Thr Glu
            145                 150                 155

aat agt gat gat tct gaa tac ttc tcc caa tac tct cgc ttt gaa atc   576
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(3/20)

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Cys Leu Ser Leu Asp Arg Ala Asp Ile Leu Tyr Asn Ile Arg Gln Thr
        -1  1               5                   10

Ser Arg Pro Asp Val Ile Pro Thr Gln Arg Asp Arg Pro Val Ala Val
    15                  20                  25

Ser Val Ser Leu Lys Phe Ile Asn Ile Leu Glu Val Asn Glu Ile Thr
30                  35                  40                  45

Asn Glu Val Asp Val Val Phe Trp Gln Gln Thr Thr Trp Ser Asp Arg
                50                  55                  60

Thr Leu Ala Trp Asn Ser Ser His Ser Pro Asp Gln Val Ser Val Pro
            65                  70                  75

Ile Ser Ser Leu Trp Val Pro Asp Leu Ala Ala Tyr Asn Ala Ile Ser
        80                  85                  90
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Lys Pro Glu Val Leu Thr Pro Gln Leu Ala Arg Val Val Ser Asp Gly
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Glu Val Leu Tyr Met Pro Ser Ile Arg Gln Arg Phe Ser Cys Asp Val
110                 115                 120                 125

Ser Gly Val Asp Thr Glu Ser Gly Ala Thr Cys Arg Ile Lys Ile Gly
                130                 135                 140

Ser Trp Thr His His Ser Arg Glu Ile Ser Val Asp Pro Thr Thr Glu
            145                 150                 155

Asn Ser Asp Asp Ser Glu Tyr Phe Ser Gln Tyr Ser Arg Phe Glu Ile
        160                 165                 170

Leu Asp Val Thr Gln Lys Lys Asn Ser Val Thr Tyr Ser Cys Cys Pro
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Glu Ala Tyr Glu Asp Val Glu Val Ser Leu Asn Phe Arg Lys Lys Gly
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               -15                 -10                  -5

tgt cta agc ttg gac cgg gca gac atc ttg tac aac ata cgt cag aca   96
Cys Leu Ser Leu Asp Arg Ala Asp Ile Leu Tyr Asn Ile Arg Gln Thr
        -1   1               5                  10

tcg aga ccg gat gtg att ccc aca cag cga gat cgc cca gtg gcg gtg   144
Ser Arg Pro Asp Val Ile Pro Thr Gln Arg Asp Arg Pro Val Ala Val
    15                  20                  25

tcc gtc tct ttg aag ttc atc aac atc ttg gaa gtg aat gaa ata acc   192
Ser Val Ser Leu Lys Phe Ile Asn Ile Leu Glu Val Asn Glu Ile Thr
30                  35                  40                  45

aat gaa gtg gac gtg gtc ttt tgg cag cag acg aca tgg tcg gac agg   240
Asn Glu Val Asp Val Val Phe Trp Gln Gln Thr Thr Trp Ser Asp Arg
                50                  55                  60

acc ctc gcc tgg aac agt tct cac tca cca gat cag gtt tcc gtg cca   288
Thr Leu Ala Trp Asn Ser Ser His Ser Pro Asp Gln Val Ser Val Pro
            65                  70                  75

ata agc tct ttg tgg gtg cct gac ctc gct gca tac aac gcc atc tcg   336
Ile Ser Ser Leu Trp Val Pro Asp Leu Ala Ala Tyr Asn Ala Ile Ser
        80                  85                  90

aaa cct gaa gtc ctt aca ccg caa ctg gcc agg gtc gta tcc gat ggt   384
Lys Pro Glu Val Leu Thr Pro Gln Leu Ala Arg Val Val Ser Asp Gly
    95                  100                 105

gaa gtg ctg tac atg ccg agt atc cgc cag cgg ttc tcc tgc gat gta   432
Glu Val Leu Tyr Met Pro Ser Ile Arg Gln Arg Phe Ser Cys Asp Val
110                 115                 120                 125

tcg ggt gtc gat acg gag tcc ggt gct acg tgt cgg atc aaa att ggt   480
Ser Gly Val Asp Thr Glu Ser Gly Ala Thr Cys Arg Ile Lys Ile Gly
                130                 135                 140
```

```
tcc tgg acc cac cac agt gga gag att tct gta gat ccc acg aca gaa   528
Ser Trp Thr His His Ser Gly Glu Ile Ser Val Asp Pro Thr Thr Glu
            145                 150                 155

aat agt gat gat tct gaa tac ttc tcc caa tac tct cgc ttt gaa atc   576
Asn Ser Asp Asp Ser Glu Tyr Phe Ser Gln Tyr Ser Arg Phe Glu Ile
        160                 165                 170

ttg gac gtc aca cag aag aag aac tcg gtt atc tac tct tgc tgt ccg   624
Leu Asp Val Thr Gln Lys Lys Asn Ser Val Ile Tyr Ser Cys Cys Pro
    175                 180                 185

gag gca tac gag gac gtt gaa gtg agt ctc aat ttc cgg aag aag gga   672
Glu Ala Tyr Glu Asp Val Glu Val Ser Leu Asn Phe Arg Lys Lys Gly
190                 195                 200                 205

cgc tcc gaa att ctt tag                                          690
Arg Ser Glu Ile Leu
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Met Arg Arg Asn Ile Phe Cys Leu Ala Cys Leu Trp Ile Val Gln Gly
                -15                 -10                 -5

Cys Leu Ser Leu Asp Arg Ala Asp Ile Leu Tyr Asn Ile Arg Gln Thr
        -1  1                   5                   10

Ser Arg Pro Asp Val Ile Pro Thr Gln Arg Asp Arg Pro Val Ala Val
    15                  20                  25

Ser Val Ser Leu Lys Phe Ile Asn Ile Leu Glu Val Asn Glu Ile Thr
30                  35                  40                  45

Asn Glu Val Asp Val Val Phe Trp Gln Gln Thr Thr Trp Ser Asp Arg
```

50 55 60

Thr Leu Ala Trp Asn Ser Ser His Ser Pro Asp Gln Val Ser Val Pro
65 70 75

Ile Ser Ser Leu Trp Val Pro Asp Leu Ala Ala Tyr Asn Ala Ile Ser
80 85 90

Lys Pro Glu Val Leu Thr Pro Gln Leu Ala Arg Val Val Ser Asp Gly
95 100 105

Glu Val Leu Tyr Met Pro Ser Ile Arg Gln Arg Phe Ser Cys Asp Val
110 115 120 125

Ser Gly Val Asp Thr Glu Ser Gly Ala Thr Cys Arg Ile Lys Ile Gly
130 135 140

Ser Trp Thr His His Ser Gly Glu Ile Ser Val Asp Pro Thr Thr Glu
145 150 155

Asn Ser Asp Asp Ser Glu Tyr Phe Ser Gln Tyr Ser Arg Phe Glu Ile
160 165 170

Leu Asp Val Thr Gln Lys Lys Asn Ser Val Ile Tyr Ser Cys Cys Pro
175 180 185

Glu Ala Tyr Glu Asp Val Glu Val Ser Leu Asn Phe Arg Lys Lys Gly
190 195 200 205

Arg Ser Glu Ile Leu
210

<210> 5
<211> 675
<212> DNA
<213> Bulinus truncatus

<220>

(8/20)

<221> CDS
<222> (1)..(672)

<220>
<221> mat_peptide
<222> (64)..(672)

<400> 5

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atg gct gaa cta cga agg atc att ctt ctg cta tgt act att gcc ttt   48
Met Ala Glu Leu Arg Arg Ile Ile Leu Leu Leu Cys Thr Ile Ala Phe
    -20                 -15                 -10

cat gtt tcc cat gga caa ata aga tgg acg ctg ctg aat cag atc acc   96
His Val Ser His Gly Gln Ile Arg Trp Thr Leu Leu Asn Gln Ile Thr
 -5              -1   1               5                  10

ggt gaa tct gac gtc att ccg ctg tct aac aac acg ccc ctg aat gtg   144
Gly Glu Ser Asp Val Ile Pro Leu Ser Asn Asn Thr Pro Leu Asn Val
            15                  20                  25

tcg ctg aat ttt aag ctg atg aat atc gta gag gcg gac aca gaa aaa   192
Ser Leu Asn Phe Lys Leu Met Asn Ile Val Glu Ala Asp Thr Glu Lys
        30                  35                  40

gat caa gtg gag gtc gtg ctg tgg aca cag gct agc tgg aaa gtg ccg   240
Asp Gln Val Glu Val Val Leu Trp Thr Gln Ala Ser Trp Lys Val Pro
    45                  50                  55

tat tac agc tca ctg ctg tcc tct agc agt tta gac cag gtg agc tta   288
Tyr Tyr Ser Ser Leu Leu Ser Ser Ser Ser Leu Asp Gln Val Ser Leu
60                  65                  70                  75

cca gtc agc aaa atg tgg acc cca gac ctt tct ttc tac aac gcc atc   336
Pro Val Ser Lys Met Trp Thr Pro Asp Leu Ser Phe Tyr Asn Ala Ile
                80                  85                  90

gct gca ccc gag ttg ctc tcc gca gac cgc gtg gtg gtc tct aag gac   384
Ala Ala Pro Glu Leu Leu Ser Ala Asp Arg Val Val Val Ser Lys Asp
            95                  100                 105
```

```
ggg agc gtc att tac gtc ccc agc cag agg gtc cgt ttc acc tgc gac   432
Gly Ser Val Ile Tyr Val Pro Ser Gln Arg Val Arg Phe Thr Cys Asp
        110                 115                 120

ctt att aat gtc gac acg gag ccg gga gcc acc tgt cgc atc aaa gtc   480
Leu Ile Asn Val Asp Thr Glu Pro Gly Ala Thr Cys Arg Ile Lys Val
    125                 130                 135

gga tcc tgg acc cac gac aac aaa cag ttc gcc ctg atc acc ggg gag   528
Gly Ser Trp Thr His Asp Asn Lys Gln Phe Ala Leu Ile Thr Gly Glu
140                 145                 150                 155

gag ggg gtg gtg aat att gca gag tac ttc gac agc cca aag ttt gac   576
Glu Gly Val Val Asn Ile Ala Glu Tyr Phe Asp Ser Pro Lys Phe Asp
                160                 165                 170

ctt ttg agt gcc aca cag agt ctg aat cgc aag aag tac agc tgt tgc   624
Leu Leu Ser Ala Thr Gln Ser Leu Asn Arg Lys Lys Tyr Ser Cys Cys
            175                 180                 185

gag aat atg tat gat gac att gaa att acc ttt gca ttc aga aag aag   672
Glu Asn Met Tyr Asp Asp Ile Glu Ile Thr Phe Ala Phe Arg Lys Lys
        190                 195                 200

taa                                                              675
```

<210> 6
<211> 224
<212> PRT
<213> Bulinus truncatus

<400> 6

```
Met Ala Glu Leu Arg Arg Ile Ile Leu Leu Leu Cys Thr Ile Ala Phe
    -20                 -15                 -10

His Val Ser His Gly Gln Ile Arg Trp Thr Leu Leu Asn Gln Ile Thr
 -5              -1   1                   5                  10

Gly Glu Ser Asp Val Ile Pro Leu Ser Asn Asn Thr Pro Leu Asn Val
```

15 20 25

Ser Leu Asn Phe Lys Leu Met Asn Ile Val Glu Ala Asp Thr Glu Lys
30 35 40

Asp Gln Val Glu Val Val Leu Trp Thr Gln Ala Ser Trp Lys Val Pro
45 50 55

Tyr Tyr Ser Ser Leu Leu Ser Ser Ser Ser Leu Asp Gln Val Ser Leu
60 65 70 75

Pro Val Ser Lys Met Trp Thr Pro Asp Leu Ser Phe Tyr Asn Ala Ile
80 85 90

Ala Ala Pro Glu Leu Leu Ser Ala Asp Arg Val Val Val Ser Lys Asp
95 100 105

Gly Ser Val Ile Tyr Val Pro Ser Gln Arg Val Arg Phe Thr Cys Asp
110 115 120

Leu Ile Asn Val Asp Thr Glu Pro Gly Ala Thr Cys Arg Ile Lys Val
125 130 135

Gly Ser Trp Thr His Asp Asn Lys Gln Phe Ala Leu Ile Thr Gly Glu
140 145 150 155

Glu Gly Val Val Asn Ile Ala Glu Tyr Phe Asp Ser Pro Lys Phe Asp
160 165 170

Leu Leu Ser Ala Thr Gln Ser Leu Asn Arg Lys Lys Tyr Ser Cys Cys
175 180 185

Glu Asn Met Tyr Asp Asp Ile Glu Ile Thr Phe Ala Phe Arg Lys Lys
190 195 200

<210> 7
<211> 675
<212> DNA

<213> Bulinus truncatus

<220>
<221> CDS
<222> (1)..(672)

<220>
<221> mat_peptide
<222> (64)..(672)

<400> 7

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atg gct gaa cta cga ggg atc att ctt ctg cta tgt act att gcc ttt   48
Met Ala Glu Leu Arg Gly Ile Ile Leu Leu Leu Cys Thr Ile Ala Phe
    -20                 -15                 -10

cat gtt tcc cat gga caa ata aga tgg acg ctg ctg aat cag atc acc   96
His Val Ser His Gly Gln Ile Arg Trp Thr Leu Leu Asn Gln Ile Thr
 -5              -1   1               5                  10

ggt gaa tct gac gtc att ccg ctg tct aac aac acg cca ctg aat gtg   144
Gly Glu Ser Asp Val Ile Pro Leu Ser Asn Asn Thr Pro Leu Asn Val
             15                  20                  25

tcg ctg aat ttt aag ctg atg aat atc tta gag gcg gac aca gag aaa   192
Ser Leu Asn Phe Lys Leu Met Asn Ile Leu Glu Ala Asp Thr Glu Lys
         30                  35                  40

gat caa gtg gag gtc gtg ctg tgg aca cag gct agc tgg aaa gtg ccg   240
Asp Gln Val Glu Val Val Leu Trp Thr Gln Ala Ser Trp Lys Val Pro
     45                  50                  55

tat tac agc tca ctg ctg tcc tct agc agt tta gac cag gtg agc tta   288
Tyr Tyr Ser Ser Leu Leu Ser Ser Ser Ser Leu Asp Gln Val Ser Leu
 60                  65                  70                  75

cca gcc agc aaa atg tgg acc cca gac ctt tct ttc tat aac gcc atc   336
Pro Ala Ser Lys Met Trp Thr Pro Asp Leu Ser Phe Tyr Asn Ala Ile
                80                  85                  90

gct gca ccc gag ttg ctc tcc aca gac cgc gtg gtg gtc tct aag gac   384
```

```
Ala Ala Pro Glu Leu Leu Ser Thr Asp Arg Val Val Val Ser Lys Asp
             95                  100                 105

ggg agc gtc att tac gtg ccc agc cag agg gtc cgt ttc acc tgc gac   432
Gly Ser Val Ile Tyr Val Pro Ser Gln Arg Val Arg Phe Thr Cys Asp
        110                 115                 120

ctt att aat gtg gac acg gag ccg gga gcc acc tgt cgc atc aaa gtc   480
Leu Ile Asn Val Asp Thr Glu Pro Gly Ala Thr Cys Arg Ile Lys Val
    125                 130                 135

gga tcc tgg acc ttc gac aac aaa cag ctc gcc ctg atc acc ggg gag   528
Gly Ser Trp Thr Phe Asp Asn Lys Gln Leu Ala Leu Ile Thr Gly Glu
140                 145                 150                 155

gag ggg gtg gtg aat att gca gag tac ttc gac agc cca aag tac gac   576
Glu Gly Val Val Asn Ile Ala Glu Tyr Phe Asp Ser Pro Lys Tyr Asp
                160                 165                 170

ctt ttg agt gcc aca cag agt ctg aat cgc aag aag tac aga tgt tgc   624
Leu Leu Ser Ala Thr Gln Ser Leu Asn Arg Lys Lys Tyr Arg Cys Cys
            175                 180                 185

gag aat atg tat gaa gac att gaa att acc ttt gca ttc aga aag aag   672
Glu Asn Met Tyr Glu Asp Ile Glu Ile Thr Phe Ala Phe Arg Lys Lys
        190                 195                 200

taa                                                              675
```

<210> 8
<211> 224
<212> PRT
<213> Bulinus truncatus

<400> 8

```
Met Ala Glu Leu Arg Gly Ile Ile Leu Leu Leu Cys Thr Ile Ala Phe
    -20                 -15                 -10

His Val Ser His Gly Gln Ile Arg Trp Thr Leu Leu Asn Gln Ile Thr
```

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-5 -1 1 5 10

Gly Glu Ser Asp Val Ile Pro Leu Ser Asn Asn Thr Pro Leu Asn Val
15 20 25

Ser Leu Asn Phe Lys Leu Met Asn Ile Leu Glu Ala Asp Thr Glu Lys
30 35 40

Asp Gln Val Glu Val Val Leu Trp Thr Gln Ala Ser Trp Lys Val Pro
45 50 55

Tyr Tyr Ser Ser Leu Leu Ser Ser Ser Ser Leu Asp Gln Val Ser Leu
60 65 70 75

Pro Ala Ser Lys Met Trp Thr Pro Asp Leu Ser Phe Tyr Asn Ala Ile
80 85 90

Ala Ala Pro Glu Leu Leu Ser Thr Asp Arg Val Val Val Ser Lys Asp
95 100 105

Gly Ser Val Ile Tyr Val Pro Ser Gln Arg Val Arg Phe Thr Cys Asp
110 115 120

Leu Ile Asn Val Asp Thr Glu Pro Gly Ala Thr Cys Arg Ile Lys Val
125 130 135

Gly Ser Trp Thr Phe Asp Asn Lys Gln Leu Ala Leu Ile Thr Gly Glu
140 145 150 155

Glu Gly Val Val Asn Ile Ala Glu Tyr Phe Asp Ser Pro Lys Tyr Asp
160 165 170

Leu Leu Ser Ala Thr Gln Ser Leu Asn Arg Lys Lys Tyr Arg Cys Cys
175 180 185

Glu Asn Met Tyr Glu Asp Ile Glu Ile Thr Phe Ala Phe Arg Lys Lys
190 195 200

<210> 9
<211> 502
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (1)..(235)

<400> 9

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Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
 1               5                  10                  15

Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
            20                  25                  30

Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
        35                  40                  45

Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
    50                  55                  60

Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
65                  70                  75                  80

Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
                85                  90                  95

Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
            100                 105                 110

Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
        115                 120                 125

Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
    130                 135                 140

Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
145                 150                 155                 160
```

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Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
165 170 175

Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
180 185 190

Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
195 200 205

Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val
210 215 220

Thr Met Arg Arg Arg Thr Leu Tyr Tyr Gly Leu Asn Leu Leu Ile Pro
225 230 235 240

Cys Val Leu Ile Ser Ala Leu Ala Leu Leu Val Phe Leu Leu Pro Ala
245 250 255

Asp Ser Gly Glu Lys Ile Ser Leu Gly Ile Thr Val Leu Leu Ser Leu
260 265 270

Thr Val Phe Met Leu Leu Val Ala Glu Ile Met Pro Ala Thr Ser Asp
275 280 285

Ser Val Pro Leu Ile Ala Gln Tyr Phe Ala Ser Thr Met Ile Ile Val
290 295 300

Gly Leu Ser Val Val Val Thr Val Ile Val Leu Gln Tyr His His His
305 310 315 320

Asp Pro Asp Gly Gly Lys Met Pro Lys Trp Thr Arg Val Ile Leu Leu
325 330 335

Asn Trp Cys Ala Trp Phe Leu Arg Met Lys Arg Pro Gly Glu Asp Lys
340 345 350

Val Arg Pro Ala Cys Gln His Lys Gln Arg Arg Cys Ser Leu Ala Ser
355 360 365

Val Glu Met Ser Ala Val Ala Pro Pro Pro Ala Ser Asn Gly Asn Leu

```
    370                 375                 380

Leu Tyr Ile Gly Phe Arg Gly Leu Asp Gly Val His Cys Val Pro Thr
385                 390                 395                 400

Pro Asp Ser Gly Val Val Cys Gly Arg Met Ala Cys Ser Pro Thr His
                405                 410                 415

Asp Glu His Leu Leu His Gly Gly Gln Pro Pro Glu Gly Asp Pro Asp
            420                 425                 430

Leu Ala Lys Ile Leu Glu Glu Val Arg Tyr Ile Ala Asn Arg Phe Arg
        435                 440                 445

Cys Gln Asp Glu Ser Glu Ala Val Cys Ser Glu Trp Lys Phe Ala Ala
    450                 455                 460

Cys Val Val Asp Arg Leu Cys Leu Met Ala Phe Ser Val Phe Thr Ile
465                 470                 475                 480

Ile Cys Thr Ile Gly Ile Leu Met Ser Ala Pro Asn Phe Val Glu Ala
                485                 490                 495

Val Ser Lys Asp Phe Ala
            500
```

<210> 10
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: N-terminus of mature LAChBP1

<400> 10

```
Leu Asp Arg Ala Asp Ile Leu Tyr Asn Ile
 1               5                  10
```

<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotides encoding N-terminal peptide of
LAChBP1

<220>
<221> modified_base
<222> (13)
<223> i

<400> 11
cggatccgay mgagcngaya thytntayaa ya 32

<210> 12
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer1 useful
for cloning cDNA encoding LAChBP (optionally with
Primer2)

<220>
<221> modified_base
<222> (14)
<223> i

<220>
<221> modified_base
<222> (20)
<223> i

<400> 12
gcgaattcga yacagarwsa ggngcnacnt g 31

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer2
useful for cloning cDNA encoding LAChBP
(optionally with Primer1)

<220>
<221> modified_base
<222> (20)
<223> i

<400> 13
gcgaagcttc rtcytcrtaa gcytcngcrc arc 33

<210> 14
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His-tag

<400> 14
Ser Arg Gly His His His His His His
1 5

<210> 15
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His-tag

<400> 15
Glu Phe Lys Asp Asp Asp Asp Lys His His His His His His
1 5 10

<210> 16
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Additonal amino acids at the N-terminus of mature LAChBP due to alpha-mating factor cleavage site

<400> 16
Glu Ala Glu Ala
1

<210> 17
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer useful for generating LAChBP/alpha7 nAChR chimera

<400> 17
gcgctcgaga aaagagaggc tgaagctttg gaccgggcag acatctt 47

<210> 18
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer useful
for generating LAChBP/alpha7 nACHR chimera

<400> 18
cgcgaattca agaatttcgg agcgtccctt 30

<210> 19
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer useful
for generating LAChBP/alpha7 nACHR chimera

<400> 19
gtggaaacca gacattctcc tctacaacgc catctcgaaa cc 42

<210> 20
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer useful
for generating LAChBP/alpha7 nACHR chimera

<400> 20
gaggagaatg tctggtttcc acaaagagct tattggcac 39